

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
24 October 2002 (24.10.2002)

PCT

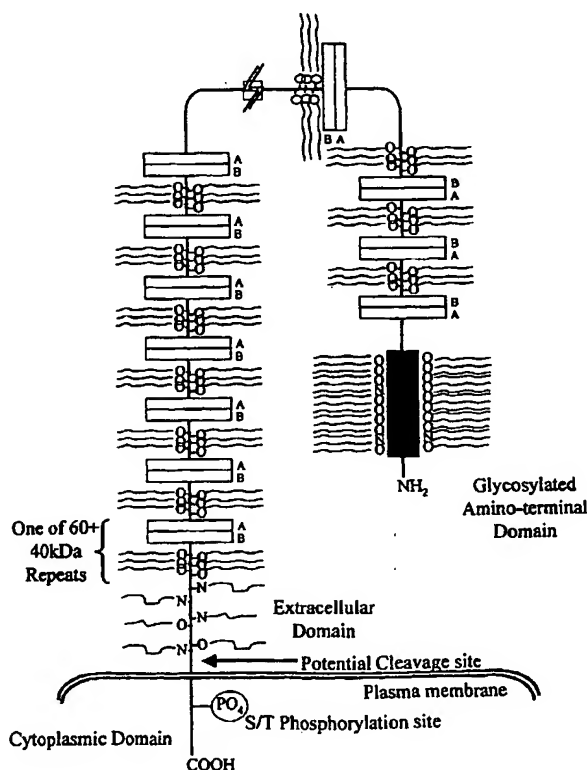
(10) International Publication Number
WO 02/083866 A2

- (51) International Patent Classification⁷: **C12N**
- (21) International Application Number: **PCT/US02/11734**
- (22) International Filing Date: **12 April 2002 (12.04.2002)**
- (25) Filing Language: **English**
- (26) Publication Language: **English**
- (30) Priority Data:
- | | | |
|------------|--------------------------------|----|
| 60/284,175 | 17 April 2001 (17.04.2001) | US |
| 60/299,380 | 19 June 2001 (19.06.2001) | US |
| 09/965,738 | 27 September 2001 (27.09.2001) | US |
| 60/345,180 | 21 December 2001 (21.12.2001) | US |
- (63) Related by continuation (CON) or continuation-in-part (CIP) to earlier application:
- | | |
|----------|--------------------------------|
| US | 09/965,738 (CIP) |
| Filed on | 27 September 2001 (27.09.2001) |
- (71) Applicant (for all designated States except US): **THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS [US/US]; 2404 North University Avenue, Little Rock, AR 72207-3608 (US).**
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **O'BRIEN, Timothy [US/US]; 2610 North Pierce, Little Rock, AR 72207 (US). BEARD, John [US/US]; 500 Green Mountain Circle, #8, Little Rock, AR 72211 (US). UNDERWOOD, Lowell [US/US]; 121 N. Jackson Street, Apt. K, Little Rock, AR 72205 (US).**
- (74) Agent: **FENTRESS, Susan, B.; Butler Snow O'Mara Stevens & Cannada, PLLC, 6075 Poplar Avenue, Suite 500, P.O. Box 171443, Memphis, TN 38119 (US).**
- (81) Designated States (national): **AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,**

[Continued on next page]

(54) Title: REPEAT SEQUENCES OF THE CA125 GENE AND THEIR USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

Proposed Structure of CA125



(57) Abstract: The CA125 gene has been cloned and multiple repeat sequences including the carboxy terminus have been identified. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. An amino terminal extension is present. The structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified. The repeat units encompass the site of OC125 and M11 binding. Expression of the repeats was demonstrated. Any one of the repeat domains has the potential for use as a new gold standard for detecting and monitoring the presence of the CA125 antigen. The repeat domains and other domains also provide a basis for the development of a vaccine.

WO 02/083866 A2



GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

REPEAT SEQUENCES OF THE CA125 GENE AND THEIR USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application Serial No. 60/284,175 filed April 17, 2001, U.S. Provisional Application Serial No. 60/299,380 filed June 19, 2001, U.S. Non-Provisional Application Serial No. 09/965,738 filed September 27, 2001, and U.S. Provisional Application Serial No. 60/345,180 filed December 21, 2001, which are incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

The present invention relates generally to the cloning, identification, and expression of the CA125 gene's glycosylated amino terminal domain, the multiple repeat domain, and the carboxy terminal domain *in vitro* and, more specifically, to the use of recombinant CA125 with epitope binding sites for diagnostic and therapeutic purposes.

CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. Elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease.

It is well established that CA125 is not uniquely expressed in ovarian carcinoma, but is also found in both normal secretory tissues and other carcinomas (i.e., pancreas, liver, colon) [Hardardottir H *et al.*, Distribution of CA125 in embryonic tissue and adult derivatives of the fetal periderm, *Am J Obstet. Gynecol.* 163;6(1):1925-1931 (1990); Zurawski VR *et al.*, Tissue distribution and characteristics of the CA125 antigen, *Cancer Rev.* 11-12:102-108 (1988); and O'Brien TJ *et al.*, CA125 antigen in human amniotic fluid and fetal membranes, *Am J Obstet Gynecol.* 155:50-55, (1986); Nap M *et al.*, Immunohistochemical characterization of 22 monoclonal antibodies against the CA125 antigen: 2nd report from the ISOBM TD-1 workshop, *Tumor Biology* 17:325-332 (1996)].

Notwithstanding, CA125 correlates directly with the disease status of affected patients (i.e., progression, regression, and no change), and has become the "gold standard" for monitoring patients with ovarian carcinoma [Bast RC *et al.*, A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N Engl J Med.* 309:883-887 (1983); and Bon GC *et al.*, Serum tumor marker immunoassays in gynecologic oncology: Establishment of reference values, *Am J Obstet. Gynecol.* 174:107-114 (1996)]. CA125 is especially useful in post-menopausal patients where endometrial tissue has become atrophic and, as a result, is not a major source of normal circulating CA125.

During the mid 1980's, the inventor of the present invention and others developed M11, a monoclonal antibody to CA125. M11 binds to a dominant epitope on the repeat structure of the CA125 molecule [O'Brien TJ *et al.*, New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol* 165:1857-64 (1991)]. More recently, the inventor and others developed a purification and stabilization scheme for CA125, which allows for the accumulation of highly purified high molecular weight CA125 [O'Brien TJ *et al.*, More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4):188-195 (1998)].

Considerable progress has been made over the years to further characterize the CA125 molecule, its structure and its function. The CA125 molecule is a high molecular weight glycoprotein with a predominance of O-linked sugar side chains. The native molecule exists as a very large complex (~2-5 million daltons). The complex appears to be composed of an epitope containing CA125 molecule and binding proteins which carry no CA125 epitopes. The CA125 molecule is heterogenous in both size and charge, most likely due to continuous deglycosylation of the side chains during its life-span in bodily fluids. The core CA125 subunit is in excess of 200,000 daltons, and retains the capacity to bind both OC125 and M11 class antibodies. While the glycoprotein has been described biochemically and metabolically by the inventor of the present invention and others, no one has yet cloned the CA125 gene, which would provide the basis for understanding its structure and its physiologic role in both normal and malignant tissues.

Despite the advances in detection and quantitation of serum tumor markers like CA125, the majority of ovarian cancer patients are still diagnosed at an advanced stage of the disease--Stage III or IV. Further, the management of patients' responses to treatment and the detection of disease recurrence remain major problems. There, thus, remains a need to significantly improve and standardize current CA125 assay systems. Further, the development of an early indicator of risk of ovarian cancer will provide a useful tool for early diagnosis and improved prognosis.

SUMMARY OF THE INVENTION

The CA125 gene has been cloned and multiple repeat sequences as well as the glycosylated amino terminal and the carboxy terminus have been identified. CA125 requires a transcript of more than 35,000 bases and occupies approximately 150,000 bp on chromosome 19q 13.2. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. Analysis of the amino terminal extension revealed that its amino acid composition is consistent with the amino acid composition of the amino terminal domain.

The extracellular repeat domain, which characterizes the CA125 molecule, also represents a major portion of the CA125 molecular structure. It is downstream from the amino terminal domain and presents itself in a much different manner to its extracellular matrix neighbors. These repeats are characterized by many features including a highly-conserved nature and a uniformity in exon structure. But most consistently, a cysteine enclosed sequence may form a cysteine loop. Domain 2 comprises 156 amino acid repeat units of the CA125 molecule. The repeat domain constitutes the largest proportion of the

CA125 molecule. The repeat units also include the epitopes now well-described and classified for both the major class of CA125 antibodies of the OC125 group and the M11 group. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. The repeat sequences demonstrated 70-85% homology to each other. The existence of the repeat sequences was confirmed by expression of the recombinant protein in *E. coli* where both OC125/M11 class antibodies were found to bind to sites on the CA125 repeat.

The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. The carboxy terminal also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain, which allows for proteolytic cleavage and release of the CA125 molecule.

The identification and sequencing of multiple repeat domains of the CA125 antigen provides potentially new clinical and therapeutic applications for detecting, monitoring and treating patients with ovarian cancer and other carcinomas where CA125 is expressed. For example, the ability to express repeat domains of CA125 with the appropriate epitopes would provide a much needed standard reagent for research and clinical applications. Current assays for CA125 utilize as standards either CA125 produced from cultured cell lines or from patient ascites fluid. Neither source is defined with regard to the quality or purity of the CA125 molecule. The present invention overcomes the disadvantages of current assays by providing multiple repeat domains of CA125 with epitope binding sites. At least one or more of any of the more than 60 repeats shown in Table 16 can be used as a "gold standard" for testing the presence of CA125. Furthermore, new and more specific assays may be developed utilizing recombinant products for antibody production.

Perhaps even more significantly, the multiple repeat domains of CA125 or other domains could also be used for the development of a potential vaccine for patients with ovarian cancer. In order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains

which encompass epitope binding sites for known murine antibodies, it will be feasible to more directly stimulate patients' immune systems to CA125 and, as a result, extend the life of ovarian carcinoma patients.

The recombinant CA125 of the present invention may also be used to develop therapeutic targets. Molecules like CA125, which are expressed on the surface of tumor cells, provide potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. Humanized or human antibodies to CA125 epitopes could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. Natural ligands having a natural binding affinity for domains on the CA125 molecule could also be utilized to deliver therapeutic agents to tumor cells.

CA125 expression may further provide a survival or metastatic advantage to ovarian tumor cells. Antisense oligonucleotides derived from the CA125 repeat sequences could be used to down-regulate the expression of CA125. Further, antisense therapy could be used in association with a tumor cell delivery system of the type described above.

Recombinant domains of the CA125 molecule also have the potential to identify small molecules, which bind to individual domains of the CA125 molecule. These small molecules could also be used as delivery agents or as biological modifiers.

In one aspect of the present invention, a CA125 molecule is disclosed comprising: (a) an extracellular amino terminal domain, comprising 5 genomic exons, wherein exon 1 comprises amino acids #1-33 of SEQ ID NO: 299, exon 2 comprises amino acids #34-1593 of SEQ ID NO: 299, exon 3 comprises amino acids #1594-1605 of SEQ ID NO: 299, exon 4 comprises amino acids #1606-1617 of SEQ ID NO: 299, and exon 5 comprises amino acids #1618-1637 of SEQ ID NO: 299; (b) an amino terminal extension, comprising 4 genomic exons, wherein exon 1 comprises amino acids #1-3157 of SEQ ID NO: 310, exon 2 comprises amino acids #3158-3193 of SEQ ID NO: 310, exon 3 comprises amino acids #3194-9277 of SEQ ID NO: 310, and exon 4 comprises amino acids #9278-10,427 of SEQ ID NO: 310; (c) a multiple repeat domain, wherein each repeat unit comprises 5 genomic exons, wherein exon 1 comprises amino acids #1-42 in any of SEQ ID NOS: 164 through 194; exon 2 comprises amino acids #43-65 in any of SEQ ID NOS: 195 through 221; exon 3 comprises amino acids #66-123 in any of SEQ ID NOS: 222

through 249; exon 4 comprises amino acids #124-135 in any of SEQ ID NOS: 250 through 277; and exon 5 comprises amino acids #136-156 in any of SEQ ID NOS: 278 through 298; and (d) a carboxy terminal domain comprising a transmembrane anchor with a short cytoplasmic domain, and further comprising 9 genomic exons, wherein exon 1 comprises amino acids #1-11 of SEQ ID NO: 300; exon 2 comprises amino acids #12-33 of SEQ ID NO: 300; exon 3 comprises amino acids #34-82 of SEQ ID NO: 300; exon 4 comprises amino acids #83-133 of SEQ ID NO: 300; exon 5 comprises amino acids #134-156 of SEQ ID NO: 300; exon 6 comprises amino acids #157-212 of SEQ ID NO: 300; exon 7 comprises amino acids #213-225 of SEQ ID NO: 300; exon 8 comprises amino acids #226-253 of SEQ ID NO: 300; and exon 9 comprises amino acids #254-284 of SEQ ID NO: 300.

In another aspect of the present invention, the N-glycosylation sites of the amino terminal domain marked (x) in Figure 8B are encoded at positions #81, #271, #320, #624, #795, #834, #938, and #1,165 in SEQ ID NO: 299.

In another aspect of the present invention, the serine and threonine O-glycosylation pattern for the amino terminal domain is marked (o) in SEQ ID NO: 299 in Figure 8B.

In another aspect of the present invention, the N-glycosylation sites of the amino terminal extension marked (x) in Table 26 are encoded at positions #139, #434, #787, #930, #957, #1266, #1375, #1633, #1840, #1877, #1890, #2345, #2375, #2737, #3085, #3178, #3501, #4221, #4499, #4607, #4614, #4625, #5048, #5133, #5322, #5396, #5422, #5691, #5865, #6090, #6734, #6861, #6963, #8031, #8057, #8326, #8620, #8686, #8915, #9204, #9495, #9787, #10,077, and #10,175.

In another aspect, the serine and threonine O-glycosylation pattern for the amino terminal extension is marked (o) in Table 26.

In another aspect of the present invention, exon 2 in the repeat domain comprises at least 31 different copies; exon 2 comprises at least 27 different copies; exon 3 comprises at least 28 different copies; exon 4 comprises at least 28 different copies, and exon 5 comprises at least 21 different copies.

In another aspect of the present invention, the repeat domain comprises 156 amino acid repeat units which comprise epitope binding sites. The epitope binding sites are located in the C-enclosure at amino acids #59-79 (marked C-C) in SEQ ID NO: 150 in Figure 5.

In another aspect, the 156 amino acid repeat unit comprises O-glycosylation sites at positions #128, #129, #132, #133, #134, #135, #139, #145, #146, #148, #150, #151, and #156 in SEQ ID NO: 150 in Figure 5C. The 156 amino acid repeat unit further comprises N-glycosylation sites at positions #33 and #49 in SEQ ID NO: 150 in Figure 5C. The repeat unit also includes at least one conserved methionine (designated M) at position #24 in SEQ ID NO: 150 in Figure 5C.

In yet another aspect, the transmembrane domain of the carboxy terminal domain is located at positions #230-252 (underlined) in SEQ ID NO: 300 of Figure 9B. The cytoplasmic domain of the carboxy terminal domain comprises a highly basic sequence adjacent to the transmembrane at positions #256-260 in SEQ ID NO: 300 of Figure 9B, serine and threonine phosphorylation sites at positions #254, #255, and #276 in SEQ ID NO: 300 in Figure 9B, and tyrosine phosphorylation sites at positions #264, #273, and #274 in SEQ ID NO: 300 of Figure 9B.

In another aspect of the present invention, an isolated nucleic acid of the CA125 gene is disclosed, which comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152; (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

In another aspect of the present invention, an isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NOS: 11-47, 50-80, 82, 146, 148, 149, 151, and 153-158; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

In yet another aspect, a vector comprising the nucleic acid of the CA125 gene is disclosed. The vector may be a cloning vector, a shuttle vector, or an expression vector. A cultured cell comprising the vector is also disclosed.

In yet another aspect, a method of expressing CA125 antigen in a cell is disclosed, comprising the steps of: (a) providing at least one nucleic acid comprising a nucleotide sequence selected from the group consisting of: (i) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152; (ii) a nucleotide sequence having at least 70% sequence

identity to any one of the sequences in (i); (iii) a degenerate variant of any one of (i) to (ii); and (iv) a fragment of any one of (i) to (iii); (b) providing cells comprising an mRNA encoding the CA125 antigen; and (c) introducing the nucleic acid into the cells, wherein the CA125 antigen is expressed in the cells.

In yet another aspect, a purified polypeptide of the CA125 gene, comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, and 153-158; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

In another aspect, a purified antibody that selectively binds to an epitope in the receptor-binding domain of CA125 protein, wherein the epitope is within the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 146, 151, and 153-158; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

A diagnostic for detecting and monitoring the presence of CA125 antigen is also disclosed, which comprises recombinant CA125 comprising at least one repeat unit of the CA125 repeat domain including epitope binding sites selected from the group consisting of amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 150, 151, 153-161, and 162 (amino acids #1,643-11,438).

A therapeutic vaccine to treat mammals with elevated CA125 antigen levels or at risk of developing a disease or disease recurrence associated with elevated CA125 antigen levels is also disclosed. The vaccine comprises recombinant CA125 repeat domains including epitope binding sites, wherein the repeat domains are selected from the group of amino acid sequences consisting of SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, 153-161, and 162 (amino acids #1,643-11,438), and amino acids #175-284 of SEQ ID NO: 300. Mammals include animals and humans.

In another aspect of the present invention, an antisense oligonucleotide is disclosed that inhibits the expression of CA 125 encoded by: (a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152; (b) a nucleotide sequence having at least 70%

sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

The preceeding and further aspects of the present invention will be apparent to those of ordinary skill in the art from the following description of the presently preferred embodiments of the invention, such description being merely illustrative of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates the cyanogen bromide digested products of CA125 on Western blot probed with M11 and OC125 antibodies. Table 1 shows the amino acid sequence derived from the amino terminal end of the 40 kDa cyanogen bromide peptide along with internal sequences obtained after protease digestion of the 40 kDa fragment (SEQ ID NOS: 1-4). SEQ ID NO: 1 is the amino terminal sequence derived of the 40 kDa peptide and SEQ ID NOS: 2, 3, and 4 reflect internal amino acid sequences derived from peptides after protease digestion of the 40 kDa fragment. Table 1 further provides a translation of the EST (BE005912) with homologous sequences (SEQ ID NOS: 5 and 6) either boxed or underlined. Protease cleavage sites are indicated by arrows.

Figure 2A illustrates PCR amplification of products generated from primers utilizing the EST sequence referred to in Figure 1, the amino acid sequence obtained from the 40 kDa fragment and EST sequence AA# 640762. Lane 1-2: normal; 3: serous ovarian carcinoma; 4: serous ovarian carcinoma; 5: mucinous ovarian carcinoma; 6: β -tubulin control. The anticipated size band 400 b is present in lane 3 and less abundantly in lane 4.

Figure 2B illustrates the RT-PCR that was performed to determine the presence or absence of CA125 transcripts in primary culture cells of ovarian tumors. This expression was compared to tubulin expression as an internal control. Lanes 1, 3, 5, 7, and 9 represent the primary ovarian tumor cell lines. Lanes 2, 4, 6, and 8 represent peripheral blood mononuclear cell lines derived from the corresponding patients in lanes 1, 3, 5, and 7. Lane 10 represents fibroblasts from the patient tumor in lane 9. Lanes 11 and 12 are CaOV3 and a primary tumor specimen, respectively.

Figure 3 illustrates repeat sequences determined by sequencing cloned cDNA from the 400 b band in Figure 2B. Placing of repeat sequences in a contiguous fashion was accomplished by PCR amplification and sequencing of overlap areas between two repeat sequences. A sample of the complete repeat sequences is shown in SEQ ID NOS: 158, 159, 160, and 161, which was obtained in this manner and placed next to each other based on overlap sequences. The complete list of repeat sequences that was obtained is shown in Table 21 (SEQ ID NO: 162).

Figure 4 illustrates three Western immunoblot patterns: Panel A = probed with M11, Panel B = probed with OC125 and Panel C = probed with antibody ISOBM 9.2. Each panel represents *E. coli* extracts as follows: lane 1 = *E. coli* extract from bacteria with the plasmid PQE-30 only. Lane 2 = *E. coli* extract from bacteria with the plasmid PQE-30 which includes the CA125 repeat unit. Lane 3 = *E. coli* extract from bacteria with the plasmid PQE-30 which includes the TADG-14 protease unrelated to CA125. Panel D shows a Coomassie blue stain of a PAGE gel of *E. coli* extract derived from either PQE-30 alone or from bacteria infected with PQE-30 - CA125 repeat (recombinant CA125 repeat).

Figure 5 represents Western blots of the CA125 repeat sequence that were generated to determine the position of the M11 epitope within the recombinant CA125 repeat. The expressed protein was bound to Ni-NTA agarose beads. The protein was left undigested or digested with Asp-N or Lys-C. The protein remaining bound to the beads was loaded into lanes 1, 2, or 3 corresponding to undigested, Asp-N digested and Lys-C digested, respectively. The supernatants from the digestions were loaded in lanes 4, 5, and 6 corresponding to undigested, Asp-N digested and Lys-C digested, respectively. The blots were probed with either anti-His tag antibody (A) or M11 antibody (B). Panel C shows a typical repeat sequence corresponding to SEQ ID NO: 150 with each exon defined by arrows. All proteolytic aspartic acid and lysine sites are marked with overhead arrow or dashes. In the lower panel, the O-glycosylation sites in exons 4 and 5 are marked with O, the N-glycosylation sites are marked with X plus the amino acid number in the repeat (#12, 33, and 49) the conserved methionine is designated with M plus the amino acid number (M#24), and the cysteine enclosure which is also present in all repeats and encompasses 19 amino acids between the cysteines is marked with C-C (amino acids #59-79). The epitopes for M11 and OC125 are located in the latter part of the C-enclosure or downstream from the C-enclosure.

Figure 6 illustrates a Northern blot analysis of RNA derived from either normal ovary (N) or ovarian carcinoma (T) probed with a P³² cDNA repeat sequence of CA125. Total RNA samples (10µg) were size separated by electrophoresis on a formaldehyde 1.2% agarose gel. After blotting to Hybond N, the lanes were probed with P³² radiolabelled 400 bp repeat (see Figure 2). Lane 1 represents RNA from normal ovarian tissue, and lane 2 represents RNA from serous ovarian tumor tissue.

Figure 7A is a schematic diagram of a typical repeat unit for CA125 showing the N-glycosylation sites at the amino end and the totally conserved methionine (M). Also shown is the proposed cysteine enclosed loop with antibody binding sites for OC125 and M11. Also noted are the highly O-glycosylated residues at the carboxy end of the repeat.

Figure 7B represents the genomic structure and exon configuration of a 156 amino acid repeat sequence of CA125 (SEQ ID NO: 163), which comprises a standard repeat unit.

Figure 7C lists the individual known sequences for each exon, which have been determined as follows: Exon 1 – SEQ ID NOS: 164-194; Exon 2 – SEQ ID NOS: 195-221; Exon 3 – SEQ ID NOS: 222-249; Exon 4 – SEQ ID NOS: 250-277; and Exon 5 – SEQ ID NOS: 278-298.

Figure 8A shows the genomic structure of the amino terminal end of the CA125 gene. It also indicates the amino composition of each exon in the extracellular domain.

Figure 8B illustrates the amino acid composition of the amino terminal domain (SEQ ID NO: 299) with each potential O-glycosylation site marked with a superscript (o) and N-glycosylation sites marked with a superscript (x). T-TALK sequences are underlined.

Figure 9A illustrates the genomic exon structure of the carboxy-terminal domain of the CA125 gene. It includes a diagram showing the extracellular portion, the potential cleavage site, the transmembrane domain and the cytoplasmic tail.

Figure 9B illustrates the amino acid composition of the carboxy terminal domain (SEQ ID NO: 300) including the exon boundaries, O-glycosylation sites (o), and N-glycosylation sites (x). The proposed transmembrane domain is underlined.

Figure 10 illustrates the proposed structure of the CA125 molecule based on the open reading frame sequence described herein. As shown, the molecule is dominated by a major repeat domain in the extracellular space along with a highly glycosylated amino terminal repeat.

The molecule is anchored by a transmembrane domain and also includes a cytoplasmic tail with potential for phosphorylation.

Figure 11 is a diagram of the CA125 gene showing the originally cloned domains of both the genomic and amino acid sequences and the extension of the glycosylated amino terminal protein sequence.

Figure 12 is a diagram of the contig alignment from overlapping chromosome 19 cosmids.

Figure 13 illustrates the genomic exon structure of the CA125 gene amino terminal extension.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, conventional molecular biology, microbiology, and recombinant DNA techniques may be used that will be apparent to those skilled in the relevant art. Such techniques are explained fully in the literature (see, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D. N. Glover ed. 1985); "Oligonucleotide Synthesis" (M. J. Gait ed. 1984); "Nucleic Acid Hybridization" (B. D. Hames & S. J. Higgins eds. (1985)); "Transcription and Translation" (B. D. Hames & S. J. Higgins eds. (1984)); "Animal Cell Culture" (R. I. Freshney, ed. (1986)); "Immobilized Cells And Enzymes" (IRL Press, (1986)); and B. Perbal, "A Practical Guide To Molecular Cloning" (1984)).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA

found, inter alia, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes.

As used herein, the term "gene" shall mean a region of DNA encoding a polypeptide chain.

"Messenger RNA" or "mRNA" shall mean an RNA molecule that encodes for one or more polypeptides.

"DNA polymerase" shall mean an enzyme which catalyzes the polymerization of deoxyribonucleotide triphosphates to make DNA chains using a DNA template.

"Reverse transcriptase" shall mean an enzyme which catalyzes the polymerization of deoxy- or ribonucleotide triphosphates to make DNA or RNA chains using an RNA or DNA template.

"Complementary DNA" or "cDNA" shall mean the DNA molecule synthesized by polymerization of deoxyribonucleotides by an enzyme with reverse transcriptase activity.

An "isolated nucleic acid" is a nucleic acid the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein.

"Oligonucleotide", as used herein in referring to the probes or primers of the present invention, is defined as a molecule comprised of two or more deoxy- or ribonucleotides, preferably more than ten. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

"DNA fragment" includes polynucleotides and/or oligonucleotides and refers to a plurality of joined nucleotide units formed from naturally-occurring bases and cyclofuranosyl groups joined by native phosphodiester bonds. This term effectively refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits. "DNA fragment" also refers to purine and pyrimidine groups and moieties which function similarly but which have non naturally-occurring portions. Thus, DNA fragments may have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. They may also contain altered base units or other modifications, provided that biological activity is retained. DNA fragments may also include species which include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the cyclofuranose portions of the nucleotide subunits may also occur as long as biological function is not eliminated by such modifications.

"Primer" shall refer to an oligonucleotide, whether occurring naturally or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, the source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 10-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the

remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

As used herein, the term "hybridization" refers generally to a technique wherein denatured RNA or DNA is combined with complementary nucleic acid sequence which is either free in solution or bound to a solid phase. As recognized by one skilled in the art, complete complementarity between the two nucleic acid sequences is not a pre-requisite for hybridization to occur. The technique is ubiquitous in molecular genetics and its use centers around the identification of particular DNA or RNA sequences within complex mixtures of nucleic acids.

As used herein, "restriction endonucleases" and "restriction enzymes" shall refer to bacterial enzymes which cut double-stranded DNA at or near a specific nucleotide sequence.

"Purified polypeptide" refers to any peptide generated from CA125 either by proteolytic cleavage or chemical cleavage.

"Degenerate variant" refers to any amino acid variation in the repeat sequence, which fulfills the homology exon structure and conserved sequences and is recognized by the M11, OC125 and ISOBM series of antibodies.

"Fragment" refers to any part of the CA125 molecule identified in a purification scheme.

"Conservative variant antibody" shall mean any antibody that fulfills the criteria of M11, OC125 or any of the ISOBM antibody series.

MATERIALS AND METHODS

A. Tissue collection, RNA Isolation and cDNA Synthesis

Both normal and ovarian tumor tissues were utilized for cDNA preparation. Tissues were routinely collected and stored at -80°C according to a tissue collection protocol.

Total RNA isolation was performed according to the manufacturer's instructions using the TriZol Reagent purchased from GibcoBRL (Catalog #15596-018). In some

instances, mRNA was isolated using oligo dT affinity chromatography. The amount of RNA recovered was quantitated by UV spectrophotometry. First strand complementary DNA (cDNA) was synthesized using 5.0 µg of RNA and random hexamer primers according to the manufacturer's protocol utilizing a first strand synthesis kit obtained from Clontech (Catalog #K1402-1). The purity of the cDNA was evaluated by PCR using primers specific for the β -tubulin gene. These primers span an intron such that the PCR products generated from pure cDNA can be distinguished from cDNA contaminated with genomic DNA.

B. Identification and Ordering of CA125 Repeat Units

It has been demonstrated that the 2-5 million dalton CA125 glycoprotein (with repeat domains) can be chemically segmented into glycopeptide fragments using cyanogen bromide. As shown in Figure 1, several of these fragments, in particular the 40 kDa and 60 kDa fragments, still bind to the two classical antibody groups defined by OC 125 and M11.

To convert CA125 into a consistent glycopeptide, the CA125 parent molecule was processed by cyanogen bromide digestion. This cleavage process resulted in two main fractions on commassie blue staining following polyacrylamide gel electrophoresis. An approximately 60 kDa band and a more dominant 40 kDa band were identified as shown in Figure 1. When a Western blot of these bands was probed with either OC125 or M11 antibodies (both of which define the CA125 molecule), these bands bound both antibodies. The 40 kDa band was significantly more prominent than the 60 kDa band. These data thus established the likelihood of these bands (most especially the 40 kDa band) as being an authentic cleavage peptide of the CA125 molecule, which retained the identifying characteristic of OC125 and M11 binding.

The 40 kDa and 60 kDa bands were excised from PVDF blots and submitted to amino terminal and internal peptide amino acid sequencing as described and practiced by Harvard Sequencing, (Harvard Microchemistry Facility and The Biological Laboratories, 16 Divinity Avenue, Cambridge, Massachusetts 02138). Sequencing was successful only for the 40 kDa band where both amino terminal sequences and some internal sequences were obtained as shown in Table 1 at SEQ ID NOS: 1-4. The 40 kDa fragment of the CA125 protein was

found to have homology to two translated EST sequences (GenBank Accession Nos. BE005912 and AA640762). Visual examination of these translated sequences revealed similar amino acid regions, indicating a possible repetitive domain. The nucleotide and amino acid sequences for EST Genbank Accession No. BE005912 (corresponding to SEQ ID NO: 5 and SEQ ID NO: 6, respectively) are illustrated in Table 1. Common sequences are boxed or underlined.

In an attempt to identify other individual members of this proposed repeat family, two oligonucleotide primers were synthesized based upon regions of homology in these EST sequences. Shown in Table 2A, the primer sequences correspond to SEQ ID NOS: 7 and 8 (sense primers) and SEQ ID NOS: 9 and 10 (antisense primers). Repeat sequences were amplified in accordance with the methods disclosed in the following references: Shigemasa K *et al.*, p21: A monitor of p53 dysfunction in ovarian neoplasia, *Int. J. Gynecol. Cancer* 7:296-303 (1997) and Shigemasa K *et al.*, p16 Overexpression: A potential early indicator of transformation in ovarian carcinoma, *J. Soc. Gynecol. Invest.* 4:95-102 (1997). Ovarian tumor cDNA obtained from a tumor cDNA bank was used.

Amplification was accomplished in a Thermal Cycler (Perkin-Elmer Cetus). The reaction mixture consisted of 1U Taq DNA Polymerase in storage buffer A (Promega), 1X Thermophilic DNA Polymerase 10X Mg free buffer (Promega), 300mM dNTPs, 2.5mM MgCl₂, and 0.25mM each of the sense and antisense primers for the target gene. A 20 µl reaction included 1 µl of cDNA synthesized from 50ng of mRNA from serous tumor mRNA as the template. PCR reactions required an initial denaturation step at 94°C/1.5 min. followed by 35 cycles of 94°C/0.5 min., 48°C/0.5 min., 72°C/0.5 min. with a final extension at 72°C/7 min. Three bands were initially identified (>400 bp, >800 bp, and >1200 bp) and isolated. After size analysis by agarose gel electrophoresis, these bands as well as any other products of interest were then ligated into a T-vector plasmid (Promega) and transformed into competent DH5α strain of *E. coli* cells. After growth on selective media, individual colonies were cultured overnight at 37°C, and plasmid DNA was extracted using the QIAprep Spin Miniprep kit (Qiagen). Positive clones were identified by restriction digests

using *Apa* I and *Sac* I. Inserts were sequenced using an ABI automatic sequencer, Model 377, T7 primers, and a Big Dye Terminator Cycle Sequencing Kit (Applied Biosystems).

Obtained sequences were analyzed using the Pileup program of the Wisconsin Genetic's Computer Group (GCG). Repeat units were ordered using primers designed against two highly conserved regions within the nucleotide sequence of these identified repeat units. Shown in Table 2B, the sense and antisense primers (5'-GTCTCTATGTCAATGGTTTCACCC-3' / 5'-TAGCTGCTCTCTGTCCAGTCC-3' SEQ ID NOS: 301 and 302, respectively) faced away from one another within any one repeat creating an overlap sequence, thus enabling amplification across the junction of any two repeat units. PCR reactions, cloning, sequencing, and analysis were performed as described above.

C. Identification and Assembly of the CA125 Amino Terminal Domain

In search of open reading frames containing sequences in addition to CA125 repeat units, database searches were performed using the BLAST program available at the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/). Using a repeat unit as the query sequence, cosmid AC008734 was identified as having multiple repeat sequences throughout the unordered (35) contiguous pieces of DNA, also known as contigs. One of these contigs, #32, was found to have exons 1 and 2 of a repeat region at its 3' end. Contig#32 was also found to contain a large open reading frame (ORF) upstream of the repeat sequence. PCR was again used to verify the existence of this ORF and confirm its connection to the repeat sequence. The specific primers recognized the 3' end of this ORF (5'-CAGCAGAGACCAGCACGAGTACTC-3')(SEQ ID NO: 51) and sequence within the repeat (5'-TCCACTGCCATGGCTGAGCT-3')(SEQ ID NO: 52). The remainder of the amino-terminal domain was assembled from this contig in a similar manner. With each PCR confirmation, a new primer (see Table 10A) was designed against the assembled sequence and used in combination with a primer designed against another upstream potential ORF (Set 1: 5'-CCAGCACAGCTCTTCCCAGGAC-3' / 5'-GGAATGGCTGAGCTGACGTCTG-3')(SEQ ID NO: 53 and SEQ ID NO: 54); Set 2: 5'-CTTCCCAGGACAACCTCAAGG-3' / 5'-GCAGGATGAGTGAGCCACGTG-3')(SEQ ID NO: 55 and SEQ ID NO: 56); Set 3: 5'-GTCAGATCTGGTGACCTCACTG-3' / 5'-GAGGCACTGGAAAGCCCAGAG-3')(SEQ ID NO: 57 and SEQ ID NO: 58). Potential

adjoining sequence (contig #7 containing EST AU133673) was also identified using contig #32 sequence as query sequence in database searches. Confirmation primers were designed and used in a typical manner (5'-CTGATGGCATTATGGAACACATCAC-3' / 5'-CCCAGAACGAGAGACCAGTGAG-3')(SEQ ID NO: 59 and SEQ ID NO: 60).

In order to identify the 5' end of the CA125 sequence, 5' Rapid Amplification of cDNA Ends (FirstChoiceTM RLM-RACE Kit, Ambion) was performed using tumor cDNA. The primary PCR reaction used a sense primer supplied by Ambion (5'-GCTGATGGCGATGAATGAACACTG-3') (SEQ ID NO: 61) and an anti-sense primer specific to confirmed contig #32 sequence (5'-CCCAGAACGAGAGACCAGTGAG-3')(SEQ ID NO: 62). The secondary PCR was then performed using nested primers, sense from Ambion (5'-CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG-3') (SEQ ID NO: 63) and the anti-sense was specific to confirmed contig #7 sequence (5'-CCTCTGTGTGCTGCTTCATTGGG-3')(SEQ ID NO: 64). The RACE PCR product (a band of approximately 300 bp) was cloned and sequenced as previously described.

D. Identification and Assembly of the CA125 Carboxy Terminal Domain

Database searches using confirmed repeat units as query also identified a cDNA sequence (GenBank AK024365) containing other repeat units, but also a potential carboxy terminal sequence. The contiguous nature of this sequence with assembled CA125 was confirmed using PCR (5'-GGACAAGGTCACCACACTCTAC-3' / 5'-GCAGATCCTCCAGGTCTAGGTGTG-3'), (SEQ ID NO: 303 and SEQ ID NO: 304, respectively) as well as contig and EST analysis.

E. Expression of 6xHis-tagged CA125 repeat in *E. coli*

The open reading frame of a CA125 repeat shown in Table 11 was amplified by PCR with the sense primer (5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3') (SEQ ID NO: 65) the antisense primer (5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC-3') (SEQ ID NO: 66) PCR was performed in a reaction mixture consisting of ovarian tumor cDNA derived from 50 ng of mRNA, 5 pmol each of sense and antisense primers for the CA125 repeat, 0.2 mmol of dNTPs, and 0.625 U of Taq polymerase in 1x buffer in a final volume of 25 ml. This mixture was subjected to 1 minute of denaturation at 95°C followed by 30 cycles of PCR consisting of the following: denaturation for 30 seconds at 95°C, 30 seconds of annealing at 62°C, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation. The PCR

product was purified and digested with the restriction enzymes *Bam* *HI* and *Hind* *III*. This digested PCR product was then ligated into the expression vector pQE-30, which had also been digested with *Bam* *HI* and *Hind* *III*. This clone would allow for expression of recombinant 6xHis-tagged CA125 repeat. Transformed *E. coli* (JM109) were grown to an OD600 of 1.5-2.0 at 37°C and then induced with IPTG (0.1 mM) for 4-6 hours at 25°C to produce recombinant protein. Whole *E. coli* lysate was electrophoresed through a 12% SDS polyacrylamide gel and Coomassie stained to detect highly expressed proteins.

F. Western Blot Analysis

Proteins were separated on a 12% SDS-PAGE gel and electroblotted at 100V for 40 minutes at 4°C to nitrocellulose membrane. Blots were blocked overnight in phosphate-buffered saline (PBS) pH 7.3 containing 5% non-fat milk. CA125 antibodies M11, OC125, or ISOBM 9.2 were incubated with the membrane at a dilution of 5µg/ml in 5% milk/PBS-T (PBS plus 0.1% TX-100) and incubated for 2 hours at room temperature. The blot was washed for 30 minutes with several changes of PBS and incubated with a 1:10,000 dilution of horseradish peroxidase (HRP) conjugated goat anti-mouse IgG antibody (Bio-Rad) for 1 hour at room temperature. Blots were washed for 30 minutes with several changes of PBS and incubated with a chemiluminescent substrate (ECL from Amersham Pharmacia Biotech) before a 10-second exposure to X-ray film for visualization.

Figure 4 illustrates three Western immunoblot patterns of the recombinant CA125 repeat purified from *E. coli* lysate (lane 2) compared to *E. coli* lysate with no recombinant protein (lane 1-negative control) and a recombinant protein TADG-14 which is unrelated to CA125 (lane 3). As shown, the M11 antibody, the OC125 antibody and the antibody ISOBM 9.2 (an OC125-like antibody) all recognized the CA125 recombinant repeat (lane 2), but did *not* recognize either the *E. coli* lysate (lane 1) or the unrelated TADG-14 recombinant (lane 3). These data confirm that the recombinant repeat encodes both independent epitopes for CA125, the OC125 epitope and the M11 epitope.

G. Northern Blot Analysis

Total RNA samples (approximately 10µg) were separated by electrophoresis through a 6.3% formaldehyde, 1.2% agarose gel in 0.02 M MOPS, 0.05 M sodium acetate (pH 7.0), and 0.001 M EDTA. The RNAs were then blotted to Hybond-N (Amersham) by capillary

action in 20x SSPE and fixed to the membrane by baking for 2 hours at 80°C. A PCR product representing one 400 bp repeat of the CA125 molecule was radiolabelled using the Prime-a-Gene Labeling System available from Promega (cat. #U1100). The blot was probed and stripped according to the ExpressHyb Hybridization Solution protocol available from Clontech (Catalog #8015-1).

RESULTS

In 1997, a system was described by a co-inventor of the present invention and others for purification of CA125 (primarily from patient ascites fluid), which when followed by cyanogen bromide digestion, resulted in peptide fragments of CA125 of 60 kDa and 40 kDa [O'Brien TJ *et al.*, More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4)188-195 (1998)]. Both fragments were identifiable by commassie blue staining on polyacrylamide gels and by Western blot. Both fragments were shown to bind both OC125 and M11 antibodies, indicating both major classes of epitopes were preserved in the released peptides (Figure 1).

Protein sequencing of the 40 kDa band yielded both amino terminal sequences and some internal sequences generated by protease digestion (Table 1 – SEQ ID NOS: 1-4). Insufficient yields of the 60 kDa band resulted in unreliable sequence information. Unfortunately, efforts to amplify PCR products utilizing redundant primers designed to these sequences were not successful. In mid 2000, an EST (#BE005912) was entered into the GCG database, which contained homology to the 40 kDa band sequence as shown in Table 1 (SEQ ID NOS: 5 and 6). The translation of this EST indicated good homology to the amino terminal sequence of the 40 kDa repeat (e.g. PGSRKFKTTE) with only one amino acid difference (i.e. an asparagine is present instead of phenylalanine in the EST sequence). Also, some of the internal sequences are partially conserved (e.g. SEQ ID NO: 2 and to a lesser extent, SEQ ID NO: 3 and SEQ ID NO: 4). More importantly, all the internal sequences are preceded by a basic amino acid (Table 1, indicated by arrows) appropriate for proteolysis by the trypsin used to create the internal peptides from the 40 kDa cyanogen bromide repeat. Utilizing the combined sequences, those obtained by amino acid sequencing and those identified in the EST (#BE005912) and a second EST (#AA640762) identified in the database, sense primers were created as follows: 5'-GGA GAG GGT TCT GCA GGG TC-3' (SEQ ID NO: 7) representing amino acids ERVLQG and anti-sense

primer, 5' GTG AAT GGT ATC AGG AGA GG-3' (SEQ ID NO: 9) representing PLLIPF. Using PCR, the presence of transcripts was confirmed representing these sequences in ovarian tumors and their absence in normal ovary and either very low levels or no detectable levels in a mucinous tumor (Figure 2A). The existence of transcripts was further confirmed in cDNA derived from multiple primary ovarian carcinoma cell lines and the absence of transcripts in matched lymphocyte cultures from the same patient (Figure 2B).

After cloning and sequencing of the amplified 400 base pair PCR products, a series of sequences were identified, which had high homology to each other but which were clearly distinct repeat entities (Figure 3) (SEQ ID NOS: 158 through 161).

Examples of each category of repeats were sequenced, and the results are shown in Tables 3, 4, and 5. The sequences represent amplification and sequence data of PCR products obtained using oligonucleotide primers derived from an EST (Genbank Accession No. BE005912). Table 3 illustrates the amino acid sequence for a 400 bp repeat in the CA125 molecule, which is identified as SEQ ID NO: 11 through SEQ ID NO: 21. Table 4 illustrates the amino acid sequence for a 800 bp repeat in the CA125 molecule, which corresponds to SEQ ID NO: 22 through SEQ ID NO: 35. Table 5 illustrates the amino acid sequence for a 1200 bp repeat in the CA125 molecule, which is identified as SEQ ID NO: 36 through SEQ ID NO: 46. Assembly of these repeat sequences (which showed 75-80% homology to each other as determined by GCG Software (GCG = Genetics Computer Group) using the Pileup application) utilizing PCR amplification and sequencing of overlapping sequences allowed for the construction of a 9 repeat structure. The amino acid sequence for the 9 repeat is shown in Table 6 as SEQ ID NO: 47. The individual C-enclosures are highlighted in the table.

Using the assembled repeat sequence in Table 6 to search genebank databases, a cDNA sequence referred to as Genbank Accession No. AK024365 (entered on 9/29/00) was discovered. Table 7 shows the amino acid sequence for AK024365, which corresponds to SEQ ID NO: 48. AK024365 was found to overlap with two repeats of the assembled repeat sequence shown in Table 6. Individual C-enclosures are highlighted in Table 7.

The cDNA for AK024365 allowed alignment of four additional repeats as well as a downstream carboxy terminus sequence of the CA125 gene. Table 8 illustrates the complete

DNA sequence of 13 repeats contiguous with the carboxy terminus of the CA125 molecule, which corresponds to SEQ ID NO: 49. Table 9 illustrates the complete amino acid sequence of the 13 repeats and the carboxy terminus of the CA125 molecule, which corresponds to SEQ ID NO: 50. The carboxy terminus domain was further confirmed by the existence of two EST's (Genbank Accession Nos. AW150602 and AI923224) in the genebank database, both of which confirmed the stop-codon indicated (TGA) as well as the poly A signal sequence (AATAA) and the poly A tail (see Table 9). The presence of these repeats has been confirmed in serous ovarian tumors and their absence in normal ovarian tissue and mucinous tumors as expected (see Figure 2A). Also, the transcripts for these repeats have been shown to be present in tumor cell lines derived from ovarian tumors, but not in normal lymphocyte cell lines (Figure 2B). Moreover, Northern blot analysis of mRNA derived from normal or ovarian carcinoma and probed with a P³² labeled CA125 repeat sequence (as shown in Figure 6) confirmed the presence of an RNA transcript in excess of 20 kb in ovarian tumor extracts (see Figure 2B).

To date, 45 repeat sequences have been identified with high homology to each other. To order these repeat units, overlapping sequences were amplified using a sense primer (5' GTC TCT ATG TCA ATG GTT TCA CCC-3') (SEQ ID NO: 305) from an upstream repeat and an antisense primer from a downstream repeat sequence (antisense 5' TAG CTG CTC TCT GTC CAG TCC-3') (SEQ ID NO: 306). Attempts have been made to place these repeats in a contiguous fashion as shown in Figure 3. There is some potential redundancy. Further, there is evidence from overlapping sequences that some repeats exist in more than one location in the sequence giving a total of more than 60 repeats in the CA125 molecule (see Table 21 SEQ ID NO: 162).

Final confirmation of the relationship of the putative CA125 repeat domain to the known CA125 molecule was achieved by expressing a recombinant repeat domain in *E. coli*. In Figure 4, expression of a recombinant CA125 repeat domain is shown in lane 2 compared to the vector alone in lane 1, Panel D. A series of Western blots representing *E. coli* extracts of vector alone in lane 1; CA125 recombinant protein lane in 2 and recombinant TADG-14 (an unrelated recombinant protease), lane 3, were probed with the CA125 antibodies M11, Panel A; OC125,

Panel B; and ISOBM 9.2, Panel C. In all cases, CA125 antibodies recognized only the recombinant CA125 antigen (lane 2 of each panel).

To further characterize the epitope location of the CA125 antibodies, recombinant CA125 repeat was digested with the endoprotease Lys-C and separately with the protease Asp-N. In both cases, epitope recognition was destroyed. As shown in Figure 5, the initial cleavage site for ASP-N is at amino acid #76 (indicated by arrow in Figure 5C). This sequence (amino acids # 1-76), a 17 kDa band, was detected with anti-histidine antibodies (Figure 5A, Lane 3) and found to have no capacity to bind CA125 antibodies (Figure 5B, Lane 3). The upper bands in Figures 5A and 5B represent the undigested remaining portion of the CA125 recombinant repeat. From these data, one can reasonably conclude that epitopes are either located at the site of cleavage and are destroyed by Asp-N or are downstream from this site and also destroyed by cleavage. Likewise, cleavage with Lys-C would result in a peptide, which includes amino acids # 68-154 (Figure 5C) and again, no antibody binding was detected. In view of the foregoing, it seems likely that epitope binding resides in the cysteine loop region containing a possible disulfide bridge (amino acids # 59-79). Final confirmation of epitope sites are being examined by mutating individual amino acids.

To determine transcript size of the CA125 molecule, Northern blot analysis was performed on mRNA extracts from both normal and tumor tissues. In agreement with the notion that CA125 may be represented by an unusually large transcript due to its known mega dalton size in tumor sera, ascites fluid, and peritoneal fluid [Nustad K *et al.*, CA125 – epitopes and molecular size, *Int. J of Biolog. Markers*, 13(4)196-199 (1998)], a transcript was discovered which barely entered the gel from the holding well (Figure 6). CA125 mRNA was only present in the tumor RNA sample and while a precise designation of its true size remains difficult due to the lack of appropriate standards, its unusually large size would accommodate a protein core structure in excess of 11,000 amino acids.

Evidence demonstrates that the repeat domain of the CA125 molecule encompasses a minimum of 45 different 156 amino acid repeat units and possibly greater than 60 repeats, as individual repeats occur more than once in the sequence. This finding may well account for the extraordinary size of the observed transcript. The amino acid composition of the repeat units (Figure 7A, 7C, Table 21) indicates that the sequence is rich in serine, threonine, and proline typical of the high STP repeat regions of the mucin genes [Gum Jr., JR, Mucin genes and the

proteins they encode: Structure, diversity and regulation, *Am J Respir. Cell Mol. Biol.* 7:557-564 (1992)]. Results suggest that the downstream end of the repeat is heavily glycosylated.

Also noteworthy is a totally conserved methionine at position 24 of the repeat (Figure 7A, 7C). It is this methionine which allowed cyanogen bromide digestion of the CA125 molecule, resulting in the 40 kDa glycopeptide that was identified with OC125 and M11 antibodies in Western blots of the CNBr digested peptides. These data predict that the epitopes for the CA125 antibodies are located in the repeat sequence. By production of a recombinant product representing the repeat sequence, results have confirmed this to be true. A potential disulfide bond is noted, which would encompass a C-enclosure comprising 19 amino acids enclosed by two cysteines at positions #59 and #79. The cysteines are totally conserved, which suggest a biological role for the resulting putative C-enclosure in each repeat. As mentioned above, it is likely that the OC125 and M11 epitopes are located in the C-enclosure, indicating its relative availability for immune detection. This is probably due to the C-enclosure structure and the paucity of glycosylation in the immediate surrounding areas. Domain searches also suggest some homology in the repeat domain to an SEA domain commonly found in the mucin genes [Williams SJ *et al.*, MUC13, a novel human cell surface mucin expressed by epithelial and hemopoietic cells, *J of Biol. Chem* 276(21)18327-18336 (2001)] beginning at amino acid #1 and ending at #131 of each repeat. No biological function has been described for this domain.

Based on homology of the repeat sequences to chromosome 19q 13.2 (cosmid #AC008734) and confirmed by genomic amplification, it has been established that each repeat is comprised of 5 exons (covering approximately 1900 bases of genomic DNA): exon 1 comprises 42 amino acids (#1-42); exon 2 comprises 23 amino acids (#43-65); exon 3 comprises 58 amino acids (#66-123); exon 4 comprises 12 amino acids (#124-135); and exon 5 comprises 21 amino acids (#136-156) (see Figure 7B). Homology pile-ups of individual exons have also been completed (see Figure 7C), which indicates that exon 1 has a minimum of 31 different copies of the exon; exon 2 has 27 copies; exon 3 has 28 copies, exon 4 has 28 copies and exon 5 has 21 copies. If all exons were only found in a single configuration relative to each other, one could determine that a minimum number of repeats of 31 were present in the CA125 molecule. Using the exon 2 pile-up data as an example, it has been established as mentioned above that there are 27 individual exon 2 sequences. Using exon 2, which was sequenced fully in both the repeat units and the overlaps, results established that a minimum of 45 repeat units are present when

exon 2 is combined with unique other exon combinations. However, based on overlap sequence information, 60+ repeat units are likely present in the CA125 molecule (Table 21). This larger number of repeat units can be accounted for by the presence of the same repeat unit occurring in more than one location.

Currently, the repetitive units of the repeat domain of the CA125 molecule constitute the majority of its extracellular molecular structure. These sequences have been presented in a tandem fashion based on overlap sequencing data. Some sequences may be incorrectly placed and some repeat units may not as yet be identified (Table 21). More recently, an additional repeat was identified in CA125 as shown in Tables 22 and 23 (SEQ. ID NOS: 307 and 308). The exact position has not yet been identified. Also, there is a potential that alternate splicing and/or mutation could account for some of the repeat variants that are listed. Studies are being conducted to compare both normal tissue derived CA125 repeats to individual tumor derived CA125 repeats to determine if such variation is present. Currently, the known exon configurations would easily accommodate the greater than 60 repeat units as projected. It is, therefore, unlikely that alternate splicing is a major contributor to the repetitive sequences in CA125. It should also be noted that the genomic database for chromosome 19q 13.2 only includes about 10 repeat units, thus indicating a discrepancy between the data of the present invention (more than 60 repeats) and the genomic database. A recent evaluation of the methods used for selection and assembly for genomic sequence [Marshall E, DNA Sequencing: Genome teams adjust to shotgun marriage, *Science* 292:1982-1983 (2001)] reports that "more research is needed on repeat blocks of almost identical DNA sequence which are more common in the human genome. Existing assembly programs can't handle them well and often delete them." The CA125 repeat units located on chromosome 19 may well be victims of deletion in the genomic database, thus accounting for most CA125 repeat units absent from the current databases.

A. Sequence Confirmation and Assembly of the Amino Terminal Domain (Domain 1) of the CA125 Molecule

As previously mentioned, homology for repeat sequences was found in the chromosome 19 cosmid AC008734 of the GCG database. This cosmid at the time consisted of 35 unordered contigs. After searching the cosmid for repeat sequences, contig #32 was found to have exons 1 and 2 of a repeat unit at its 3' end. Contig #32 also had a large open reading frame upstream

from the two repeat units, which suggested that this contig contained sequences consistent with the amino terminal end of the CA125 molecule. A sense primer was synthesized to the upstream non-repeat part of contig #32 coupled with a specific primer from within the repeat region (see Methods). PCR amplification of ovarian tumor cDNA confirmed the contiguous positioning of these two domains. The PCR reaction yielded a band of approximately 980bp. The band was sequenced and found to connect the upstream open reading frame to the repeat region of CA125. From these data, more primer sets (see Methods) were synthesized and used in PCR reactions to piece together the entire open reading frame contained in contig #32. To find the 5' most end of the sequence, an EST (AU133673) was discovered, which linked contig #32 to contig #7 of the same cosmid. Specific primers were synthesized, (5'-CTGATGGCATTATGGAACACATCAC-3' (SEQ ID NO: 59) and 5'-CCCAGAACGAGAGACCACTGAG-3' (SEQ ID NO: 60)), to the EST and contig #32. A PCR reaction was performed to confirm that part of the EST sequence was in fact contiguous with contig #32. Confirmation of this contiguous 5' prime sequencing strategy using overlapping sequences allowed the assembly of the 5' region (Domain 1) (Figure 8A). 5' RACE PCR was performed on tumor cDNA to confirm the amino terminal sequence to CA125. The test confirmed the presence of contig #7 sequence at the amino terminal end of CA125.

The amino terminal domain comprises five genomic exons covering approximately 13,250 bp. Exon 1, a small exon, (amino acids #1-33) is derived from contig #7 (Figure 8A). The remaining exons are all derived from contig #32: Exon 2 (amino acids #34-1593), an extraordinarily large exon, Exon 3 (amino acids #1594-1605), Exon 4 (amino acids #1606-1617) and Exon 5 (amino acids #1618-1637) (see Figure 8A).

Potential N-glycosylation sites marked (x) are encoded at positions #81, #271, #320, #624, #795, #834, #938, and #1,165 (see Figure 8B). O-glycosylation sites are extraordinarily abundant and essentially cover the amino terminal domain (Figure 8B). As shown by the O-glycosylation pattern, Domain 1 is highly enriched in both threonine and serine (Figure 8B).

With additional research, an extension of the glycosylated amino terminal sequence was identified and cloned. Table 24 (SEQ ID NO: 309) illustrates the DNA sequence of the CA125 amino terminal extension. Table 25 (SEQ ID NO: 310) illustrates the protein sequence for the amino terminal extension of the CA125 gene. It should be noted that the last four amino acids,

TDGI, in SEQ ID NO: 310 belong to exon 1 of the amino terminal domain. Table 26 illustrates the serine/threonine o-glycosylation pattern for the CA125 amino terminal extension.

B. Sequence Confirmation and Assembly of the CA125 Carboxy Terminal End (Domain 3)

A search of Genbank using the repeat sequences described above uncovered a cDNA sequence referred to as Genbank accession number AK024365. This sequence was found to have 2 repeat sequences, which overlapped 2 known repeat sequences of a series of 6 repeats. As a result, the cDNA allowed the alignment of all six carboxy terminal repeats along with a unique carboxy terminal sequence. The carboxy terminus was further confirmed by the existence of two other ESTs (Genbank accession numbers AW150602 and A1923224), both of which confirmed a stop codon as well as a poly-A signal sequence and a poly-A tail (see GCG database #AF414442). The sequence of the carboxy terminal domain was confirmed using primers designed to sequence just downstream of the repeat domain (sense primer 5' GGA CAA GGT CAC CAC ACT CTA C-3') (SEQ ID NO: 303) and an antisense primer (5'-GCA GAT CCT CCA GGT CTA GGT GTG-3') (SEQ ID NO: 304) designed to carboxy terminus (Figure 9A).

The carboxy terminal domain covers more than 14,000 genomic bp. By ligation, this domain comprises nine exons as shown in Figure 9A. The carboxy-terminus is defined by a 284 amino acid sequence downstream from the repeat domains (see Figure 9B). Both N-glycosylation sites marked (x) (#31, #64, #103, #140, #194, #200) and a small number of O-glycosylation sites marked (o) are predicted for the carboxy end of the molecule (Figures 9A, 9B). Of special note is a putative transmembrane domain at positions #230-#252 followed by a cytoplasmic domain, which is characterized by a highly basic sequence adjacent to the membrane (#256-#260) as well as several potential S/T phosphorylation sites (#254, #255, #276) and tyrosine phosphorylation sites (at # 264, #273, #274) (Figures 9A, 9B).

Assembly of the CA125 molecule as validated by PCR amplification of overlap sequence provides a picture of the whole molecule (see Figure 10 and Table 21). The complete nucleotide sequence is available in Genebank, Accession #AF414442 and the amino acid sequence as currently aligned is shown in Table 21.

DISCUSSION

The CA125 molecule comprises three major domains; an extracellular amino terminal domain (Domain 1), a large multiple repeat domain (Domain 2) and a carboxy terminal domain (Domain 3), which includes a transmembrane anchor with a short cytoplasmic domain (Figure 10). The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon, which often typifies mucin extracellular glycosylated domains [Desseyn JL *et al.*, Human mucin gene MUC5B, the 10.7-kb large central exon encodes various alternate subdomains resulting in a super-repeat. Structural evidence for a 11p15.5 gene family, *J. Biol. Chem.* 272(6):3168-3178 (1997)]. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Overall, the potential for O-glycosylation essentially covers this domain and, as such, may allow the carbohydrate superstructure to influence ECM interaction at this end of the CA125 molecule (Figure 8). There is one short area (amino acids # 74-120) where little or no glycosylation is predicted, which could allow for protein-protein interaction in the extracellular matrix.

Efforts to purify CA125 over the years were obviously complicated by the presence of this amino terminal domain, which is unlikely to have any epitope sites recognized by the OC125 or M11 class antibodies. As the CA125 molecule is degraded *in vivo*, it is likely that this highly glycosylated amino terminal end will be found associated with varying numbers of repeat units. This could very well account for both the charge and size heterogeneity of the CA125 molecule so often identified from serum and ascites fluid. Also of note are two T-TALK sequences at amino acids # 45-58 (underlined in Figure 8B), which are unique to the CA125 molecule.

The extracellular repeat domain, which characterizes the CA125 molecule, also represents a major portion of the molecular structure. It is downstream from the amino terminal domain and presents itself in a much different manner to its extracellular matrix neighbors. These repeats are characterized by many features including a highly-conserved nature (Figure 3) and a uniformity in exon structure (Figure 7). But most consistently, a cysteine enclosed sequence may form a cysteine loop (Table 21). This structure may provide extraordinary potential for interaction with neighboring matrix molecules. Domain 2 encompasses the 156 amino acid repeat units of the CA125 molecule. The repeat domain constitutes the largest proportion of the CA125 molecule (Table 21 and Figure 10). Because it has been known for more than 15 years that antibodies bind in a multivalent fashion to CA125, it has been predicted

that the CA125 molecule would include multiple repeat domains capable of binding the OC125 and M11 class of sentinel antibodies which define this molecule [O'Brien *et al.*, New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol.* 165:1857-1964 (1991); Nustad K *et al.*, Specificity and affinity of 26 monoclonal antibodies against the CA125 antigen: First report from the ISOBM TD-1 workshop, *Tumor Biology* 17:196-219 (1996); and Bast RC *et al.*, A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N. Engl. J. Med.* 309:883-887 (1983)]. In the present invention, more than 60 repeat units have been identified, which are in tandem array in the extracellular portion of the CA125 molecule. Individual repeat units have been confirmed by sequencing and further identified by PCR amplification of the overlapping repeat sequences. Results confirm the contiguous placement of most repeats relative to its neighbor (Table 21).

Initial evidence suggests that this area is a potential site for antibody binding and also for ligand binding. The highly conserved methionine and several highly conserved sequences within the repeat domain also suggests a functional capacity for these repeat units. The extensive glycosylation of exons 4 & 5 of the repeat unit and the N-glycosylation potential in exon 1 and the 5' end of exon 2 might further point to a functional capacity for the latter part of exon 2 and exon 3 which includes the C-enclosure (see Figure 7). It should be apparent that the C-enclosure might be a prime target for protease activity and such cleavage may well explain the difficulty experienced by many investigators in obtaining an undigested CA125 parent molecule. Such activity might explain the diffuse pattern of antibody binding and the loss of antibody binding for molecules of less than 200,000 kDa. Proteolysis would destroy the epitopes and, therefore, only multiple repeats could be identified by blotting with CA125 antibodies. The repeat unit organization also suggests the potential for a multivalent interaction with extracellular entities.

The carboxy terminal domain of the CA125 molecule comprises an extracellular domain, which does not have any homology to other known domains. It encodes a typical transmembrane domain and a short cytoplasmic tail. It also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain. This would allow for proteolytic cleavage and release of the CA125 molecule (Figure 9). As indicated by Fendrick, *et al.* [CA125 phosphorylation is associated with its secretion from the WISH human amnion cell line, *Tumor Biology* 18:278-289 (1997)], release of the CA125 molecule is preceded by

phosphorylation and sustained by inhibitors of phosphatases, especially inhibition of phosphatase 2B. The cytoplasmic tail which contains S/T phosphorylation sites next to the transmembrane domain and tyrosine phosphorylation sites downstream from there could accommodate such phosphorylation. A very distinguishable positively charged sequence is present upstream from the tyrosine, suggesting a signal transduction system involving negatively charged phosphate groups and positively charged lysine and arginine groups.

These features of the CA125 molecule suggest a signal transduction pathway involvement in the biological function of CA125 [Fendrick JL *et al.*, CA125 phosphorylation is associated with its secretion from the WISH human amnion cell line, *Tumor Biology* 18:278-289 (1997); and Konish I *et al.*, Epidermal growth factor enhances secretion of the ovarian tumor-associated cancer antigen CA125 from the human amnion WISH cell line, *J Soc. Gynecol. Invest.* 1:89-96 (1994)]. It also reinforces the prediction of phosphorylation prior to CA125 release from the membrane surface as previously proposed [Fendrick JL *et al.*, CA125 phosphorylation is associated with its secretion from the WISH human amnion cell line, *Tumor Biology* 18:278-289 (1997); and Konish I *et al.*, Epidermal growth factor enhances secretion of the ovarian tumor-associated cancer antigen CA125 from the human amnion WISH cell line, *J Soc. Gynecol. Invest.* 1:89-96 (1994)]. Furthermore, a putative proteolytic cleavage site on the extra-cellular side of the transmembrane domain is present at position #176-181.

How well does the CA125 structure described in the present invention compare to the previously known CA125 structure? O'Brien *et al.* reported that a number of questions needed to be addressed: 1) the multivalent nature of the molecule; 2) the heterogeneity of CA125; 3) the carbohydrate composition; 4) the secretory or membrane bound nature of the CA125 molecule; 5) the function of the CA125 molecule; and 6) the elusive CA125 gene [More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4)188-195 (1998)]. Several of these questions have been addressed in the present invention including, of course, the gene and its protein core product. Perhaps, most interestingly is the question of whether an individual large transcript accounted for the whole CA125 molecule, or a number of smaller transcripts which represented subunits that specifically associated to produce the CA125 molecule. From the results produced by way of the present invention, it is now apparent that the transcript of CA125 is large - similar to some of the mucin gene transcripts e.g. MUC 5B [see Verma M *et al.*, Mucin genes: Structure, expression and regulation,

Glycoconjugate J. 11:172-179 (1994); and Gendler SJ *et al.*, Epithelial mucin genes, *Annu. Rev. Physiol.* 57:607-634 (1995)]. The protein core extracellular domains all have a high capacity for O-glycosylation and, therefore, probably accounts for the heterogeneity of charge and size encountered in the isolation of CA125. The data also confirm the O-glycosylation inhibition data, indicating CA125 to be rich in O-glycosylation [Lloyd KO *et al.*, Synthesis and secretion of the ovarian cancer antigen CA125 by the human cancer cell line NIH: OVCAR-3, *Tumor Biology* 22, 77-82 (2001); Lloyd KO *et al.*, Isolation and characterization of ovarian cancer antigen CA125 using a new monoclonal antibody (VK-8): Identification as a mucin-type molecule, *Int. J. Cancer*, 71:842-850 (1997); and Fendrick JL *et al.*, Characterization of CA125 synthesized by the human epithelial amnion WISH cell line, *Tumor Biology* 14:310-318 (1993)].

The repeat domain which includes more than 60 repeat units accounts for the multivalent nature of the epitopes present, as each repeat unit likely contains epitope binding sites for both OC125-like antibodies and M11-like antibodies. The presence of a transmembrane domain and cleavage site confirms the membrane association of CA125, and reinforces the data which indicates a dependence of CA125 release on proteolysis. Also, the release of CA125 from the cell surface may well depend on cytoplasmic phosphorylation and be the result of EGF signaling [Nustad K *et al.*, Specificity and affinity of 26 monoclonal antibodies against the CA125 antigen: First report from the ISOBM TD-1 workshop, *Tumor Biology* 17:196-219 (1996)]. As for the question of inherent capacity of CA125 for proteolytic activity, this does not appear to be the case. However, it is likely that the associated proteins isolated along with CA125 (e.g. the 50 kDa protein which has no antibody binding ability) may have proteolytic activity. In any case, proteolysis of an extracellular cleavage site is the most likely mechanism of CA125 release. Such cleavage would be responsive to cytoplasmic signaling and mediated by an associated extracellular protease activity.

In summary, the large number of tandem repeats of the CA125 molecule, which dominate its molecular structure and contain the likely epitope binding sites of the CA125 molecule, was unexpected. Also, one cannot as yet account for the proteolytic activity, which has plagued the isolation and characterization of this molecule for many years. While no protease domain per se is constitutively part of the CA125 molecule, there is a high likelihood of a direct association by an extracellular protease with the ligand binding domains of the CA125 molecule. Finally, what is the role of the dominant repeat domain of this extracellular structure? Based on the expression

data of CA125 on epithelial surfaces and in glandular ducts, it is reasonable to conclude that the unique structure of these repeat units with their cysteine loops plays a role both as glandular anti-invasive molecules (bacterial entrapment) and/or a role in anti-adhesion (maintaining patency) between epithelial surfaces and in ductal linings.

Recently, Yin and Lloyd described the partial cloning of the CA125 antigen using a completely different approach to that described in the present invention [Yin TWT *et al.*, Molecular cloning of the CA125 ovarian cancer antigen. Identification as a new mucin (MUC16), *J Biol. Chem.* 276:27371-27375 (2001)]. Utilizing a polyclonal antibody to CA125 to screen an expression library of the ovarian tumor cell line OVCAR-3, these researchers identified a 5965 bp clone containing a stop codon and a poly A tail, which included nine partially conserved tandem repeats followed by a potential transmembrane region with a cytoplasmic tail. The 5965 bp sequence is almost completely homologous to the carboxy terminus region shown in Table 21. Although differing in a few bases, the sequences are homologous. As mentioned above, the cytoplasmic tail has the potential for phosphorylation and a transmembrane domain would anchor this part of the CA125 molecule to the surface of the epithelial or tumor cell. In the extracellular matrix, a relatively short transition domain connects the transmembrane anchor to a series of tandem repeats - in the case of Yin and Lloyd, nine.

By contrast, the major extracellular part of the molecule of the present invention as shown is upstream from the sequence described by Yin and includes a large series of tandem repeats. These results, of course, provide a different picture of the CA125 molecule, which suggest that CA125 is dominated by the series of extracellular repeats. Also included is a major amino terminal domain (~1638 amino acids) for the CA125 molecule, which it is believed accounts for a great deal of the O-glycosylation known to be an important structural component of CA125.

In conclusion, a CA125 molecule is disclosed which requires a transcript of more than 35,000 bases and occupies approximately 150,000 bp on chromosome 19q 13.2. It is dominated by a large series of extracellular repeat units (156 amino acids), which offer the potential for molecular interactions especially through a highly conserved unique cysteine loop. The repeat units also include the epitopes now well-described and classified for both the major class of CA125 antibodies (i.e., the OC125 and the M11 groups). The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. CA125 also

contains a highly glycosylated amino terminal domain, which includes a large extracellular exon typical of some mucins. Given the massive repeat domain presence of both epithelial surfaces and ovarian tumor cell surfaces, it might be anticipated that CA125 may play a major role in determining the extracellular environment surrounding epithelial and tumor cells.

Advantages and Uses of the CA125 Recombinant Products

1) Current assays to CA125 utilize as standards either CA125 produced from cultured cell lines or from patient ascites fluid. Neither source is defined with regard to the quality or purity of the CA125 molecule. Therefore arbitrary units are used to describe patient levels of CA125. Because cut-off values are important in the treatment of patients with elevated CA125 and because many different assay systems are used clinically to measure CA125, it is relevant and indeed necessary to define a standard for all CA125 assays. Recombinant CA125 containing epitope binding sites could fulfill this need for standardization. Furthermore, new and more specific assays may be developed utilizing recombinant products for antibody production.

2) Vaccines: Adequate data now exists [see Wagner U *et al.*, Immunological consolidation of ovarian carcinoma recurrences with monoclonal anti-idiotypic antibody ACA125: Immune responses and survival in palliative treatment, *Clin. Cancer Res.* 7:1112-1115 (2001)], which suggest and support the idea that CA125 could be used as a therapeutic vaccine to treat patients with ovarian carcinoma. Heretofore, in order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains which encompass epitope binding sites for known murine antibodies and domains directly anchoring CA125 on the tumor cell, it will be feasible to more directly stimulate patients' immune systems to CA125 and as a result, extend the life of ovarian carcinoma patients as demonstrated by Wagner et al.

Several approaches can be utilized to achieve such a therapeutic response in the immune system by: 1) directly immunizing the patient with recombinant antigen containing the CA125 epitopes or other domains; 2) harvesting dendritic cells from the patient; 3)

expanding these cells in *in vitro* culture; 4) activating the dendritic cells with the recombinant CA125 epitope domain or other domains or with peptides derived from these domains [see Santin AD *et al.*, Induction of ovarian tumor-specific CD8+ cytotoxic T lymphocytes by acid-eluted peptide-pulsed autologous dendritic cells, *Obstetrics & Gynecology* 96(3):422-430 (2000)]; and then 5) returning these immune stem cells to the patient to achieve an immune response to CA125. This procedure can also be accomplished using specific peptides which are compatible with histocompatibility antigens of the patient. Such peptides compatible with the HLA-A2 binding motifs common in the population are indicated in Figure 12.

3) Therapeutic Targets: Molecules, which are expressed on the surface of tumor cells as CA125 is, offer potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. CA125 offers such potential as a target: 1) Antibodies to CA125 epitopes or newly described potential epitopes: Most especially humanized or human antibodies to CA125 which could directly activate the patients' immune system to attack and kill tumor cells. Antibodies could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. 2) Natural ligands: Under normal circumstances, molecules are bound to the CA125 molecule e.g. a 50 k dalton protein which does not contain CA125 epitopes co-purifies with CA125. Such a molecule, which might have a natural binding affinity for domains on the CA125 molecule, could also be utilized to deliver therapeutic agents to tumor cells.

4) Anti-sense therapy: CA125 expression may provide a survival or metastatic advantage to ovarian tumor cells as such antisense oligonucleotide derived from the CA125 sequence could be used to down-regulate the expression of CA125. Antisense therapy could be used in association with a tumor cell delivery system such as described above.

5) Small Molecules: Recombinant domains of CA125 also offer the potential to identify small molecules which bind to individual domains of the molecule. Small molecules either from combinatorial chemical libraries or small peptides can also be used as delivery agents or as biological modifiers.

All references referred to herein are hereby incorporated by reference in their entirety.

It should be understood that various changes and modifications to the presently preferred embodiments described herein will be apparent to those skilled in the art. Such changes and modifications can be made without departing from the spirit and scope of the present invention and without diminishing its attendant advantages.

TABLE 1

Comparison of the Amino Acid Terminal Sequences and Several Internal Sequences for the 40kD Band for CA125 glycoprotein (SEQ ID NO: 1 through SEQ ID NO: 4) to the Nucleotide and Amino Acid Sequences for EST Genbank Accession No. AA640762

(SEQ ID NO: 5 and SEQ ID NO: 6, respectively)

40kDa Nterm - QHPSRKFKTTEG (SEQ ID NO: 1)

Peak 68 - FLTVERVLQGL (SEQ ID NO: 2)

Peak 65 - DTYVGPLY (SEQ ID NO: 3)

Peak 30 - DGAANGVD (SEQ ID NO: 4)

(SEQ ID NO: 5 and SEQ ID NO: 6)

↓

```

1  CGTCGACCTGGCTCTAGAAAGTTTAACACCACGGAGAGAGTCCTTCAGGGTCTGCTCAGG
   R R P G S R K F N T T E R V L Q G L L R
61  CCTGTGTTCAAGAACCACAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACCTTGCTC
   P V F K N T S V G P L Y S G C R L T L L
121 AGGCCCAAGAAGGATGGGGCAGCCACCAAAGTGGATGCCATCTGCACCTACCGCCCTGAT
    R P K K D G A A T K V D A I C T Y R P D
181 CCCAAAAGCCCTGGACTGGACAGAGAGCAGCTATACTGGGAGCTGAGCCAGGGTGATGCA
    P K S P G L D R E Q L Y W E L S Q G D A
  
```

TABLE 2A

Nucleotide and Amino Acid Sequences for Sense Primer 5' 3' (SEQ ID NO: 7 and SEQ ID NO: 8 respectively) and Antisense Primer 5' 3' (SEQ ID NO: 9 and SEQ ID NO: 10 respectively) based upon Regions of Homology for EST Genbank Accession Nos. BE005912 and AA640762

GGA GAG GGT TCT GCA GGG TC (SEQ ID NO: 7)

E R V L Q G (SEQ ID NO: 8)

GTG AAT GGT ATC AGG AGA GG (SEQ ID NO: 9)

P L L I P F (SEQ ID NO: 10)

TABLE 2B

Sense and Anti-Sense Primers Used for Ordering Repeat Units
(SEQ ID NO: 301 and SEQ ID NO: 302, respectively)

5'-GTCTCTATGTCAATGGTTTCACCC-3' (SEQ ID NO: 301)

5'-TAGCTGCTCTCTGTCCAGTCC-3' (SEQ ID NO: 302)

TABLE 3

Amino Acid Sequence for a 400 bp Repeat in the CA125 Molecule
(SEQ ID NO: 11 thru SEQ ID NO: 21)

	1				50	
12	ERVLOGLLRS	LFKSTSVGPL	YSGCRLTLR	PEKDGATATGV	DAICTHHHPDP	(SEQ ID NO: 11)
34	ERVLOGLLMP	LFKNTSVSSL	YSGCRLTLR	PEKDGAATRA	DAVCTHRPDP	(SEQ ID NO: 12)
32	ERVLOGLLGP	IFKNTSVGPL	YSGCRLTSLR	SEKDGAATGV	DAICIHRLDP	(SEQ ID NO: 13)
46	ERVLOGLLGP	MEKNTSVGGL	YSGCRLTLR	PEKNGAATGM	DAICSHRLDP	(SEQ ID NO: 14)
33	ERVLOGLLGP	LFKNSSVGPL	YSGCRLTSLR	SEKDGAATGV	DAICTHHLNP	(SEQ ID NO: 15)
15	ERVLOGLLRP	LFKSTSAGPL	YSGCRLTLR	PEKHGAATGV	DAICTLRLDP	(SEQ ID NO: 16)
35	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 17)
111	ERVLOGLLTP	LFKNTSVGPL	YSGCRLTLR	PEKQEAATGV	DTICTHRVDP	(SEQ ID NO: 18)
42	ERVLOGLLKP	LFKNTSVGPL	YSGCRLTLR	PEKHEAATGV	DTICTHRLDP	(SEQ ID NO: 19)
116	ERVLOGLLSP	IFKNSSVGPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 20)
23	ERVLOGLLRP	LFKNTSIGPL	YSSCRLTLR	PEKDKAATRV	DAICTHHHPDP	(SEQ ID NO: 21)
	51				100	
12	KSPRLDREQL	YWELSQLTHN	ITELGPYALD	NDSLFGVNGFT	HRSSVSTTST	
34	KSPGLDRERL	YWKLSQLTHG	ITELGPYTLD	RHSLYVNGFT	HQSSMTTTRT	
32	KSPGLNREQL	YWELSKLTND	IEELGPYTLD	RNSLYVNGFT	HQSSVSTTST	
46	KSPGLNREQL	YWELSQLTHG	IKELGPYTLD	RNSLYVNGFT	HRSSVAPTST	
33	QSPGLDREQL	YWQLSQMTNG	IKELGPYTLD	RNSLYVNGFT	HRSSGLTTST	
15	TGPGLDRERL	YWELSQLTNS	VTELGPYTLD	RDSLYVNGFT	HRSSVPPTSI	
35	LNPGLDREQL	YWELSKLTRG	IIELGPYTLD	RDSLYVNGFT	HRSSVPPTSI	
111	IGPGLDRERL	YWELSQLTNS	ITELGPYTLD	RDSLYVDGFN	PWSSVPPTTST	
42	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST	
116	KRPGLDREQL	YWELSQLTHN	ITELGPYSLD	RDSLYVNGFT	HQNSVPPTTST	
23	QSPGLNREQL	YWELSQLTHG	ITELGPYTLD	RDSLYVDGFT	HWSPIPTTST	
	101				150	
12	PGTPTVYLGA	SKTPASIFGP	S..AASPLLI	PFT~~~~~	~~~~~	
34	PDTSTMHLAT	S RTPASLSGP	T..TASPLLI	PF~~~~~	~~~~~	
32	PGTSTVDLRT	SGTPSSLSSP	TIMAAGPLLI	PF~~~~~	~~~~~	
46	PGTSTVDLGT	SGTPSSLSP	T..TAVPLLI	PF~~~~~	~~~~~	
33	PWTSTVDLGT	SGTPSPVPSP	T..TAGPFLI	PF~~~~~	~~~~~	
15	PGTSAVHLET	SGTPASLPGH	T..APGPLLI	PF~~~~~	~~~~~	
35	PGTSAVHLET	SGTPASLPGH	I..VPGPLLI	PF~~~~~	~~~~~	
111	PGTSTVHLAT	SGTPSPLPGH	T..APVPLLI	PFT~~~~~	~~~~~	
42	PGTSTVHLGT	SETPSSLPRP	I..VPGPLLV	PFT~~~~~	~~~~~	
116	PGTSTVYWAT	TGTPSSFPGH	T..EPGPLLI	PF~~~~~	~~~~~	
23	PGTSIVNLGT	SGIPPSLPET	T..ATGPLLI	PFT~~~~~	~~~~~	

TABLE 3-continued

Amino Acid Sequence for a 400 bp Repeat in the CA125 Molecule
(SEQ ID NO: 11 thru SEQ ID NO: 21)

	151	170
12	~~~~~	~~~~~
34	~~~~~	~~~~~
32	~~~~~	~~~~~
46	~~~~~	~~~~~
33	~~~~~	~~~~~
15	~~~~~	~~~~~
35	~~~~~	~~~~~
111	~~~~~	~~~~~
42	~~~~~	~~~~~
116	~~~~~	~~~~~
23	~~~~~	~~~~~

TABLE 4

Amino Acid Sequence for a 800 bp Repeat in the CA125 Molecule
(SEQ ID NO: 22 thru SEQ ID NO: 35)

	1				50	
79	ERVLOGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP	(SEQ ID NO: 22)
811	ERVLOGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP	(SEQ ID NO: 23)
21	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 24)
89	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 25)
85	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 26)
712	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 27)
86	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKHGAATGV	DAICTLRLDP	(SEQ ID NO: 28)
87	ERVLOGLLTP	LFKNTSVGPL	YSGCRLTLLR	PEKQEAATGV	DTICTHRVDP	(SEQ ID NO: 29)
810	ERVLOGLLRP	LFKNTSIGPL	YSSCRLTLLR	PEKDKAATRV	DAICTHHPDP	(SEQ ID NO: 30)
83	ERVLOGLLRP	VFKNTSVGPL	YSGCRLTLLR	PKKDGAATKV	DAICTYRPDP	(SEQ ID NO: 31)
81	ERVLOGLLGP	MFKNTSVGLL	YSGCRLTLLR	PKKDGAATKV	DAICTYRPDP	(SEQ ID NO: 32)
44	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 33)
812	ERVLOGLLSP	ISKNSSVGPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 34)
76	ERVLOGLLSP	IFKNSSVGSL	YSGCRLTLLR	PEKDGAATRV	DAVCTHRPDP	(SEQ ID NO: 35)
	51				100	
79	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSMPTTST	
811	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSGLTTST	
21	LNPGLDREQ	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRTSVPTTST	
89	LNPGLDREQ	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST	
85	LNPGLDREQ	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFS	RQSSMTTTRT	
712	LNPGLDREQ	YWELSKLTRG	IIELGPYLLD	RDSLYVNGFT	HRSSVPTTSI	
86	TGPGLDRERL	YWELSQTNS	YTELGPYTLD	RDSLYVNGFT	HRSSVPTTSI	
87	IGPGLDRERL	YWELSQTNS	ITELGPYTLD	RDSLYVNGFN	PWSSVPTTST	
810	QSPGLNREQ	YWELSQTTHG	ITELGPYTLD	RDSLYVDGFT	HWSPIPTTST	
83	KSPGLDREQ	YWELSQTTHS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTSI	
81	KSPGLDREQ	YWELSQTTHS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTSI	
44	KRPGLDREQ	YCELSQTTHD	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST	
812	KRPGLDREQ	YWELSQTTHN	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST	
76	KSPGLDRERL	YWKLSQTTHG	ITELGPYTLD	RHSLYVNGFT	HQSSMTTTRT	
	101				150	
79	PGTSTVDVGT	SGTPSSSPSP	TTAGPLLMPF	TLNFTITNLQ	YEEDMRRTGS	
811	PWTSTVDLGT	SGTPSPVPSP	TTAGPLLIPF	TLNFTITNLQ	YEENMGHPGS	
21	PGTSTVDLGT	SGTPFSLPSP	ATAGPLLVL	TLNFTITNLK	YEEDMHRPGS	
89	PGTSTVHLGT	SETPSSLPRP	IVPGPLLIPF	TINFTITNLR	YEENMHHPGS	
85	PDTSTMHLAT	SRTPASLSGP	TTASPLLIPF	TLNFTITNLQ	YEENMGHPGS	
712	PGTSAVHLET	FGTPASLHGH	TAPGPVLVPF	TLNFTITNLQ	YEEDMRHPGS	
86	PGTSAVHLET	SGTPASLPGH	TAPGPVLVPF	TLNFTITNLQ	YEEDMRHPGS	
87	PGTSTVHLAT	SGTPSSLPGH	TAPVPLLIPF	TLNFTITNLH	YEENMQHPGS	
810	PGTSIVNLGT	SGIPPSLPET	TATGPLLIPF	TPNFTITNLQ	YEEDMRRTGS	
83	PGTPTVDLGT	SGTPVSKPGP	SAASPLLVPF	TLNFTITNLQ	YEEDMHRPGS	
81	PGTPTVDLGT	SGTPVSKPGP	SAASPLLIPF	TINFTITNLR	YEENMGHPGS	
44	PGTSTVYWAT	TGTPSSFPGH	TEPGPLLIPF	TNFTITNLH	YEENMQHPGS	
812	PGTSTVYWAT	TGTPSSFPGH	TEPGPLLIPF	TVNFTITNLR	YEENMHHPGS	
76	PDTSTMHLAT	SRTPASLSGP	TTASPLLVL	TINFTITNQR	YEENMHHPGS	

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

TABLE 4-continued

Amino Acid Sequence for a 800 bp Repeat in the CA125 Molecule
(SEQ ID NO: 22 thru SEQ ID NO: 35)

	151				200
79	RKFNTMERVL	QGLLSPIFKN	SSVGPLYSGC	RLTSLRPEKD	GAATGMDAVC
811	RKFNIMERVL	QGLLMPLFKN	TSVSSLYSGC	RLTLLRPEKD	GAATRVDVAVC
21	RKFNTTTERVL	QTLTGPMFKN	TSVGLLYSGC	RLTLLRSEKD	GAATGVDAIC
89	RKFNIMERVL	QGLLGPLEFKN	SSVGPLYSGC	RLISLRSEKD	GAATGVDAIC
85	RKFNIMERVL	QGLLNPIFKN	SSVGPLYSGC	RLTSLKPEKD	GAATGMDAVC
712	RKFNTTTERVL	QGLLKPLFKS	TSVGPLYSGC	RLTLLRPEKR	GAATGVDITC
86	RKFNTTTERVL	QGLLKPLFKS	TSVGPLYSGC	RLTLLRPEKR	GAATGVDITC
87	RKFNTTTERVL	QGLLKPLFKS	TSVGPLYSGC	RLTLLRPEKH	GAATGVDAIC
810	RKFNTMERVL	QGLLSPIFKN	SSVGPLYSGC	RLTSLRPEKD	GAATGMDAVC
83	RKFNTATERVL	QGLLSPIFKN	SSVGPLYSGC	RLTSLRPEKD	GAATGMDAVC
81	RKFNIMERVL	QGLLKPLFKN	TSVGPLYSGC	RLTLLRPPKD	GAATGVDAIC
44	RKFNTTTERVL	QGLLKPLFKN	TSVGPLYSGC	RLTLLRPEKH	EAATGVDITC
812	RKFNTTTERVL	QGLLRPVFKN	TSVGPLYSGC	RLTLLRPPKD	GAATKVDAIC
76	RKFNTTTERVL	QGLLRPVFKN	TSVGPLYSGC	RLTLLRPPKD	GAATKVDAIC
	201				250
79	LYHPNPKRPG	LDREQLYWEL	SQLTNHNITEL	GPYSLDRDSL	YVNGFTHQNS
811	TQRPDPKSPG	LDREQLYWEL	SQLTNGITEL	GPYTLDRHSL	YVNGFTHQSS
21	THRLDPKSPG	VDREQLYWEL	SQLTNGIKEL	GPYTLDRNSL	YVNGFTHWIP
89	THHLNPQSPG	LDREQLYWEL	SQMTNGIKEL	GPYTLDRNSL	YVNGFTHRSS
85	LYHPNPKRPG	LDREQLYWEL	SQLTNGIKEL	GPYTLDRNSL	YVNGFTHRSS
712	THRLDPLNPG	LDREQLYWEL	SKLTRGIIEL	GPYLLDRGSL	YVNGFTHRNF
86	THRLDPLNPG	LDREQLYWEL	SKLTRGIIEL	GPYLLDRGSL	YVNGFTHRNF
87	THRLDPKSPG	VDREQLYWEL	SQLTNGIKEL	GPYTLDRNSL	YVNGFTHWIP
810	LYHPNPKRPG	LDREQLY~~~	~~~~~	~~~~~	~~~~~
83	LYHPNPKRPG	LDREQLYWEL	SQLTNHNITEL	GPYSLDRDSL	YVNGFTHQSS
81	THRLDPKSPG	LNREQLYWEL	SKLTNDIEEL	GPYTLDRNSL	YVNGFTHQSS
44	THRVDPKSPG	LDREQLYWEL	SQLTNSIHEL	GPYTLDRDSL	YVNGFTHRSS
812	TYRPDPKSPG	LDREQLYWEL	SKLTNDIEEL	GPYTLDRNSL	YVNGFTHQSS
76	TYRPDPKSPG	LDREQLYWEL	SQLTNSITEL	GPYTQDRDSL	YVNGFTHRSS
	251				288
79	VPTTSTPGTS	TVYWATTGTP	SSFPGHT..E	PGPL~~~~	
811	MTTTRTPDTS	TMHLATS RTP	ASLSGPT..T	ASPLLIPF	
21	~~~~~	~~~~~	~~~~~	~~~~~	
89	GLTTSTPWTS	TVDLGTSGTP	SPVPSPT..T	AGPLLIPF	
85	VAPTSTPGTS	TVDLGTSGTP	SSLPSPT..T	AVPLLIPF	
712	VPITSTPGTS	TVHLGTSETP	SSLPRPI..V	PGPLLIPF	
86	VPITSTPGTS	TVHLGTSETP	SSLPRPI..V	PGPLLIPF	
87	VPTSSTPGTS	TVDLG.SGTP	SSLPSPT..T	AGPL~~~~	
810	~~~~~	~~~~~	~~~~~	~~~~~	
83	MTTTRTPDTS	TMHLATS RTP	ASLSGPT..T	ASPLLIPF	
81	VSTTSTPGTS	TVDLRTSGTP	SSLSSPTIMA	AGPLLIPF	
44	VPTTSTPGTS	TVHLATSGTP	SSLPGHT..A	PVPLLI~~	
812	VSTTSTPGTS	TVDLRTSGTP	SSLSSPTIMA	AGPLLIPF	
76	VPTTSIPGTS	AVHLETSGTP	ASLP~~~~~	~~~~~	

TABLE 5

Amino Acid Sequence for a 1200 bp Repeat in the CA125 Molecule
(SEQ ID NO: 36 thru SEQ ID NO: 46)

	1				50	
910	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 36)
99	ERVLHGLLTP	LFKNTRVGPL	YSGCRLTLLR	PEKQEAATGV	DTICTHRVDP	(SEQ ID NO: 37)
112	~~~~~	~~~~~GPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 38)
95	ERVLQGPLSP	IFKNSSVGPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 39)
71	~~~~~	~~~~~TSVGPL	YSGCRLTLLR	SEKDGAATGV	DAIYTHRLDP	(SEQ ID NO: 40)
78	~~~~~	~~~~~	~~~~~TLLR	PKKDGVAATGV	DAICTHRLDP	(SEQ ID NO: 41)
115	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKDGVAATRV	DAICTHRPDP	(SEQ ID NO: 42)
91	ERVLQGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP	(SEQ ID NO: 43)
92	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAAATGV	DTICTHRLDP	(SEQ ID NO: 44)
113	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PEKNGAATGM	DAICSHRLDP	(SEQ ID NO: 45)
711	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKHGAATGV	DAICTLRLDP	(SEQ ID NO: 46)
	51				100	
910	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST	
99	IGPGLDRERL	YWELSQTNS	ITELGPYTLD	RDSLYVNGFN	PWSSVPTTST	
112	KRPGLDREQL	YWELSQTNS	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST	
95	KRPGLDREQL	YWELSQTNS	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST	
71	KSPGVDREQL	YWELSQTNG	IKELGPYTLD	RNSLYVNGFT	HQTSAPNTST	
78	KSPGLNREQL	YWELSKLTND	IEELGPYTLD	RNSLYVNGFT	HQSSVSTTST	
115	KIPGLDRQQL	YWELSQTNS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTST	
91	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSMPTTST	
92	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST	
113	KSPGLNREQL	YWELSQTNS	IKELGPYTLD	RNSLYVNGFT	HRSSVAPTST	
711	TGPGLDRERL	YWELSQTNS	VTELGPYTLD	RDSLYVNGFT	HRSSVPTTST	
	101				150	
910	PGTSTVHLGT	SETPSSLPRP	IV..PGPLLV	PFTLNFTITN	LQYEEAMRHP	
99	PGTSTVHLAT	SGTPSSLPGH	TA..PVPLLI	PFTLNFTITN	LHYEENMQHP	
112	PGTSTVYWT	TGTPSSFPGH	T..EPGPLLI	PFTLNFTITN	LQYEEAMGHP	
95	PGTSTVYWT	TGTPSSFPGH	T..EPGPLLI	PFTLNFTITN	LQYEEAMGHP	
71	PGTSTVDLGT	SGTPSSLPRP	T..SAGPLLI	PFTLNFTITN	LRYEENMHHP	
78	PGTSTVDLRT	SGTPSSLSP	TIMAAGPLLI	PFTLNFTITN	LRYEENMHHP	
115	PGTFTVQPET	SETPSSLPGP	T..ATGPVLL	PFTLNFTIIN	LQYEEAMHRP	
91	PGTSTVDVGT	SGTPSSSPSP	T..TAGPLLM	PFTLNFTITN	LQYEEAMRRT	
92	PGTSTVHLGT	SETPSSLPRP	IV..PGPLLI	PFTLNFTITN	LQYEEAMGHP	
113	PGTSTVDLGT	SGTPSSLPRP	T..TAVPLLI	PFTLNFTITN	LQYEEAMHCP	
711	PGTSAVHLET	SGTPASLPGH	T..APGPLLI	PFTLNFTITN	LHYEENMQHP	
	151				200	
910	GSRKFNTTER	VLQGLLRPLF	KNTSVSSLYS	GCRLTLLRPE	KDGAATRVD	
99	GSRKFNTTER	VLQGLLKPLF	KNTSVGPLY	GCRLTLFKPE	KHEAATGVDA	
112	GSRKFNTES	VLQGLLTPLF	KNSSVGPLY	GCRLISLRSE	KDGAATGVDA	
95	GSRKFNTES	VLQGLLNPIF	KNSSVGPLY	GCRLTSLRPE	KDGAATGVDA	
71	GSRKFNTMER	VLQGLLKPLF	KSTSVGPLY	GCRLTLLRPE	KDGAATRVD	
78	GSRKFNTMER	VLQGLLMPLF	KNTSVSSLYS	GCRLTLLRPE	KDGAATRVD	
115	GSRKFNTTER	VLQGLLMPLF	KNTSVGPLY	GCRLTLLRPE	KQEAATGVDT	
91	GSRKFNTMES	VLQGLLKPLF	KNTSVGPLY	GCRLTLLRPE	KDGAATGVDA	
92	GSRKFNTES	VLQGLLKPLF	RNSSLEYLYS	GCRLTSLRPE	KDSSTMAVDA	

TABLE 5-continued

Amino Acid Sequence for a 1200 bp Repeat in the CA125 Molecule
(SEQ ID NO: 36 thru SEQ ID NO: 46)

113	GSRKFNTTER	VLQSLFGPMF	KNTSVGPLY	GCRLTLFRSE	KDGAATGVDA
711	GSRKFNTMER	VLQGCLVPCS	RNTNVGLLYS	GCRLTLLXXX	XXXXXXXXXX
	201				250
910	ACTYRPDEKS	PGLDREQLYW	ELSQLTHSIT	ELGPYTLDLV	SLYVNGFNPR
99	ICTLRLDPTG	PGLDRERLYW	ELSQLTNSVT	ELGPYTLDLD	SLYVNGFTHR
112	ICTHHLNPQS	PGLDREQLYW	QLSQMTNGIK	ELGPYTLDLD	SLYVNGFTHR
95	VCLYHPNPKR	PGLDREQLYC	ELSQLTHNIT	ELGPYSLDRD	SLYVNGFTHQ
71	ICTHRPDPKI	PGLDRQQLYW	ELSQLTHSIT	ELGPYTLDLD	SLYVNGFTQR
78	VCTHRPDEKS	PGLDRERLYW	KLSQLTHGIT	ELGPYTLDLD	SLYVNGFTHR
115	ICTHRLDPSE	PGLDREQLYW	ELSQLTNSIT	ELGPYTLDLD	SLYVNGFTHS
91	ICTHRLDPKS	PGLNREQLYW	ELSKLTNDIE	EVGPYTLDLD	SLYVNGFTHR
92	ICTHRPDPED	LGLDRERLYW	ELSNLTNGIQ	ELGPYTLDLD	SLYVNGFTHR
113	ICTHRLDPKS	PGVDREQLYW	ELSQLTNGIK	ELGPYTLDLD	SLYVNGFTHQ
711	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXGPYTLDLD	SLYVNGFTHR
	251				300
910	SSV.PTTSTP	GTSTVHLATS	GTPSSLPGHT	APVPLLIPFT	LNFTITNLQY
99	SSV.PTTSIP	GTSVHLETS	GTPASLPGHT	APGPLLIPFT	LNFTITNLQY
112	SL.GLTTSTP	WTSTVDLGTS	GTPSPVPSPT	TAGPLLIPFT	LNFTITNLQY
95	NS.VPTTSTP	GTSTVYWATT	GTPSSFPGHT	EPGPLLIPFT	LNFTITNLQY
71	SSV.PTTSTP	GTFTVQPETS	ETPSSLPGPT	ATGPVLLPFT	LNFTIINLQY
78	SSM.PTTSTP	GTSTVDVGTS	GTPSSSPSPT	TAGPLLMPFT	LNFTITNLQY
115	GVLCPPPSIL	GIFTVQPETF	ETPSSLPGPT	ATGPVLLPFT	LNFTIINLQY
91	SFVAP.TSTL	GTSTVDLGTS	GTPSSLPSPT	TGVPLLIPFT	LNFTITNLQY
92	SFM.PTTSTL	GTSTVDVGTS	GTPSSSPSPT	TAGPLLMPFT	LNFTITNLQY
113	TS.APNTSTP	GTSTVDLGTS	GTPSSLPSPT	SAGPLLVPFT	LNFTITNLQY
711	SSVAP.TSTP	GTSTVDLGTS	GTPSSLPSPT	TV.PLLVPFT	LNFTITNLQY
	301				350
910	EEDMRHPGSR	KFNTMERVLQ	GLLRPLFKNT	SIGPLYSSCR	LTLLRPEKDK
99	EEDMRRTGSR	KFNTMERVLQ	GLLKPLFKST	SVGPLYSGCR	LTLLRPEKRG
112	EENMGHPGSR	KFNIMERVLQ	GLLRPVFKNT	SVGPLYSGCR	LTLLRPEKDG
95	EEDMRRTGSR	KFNTMERVLQ	GLLKPLFKST	SVGPLYSGCR	LTLLRPEKHG
71	EEDMRHPGSR	KFNTTERVLQ	GLLKPLFKST	SVGPLYSGCR	LTLLRPEKHG
78	EEDMRRTGSR	KFNTMERVLQ	GLLKPLFKST	SVGPLYSGCR	LTLLRPEKHG
115	EEDMRHPGSR	KFNTTERVLQ	GLLMPLFKNT	SVGPLYSGCR	LTLLRPEKQE
91	EENMGHPGSR	KFNIMERVLQ	GLLMPLFKNT	SVSSLYSGCR	LTLLRPEKDG
92	EEDMRRTGSR	KFNTMESVLQ	GLLKPLFKNT	SVGPLYSGCR	LTLLRPEKDG
113	EEDMRRTGSR	KFNTMESVLQ	GLLKPLFKNT	SVGPLYSGCR	LTLLRPEKDG
711	GEDMRHPGSR	KFNTTERVLQ	GLLGPLFKNS	SVGPLYSGCR	LISLRSEKDG
	351				400
910	AATRVDAICT	HHPDPQSPGL	NREQLYWELS	QLTHGITEL~	~~~~~
99	AATGVDTICT	HRLDPLNPGL	DREQLYWELS	KLTRGIIELG	PYLLDRGSly
112	AATKVDAICT	YRPDPKSPGL	DREQLYWELS	QLTHSITELG	PYTLDSDSLY
95	AATGVDAICT	LRLDPTGPGL	DRERLYWELS	QLTNSVTELG	PYTLDSDSLY
71	AATGVDAICT	LRLDPTGPGL	DRERLYWELS	QLTNSITELG	PYTLDSDSLY
78	AATGVDAICT	LRLDPTGPGL	DRERLYWELS	QLTNSVTELG	PYTLDSDSLY

TABLE 5-continued

Amino Acid Sequence for a 1200 bp Repeat in the CA125 Molecule
(SEQ ID NO: 36 thru SEQ ID NO: 46)

115	AATGVDTICT	HRVDPIGPGL	DRERLYWELS	QLTNSITELG	PYTLD RDSLY
91	AATRVVAVCT	HRPDPKSPGL	DRERLYWKLS	QLTHGITELG	PYTLD RHSLY
92	AATGVDAICT	HRLDPKSPGL	NREQLYWELS	KLTDNIEELG	PYTLD RNSLY
113	AATGVDAICT	HRLDPKSPGL	NREQLYWELS	KL~~~~~	~~~~~
711	AATGVDAICT	HHLNPQSPGL	DREQLYWQLS	QVTNGIKELG	PYTLD RNSLY

	401		447
910	~~~~~	~~~~~	~~~~~
99	VNGFTHRNFV	PITSTPGTST	VHLGTSEIHP SLPRPI..VP GPL~~~~
112	VNGFTQRSSV	PTTSIPGTPT	VDLGTSGTPV SKPGPS..AA SP~~~~~
95	VNGFTHRSSV	PTTSIPGTSA	VHLETSGTPA SLPGHT..AP GPLL~~~~
71	VNGFNPWSSV	PTTSTPGTST	VHLATSGTPS SLPGHT..AP VPL~~~~~
78	VNGFTHRSSV	PTTSIPGTSA	VHLETSGTPA SLPGHT..AP GPLLIPF
115	VNGFNPWSSV	PTTSTPGTST	VHLATSGTPS SLPGHT..AP VPLLIPF
91	VNGFTHQSSM	TTTRTPDTST	MHLATSRTPA SLSGPT..TA SPLLI PF
92	VNGFTHQSSV	STTSTPGTST	VDPRTSGTPS SLSSPTIMAA GPLLI~~
113	~~~~~	~~~~~	~~~~~
711	VNGFTHRSSG	LTTSTPWTST	VDLGTSGTPS PVPSPT..TA GPLLI~~

TABLE 6

Amino Acid Sequence for a 9 Repeat Structure in the CA125 Molecule
(SEQ ID NO: 47)

ERVLOGLLKP	LERNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP
EDLGDRERL	YWELSNLTNG	IQELGPYTL	RNSLYVNGFT	HRSSMPTTST
PGTSTVDVGT	SGTPSSSPSP	TTAGPLLMPF	TLNFTITNLQ	YEEDMRRTGS
RKFNTMERVL	QGFLSPIFKN	SSVGPLYSGC	RLTSLRPEKD	GAATGM DAV
CLYHPNPKRP	GLDREQLYWE	LSQLTHNITE	LGPYSLDRDS	LYVNGFTHQN
SVPTTSTPGT	STVYWATTGT	PSSFPGHTEP	GPLLIPFTLN	FTITNLQYEE
NMGHPGSRKF	NITERVLQGL	LNPIFKNSSV	GPLYSGCRLT	SLRPEKDGAA
TGMDAVCLYH	PNPKRPGLDR	EQLYCELSQL	THNITELGPY	SLDRDSLYVN
GFTHQNSVPT	TSTPGTSTVY	WATTGTPSSF	PGHTEPGPLL	IPFTLNFTIT
NLQYEEDMRR	TGSRKFNTME	RVLOGLLKPL	FKSTSVGPLY	SGCRLTLLRP
EKHGAATGVD	AICTLRDPT	GPGLDRERLY	WELSOLTNV	TELGPYTLDR
DSLYVNGFTH	RSSVPTTSIP	GTSAVHLETS	GTPASLPGHT	APGPLLVPFT
LNFTITNLQY	EEDMRHPGSR	KFNTTTERVLQ	GLLKPLFKST	SVGPLYSGCR
LTLLRPEKRG	AATGVDITCT	HRLDPLNPGL	DREQLYWELS	KLTRGIELG
PYLLDRGSly	VNGFTHRNFT	PITSTPGTST	VHLGTSETPS	SLPRPIVPGP
LLIPFTLNFT	ITNLQYEENM	GHPGSRKFNI	TERVLOGLLK	PLFRNSSLEY
LYSGCRLASL	RPEKDSSAMA	VDAICTHRPD	PEDLGDRER	LYWELSNLTN
GIQELGPYTL	DRNSLYVNGF	THRSMPTTS	TPGTSTVDVG	TSCTPSSSPS
PTTAGPLLMP	FTLNFTITNL	QYEEDMRRTG	SRKFNTMESV	LQGLLKPLFK
NTSVGPLYSG	CRLTLLRPKK	DGAATGVDAI	CTHRLDPKSP	GLNREQLYWE
LSKLNDIEE	VGPYTLDRNS	LYVNGFTHRS	FVAPTSTLGT	STVDLGTSGT
PSSLPSPTTG	VPLLIPFTLN	FTITNLQYEE	NMGHPGSRKF	NIMERVLOGL
LSPIFKNSSV	GSLYSGCRLT	LLRPEKDGAA	TRVDAVCTHR	PDPKSPGLDR
ERLYWKLSQL	THGIELGPY	TLDRHSFYVN	GFTHQSSMTT	TRTPDTSTMH
LATSRTPASL	SGPTTASPLL	VLFTINFIT	NQRYEENMH	PGSRKFNTTE
RVLOGLLRPV	FKNTSVGPLY	SGCRLTLLRP	KKDGAATKVD	AICTYRPDPK
SPGLDREQLY	WELSOLTHSI	TELGPYTQDR	DSLYVNGFTH	RSSVPTTSIP
GTSAVHLETS	GTPASLP			

TABLE 7

cDNA Genbank Accession # AK024365 Encompasses Repeat Sequences (Repeats 1 & 2) Homologous to Two Repeats Shown in Table 6
(SEQ ID NO: 48)

```

MPLFKNTSVS SLYSGCRLTL LRPEKDGAAT RVDAVCTHRP DPKSPGLDRE
RLYWKLSQLT HGIIELGPYT LDRHSFYVNG FTHQSSMTT RT PDTSTMHL
ATSRTPASLS GPTTASPLLV LFTINFITN QRYEENMHHP GSRKFNTTER
VLQGLLRPVF KNTSVGPLY S GCRLTLLRPK KDGAATKVDA ICTYRPDPKS
PGLDREQLYW ELSQLTHSIT ELGPYTQDRD SLYVNGFTHR SSVPTTSIPG
TSAVHLETSG TPASLPGPSA ASPLLVLFTL NFFTITNLRYE ENMQHPGSRK
FNTTTERVLQG LLRSLEFKSTS VGPLYSGCRL TLLRPEKDGT ATGVDAICTH
HPDPKSPRLD REQLYWELSQ LTHNITELGH YALDNDSLFV NGFTHRSSVS
TTSTPGTPTV YLGASKTPAS IFGPSAASHL LILFTLNFTI TNLRYEENMW
PGSRKFNTTE RVLQGLLRPL FKNTSVGPLY SGSRLTLLRP EKDGEATGVD
AICTHRPDPT GPGLDREQLY LE LSQLTHSI TELGPYTLDR DS LYVNGFTH
RSSVPTTSTG VVSEEPFTLN FTINNLRMA DMGQPGSLKF NITDNVMKHL
LSPLFQRSSL GARYTGCRVI ALRSVKNGAE TRVDLLCTYL QPLSGPGLPI
KQVFHELSQL THGITRLGPY SLDKDSLYLN GYNEPGLDEP PTTPKPATTF
LPPLSEATTA MGYHLKTLTL NFFTISNLQYS PDMGKGSATF NSTEGLVQLHL
LRPLFQKSSM GPFYLGQCLI SLRPEKDGA TGVDTTCTYH PDPVGPGLDI
QQLYWELSQL THGVTQLGFY VLDRDSLFIN GYAPQNL SIR GEYQINFHIV
NWNLSNPDPT SSEYITLLRD IQDKVTTLYK GSQLHDTFRF CLVTNLTMDS
VLVTVKALFS SNLDPSLVEQ VF LDKTLNAS FHWLGSTYQL VDIHVTEMES
SVYQPTSSSS TQHFYLNFTI TNLPSYQDKA QPGTTNYQRN KRNIEDALNQ
LFRNSSIKSY FSDCQVSTFR SVPNRHHTGV DSLCNFSPLA RRVDRVAIYE
EFLRMTRNGT QLQNF TLD RS SVLV DGYS PN RNEPLTGNSD LPFWAVILIG
LAGLLGLITC LICGVLVTRR RRRKKEGEYNV QQQCPGYYS HLDLEDLQ

```

TABLE 8

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125
(SEQ ID NO: 49)

1 GAGAGGGTTC TGCAGGGTCT GCTCAAACCC TTGTTTCAGGA ATAGCAGTCT
51 GGAATACCTC TATTCAGGCT GCAGACTAGC CTCCTCAGG CCAGAGAAGG
101 ATAGCTCAGC CATGGCAGTG GATGCCATCT GCACACATCG CCCTGACCCCT
151 GAAGACCTCG GACTGGACAG AGAGCGACTG TACTGGGAGC TGAGCAATCT
201 GACAAATGGC ATCCAGGAGC TGGGCCCCCTA CACCCTGGAC CGGAACAGTC
251 TCTATGTCAA TGGTTTCACC CATCGAAGCT CTATGCCCAC CACCAGCACT
301 CCTGGGACCT CCACAGTGGG TGTGGGAACC TCAGGGACTC CATCCTCCAG
351 CCCAGCCCC ACGACTGCTG GCCCTCTCCT GATGCCGTTT ACCCTCAACT
401 TCACCATCAC CAACCTGCAG TACGAGGAGG ACATGCGTCG CACTGGCTCC
451 AGGAAGTTCA ACACCATGGA GAGGGTTCTG CAGGGTCCGC TTAGTCCCAT
501 ATTCAAGAAC TCCAGTGTG GCCCTCTGTA CTCTGGCTGC AGACTGACCT
551 CTCTCAGGCC CGAGAAGGAT GGGGCAGCAA CTGGAATGGA TGCTGTCTGC
601 CTCTACCACC CTAATCCCAA AAGACCTGGG CTGGACAGAG AGCAGCTGTA
651 CTGGGAGCTA AGCCAGCTGA CCCACAACAT CACTGAGCTG GGGCCCTACA
701 GCCTGGACAG GGACAGTCTC TATGTCAATG GTTTCACCCA TCAGAACTCT
751 GTGCCCACCA CCAGTACTCC TGGGACCTCC ACAGTGTACT GGGCAACCAC
801 TGGGACTCCA TCCTCCTTCC CCGGCCACAC AGAGCCTGGC CCTCTCCTGA
851 TACCATTAC GCTCAACTTC ACCATCACTA ACCTACAGTA TGAGGAGAAC
901 ATGGGTCACC CTGGCTCCAG GAAGTTCAAC ATCACGGAGA GGGTTCTGCA
951 GGGTCTGCTT AATCCCATTT TCAAGAACTC CAGTGTGGC CCTCTGTACT
1001 CTGGCTGCAG ACTGACCTCT CTCAGGCCCG AGAAGGATGG GGCAGCAACT
1051 GGAATGGATG CTGTCTGCCT CTACCACCCT AATCCCAAAA GACCTGGGCT
1101 GGACAGAGAG CAGCTGTACT GCGAGCTAAG CCAGCTGACC CACAACATCA
1151 CTGAGCTGGG CCCCTACAGC TTGGACAGGG ACAGTCTTTA TGTCAATGGT

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125
(SEQ ID NO: 49)

1201 TTCACCCATC AGAACTCTGT GCCCACCACC AGTACTCCTG GGACCTCCAC
1251 AGTGTACTGG GCAACCACTG GGACTCCATC CTCCTTCCCC GGCCACACAG
1301 AGCCTGGCCC TCTCCTGATA CCATTACCCC TCAACTTCAC CATCACCAAC
1351 CTGCAGTACG AGGAGGACAT GCGTCGCACT GGCTCCAGGA AGTTCAACAC
1401 CATGGAGAGG GTTCTGCAGG GTCTGCTCAA GCCCTTGTTT AAGAGCACCA
1451 GCGTTGGCCC TCTGTACTCT GGCTGCAGAC TGACCTTGCT CAGACCTGAG
1501 AAACATGGGG CAGCCACTGG AGTGGACGCC ATCTGCACCC TCCGCCTTGA
1551 TCCCACTGGT CCTGGACTGG ACAGAGAGCG GCTATACTGG GAGCTGAGCC
1601 AGCTGACCAA CAGCGTTACA GAGCTGGGCC CCTACACCCT GGACAGGGAC
1651 AGTCTCTATG TCAATGGCTT CACCCATCGG AGCTCTGTGC CAACCACCAG
1701 TATTCCTGGG ACCTCTGCAG TGCACCTGGA AACCTCTGGG ACTCCAGCCT
1751 CCCTCCCTGG CCACACAGCC CCTGGCCCTC TCCTGGTGCC ATTCACCCTC
1801 AACTTCACTA TCACCAACCT GCAGTATGAG GAGGACATGC GTCACCCTGG
1851 TTCCAGGAAG TTCAACACCA CGGAGAGAGT CCTGCAGGGT CTGCTCAAGC
1901 CCTTGTTCAA GAGCACCAGT GTTGGCCCTC TGTACTCTGG CTGCAGACTG
1951 ACCTTGCTCA GGCCTGAAAA ACGTGGGGCA GCCACCGGCG TGGACACCAT
2001 CTGCACTCAC CGCCTTGACC CTCTAAACCC TGGACTGGAC AGAGAGCAGC
2051 TATACTGGGA GCTGAGCAAA CTGACCCGTG GCATCATCGA GCTGGGCCCC
2101 TACCTCCTGG ACAGAGGCAG TCTCTATGTC AATGGTTTCA CCCATCGGAA
2151 CTTTGTGCCC ATCACCAGCA CTCCTGGGAC CTCCACAGTA CACCTAGGAA
2201 CCTCTGAAAC TCCATCCTCC CTACCTAGAC CCATAGTGCC TGGCCCTCTC
2251 CTGATACCAT TCACACTCAA CTTCAACATC ACTAACCTAC AGTATGAGGA
2301 GAACATGGGT CACCCTGGCT CCAGGAAGTT CAACATCACG GAGAGGGTTC
2351 TGCAGGGTCT GCTCAAACCC TTGTTGAGGA ATAGCAGTCT GGAATACCTC

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125
(SEQ ID NO: 49)

2401 TATTCAGGCT GCAGACTAAC CTCACTCAGG CCAGAGAAGG ATAGCTCAAC
 2451 CATGGCAGTG GATGCCATCT GCACACATCG CCCTGACCCT GAAGACCTCG
 2501 GACTGGACAG AGAGCGACTG TACTGGGAGC TGAGCAATCT GACAAATGGC
 2551 ATCCAGGAGC TGGGCCCTTA CACCTTGGAC CGGAACAGTC TCTATGTCAA
 2601 TGGTTTCACC CATCGAAGCT CTATGCCCAC CACCAGCACT CCTGGGACCT
 2651 CCACAGTGGA TGTGGGAACC TCAGGGACTC CATCCTCCAG CCCCAGCCCC
 2701 ACGACTGCTG GCCCTCTCCT GATGCCGTTT ACCCTCAACT TCACCATCAC
 2751 CAACCTGCAG TACGAGGAGG ACATGCGTCG CACTGGCTCC AGGAAGTTCA
 2801 ACACCATGGA GAGTGTCTTG CAGGGTCTGC TCAAGCCCTT GTTCAAGAAC
 2851 ACCAGTGTG GCCCTCTGTA CTCTGGCTGC AGATTGACCT TGCTCAGGCC
 2901 CAAGAAAGAT GGGGCAGCCA CTGGAGTGGA TGCCATCTGC ACCCACCGCC
 2951 TTGACCCCAA AAGCCCTGGA CTCAACAGGG AGCAGCTGTA CTGGGAGTTA
 3001 AGCAAAGTGA CCAATGACAT TGAAGAGGTG GGCCCTACA CCTTGGACAG
 3051 GAACAGTCTC TATGTCAATG GTTTCACCCA TCGGAGCTTT GTGGCCCCCA
 3101 CCAGCACTCT TGGGACCTCC ACAGTGGACC TTGGGACCTC AGGGACTCCA
 3151 TCCTCCCTCC CCAGCCCCAC AACAGGTGTT CCTCTCCTGA TACCATTAC
 3201 ACTCAACTTC ACCATCACTA ACCTACAGTA TGAGGAGAAC ATGGGTCACC
 3251 CTGGCTCCAG GAAGTCAAC ATCATGGAGA GGGTCTGCA GGGTCTGCTT
 3301 ATGCCCTTGT TCAAGAACAC CAGTGTGAGC TCTCTGTACT CTGGTTGCAG
 3351 ACTGACCTTG CTCAGGCCTG AGAAGGATGG GGCAGCCACC AGAGTGGTTG
 3401 CTGTCTGCAC CCATCGTCCT GACCCCAAAA GCCCTGGACT GGACAGAGAG
 3451 CGGCTGTACT GGAAGCTGAG CCAGCTGACC CACGGCATCA CTGAGCTGGG
 3501 CCCCTACACC CTGGACAGGC ACAGTCTCTA TGTCAATGGT TTCACCCATC
 3551 AGAGCTCTAT GACGACCACC AGAACTCCTG ATACCTCCAC AATGCACCTG

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125
(SEQ ID NO: 49)

3601 GCAACCTCGA GAACTCCAGC CTCCCTGTCT GGACCTACGA CCGCCAGCCC
3651 TCTCCTGATA CCATTCACAA TTAAC TTCAC CATCACTAAC CTGCGGTATG
3701 AGGAGAACAT GCATCACCTT GGCTCTAGAA AGTTTAACAC CACGGAGAGA
3751 GTCCTTCAGG GTCTGCTCAG GCCTGTGTTC AAGAACACCA GTGTTGGCCC
3801 TCTGTACTCT GGCTGCAGAC TGACCTTGCT CAGGCCCAAG AAGGATGGGG
3851 CAGCCACCAA AGTGGATGCC ATCTGCACCT ACCGCCCTGA TCCCAAAGC
3901 CCTGGACTGG ACAGAGAGCA GCTATACTGG GAGCTGAGCC AGCTAACCCA
3951 CAGCATCACT GAGCTGGGCC CCTACACCCT GGACAGGGAC AGTCTCTATG
4001 TCAATGGTTT CACACAGCGG AGCTCTGTGC CCACCACTAG CATTCCTGGG
4051 ACCCCACAG TGGACCTGGG AACATCTGGG ACTCCAGTTT CTAAACCTGG
4101 TCCCTCGGCT GCCAGCCCTC TCCTGGTGCT ATCACTCTC AACTTCACCA
4151 TCACCAACCT GCGGTATGAG GAGAACATGC AGCACCTGG CTCCAGGAAG
4201 TTCAACACCA CGGAGAGGGT CCTTCAGGGC CTGCTCAGGT CCCTGTTCAA
4251 GAGCACCAGT GTTGGCCCTC TGTACTCTGG CTGCAGACTG ACTTTGCTCA
4301 GGCCTGAAAA GGATGGGACA GCCACTGGAG TGGATGCCAT CTGCACCCAC
4351 CACCCTGACC CCAAAGCCC TAGGCTGGAC AGAGAGCAGC TGTATTGGGA
4401 GCTGAGCCAG CTGACCCACA ATATCACTGA GCTGGGCCAC TATGCCCTGG
4451 ACAACGACAG CCTCTTTGTC AATGGTTTCA CTCATCGGAG CTCTGTGTCC
4501 ACCACCAGCA CTCCTGGGAC CCCACAGTG TATCTGGGAG CATCTAAGAC
4551 TCCAGCCTCG ATATTTGGCC CTTGAGCTGC CAGCCATCTC CTGATACTAT
4601 TCACCCTCAA CTTACCATC ACTAACCTGC GGTATGAGGA GAACATGTGG
4651 CCTGGCTCCA GGAAGTTCAA CACTACAGAG AGGGTCCTTC AGGGCCTGCT
4701 AAGGCCCTTG TTCAAGAACA CCAGTGTGG CCCTCTGTAC TCTGGCTCCA
4751 GGCTGACCTT GCTCAGGCCA GAGAAAGATG GGAAGCCAC CGGAGTGGAT

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125
(SEQ ID NO: 49)

4801 GCCATCTGCA CCCACCGCCC TGACCCACACA GGCCCTGGGC TGGACAGAGA
 4851 GCAGCTGTAT TTGGAGCTGA GCCAGCTGAC CCACAGCATC ACTGAGCTGG
 4901 GCCCCTACAC ACTGGACAGG GACAGTCTCT ATGTCAATGG TTTCACCCAT
 4951 CGGAGCTCTG TACCCACCAC CAGCACCGGG GTGGTCAGCG AGGAGCCATT
 5001 CACACTGAAC TTCACCATCA ACAACCTGCG CTACATGGCG GACATGGGCC
 5051 AACCCGGCTC CCTCAAGTTC AACATCACAG ACAACGTCAT GAAGCACCTG
 5101 CTCAGTCCTT TGTTCAGAG GAGCAGCCTG GGTGCACGGT ACACAGGCTG
 5151 CAGGGTCATC GCACTAAGGT CTGTGAAGAA CGGTGCTGAG ACACGGGTGG
 5201 ACCTCCTCTG CACCTACCTG CAGCCCCCTCA GCGGCCCAGG TCTGCCTATC
 5251 AAGCAGGTGT TCCATGAGCT GAGCCAGCAG ACCCATGGCA TCACCCGGCT
 5301 GGGCCCCTAC TCTCTGGACA AAGACAGCCT CTACCTTAAC GGTTACAATG
 5351 AACCTGGTCT AGATGAGCCT CCTACAATC CCAAGCCAGC CACCACATTC
 5401 CTGCCTCCTC TGTCAGAAGC CACAACAGCC ATGGGGTACC ACCTGAAAGAC
 5451 CCTCACACTC AACTTCACCA TCTCCAATCT CCAGTATTCA CCAGATATGG
 5501 GCAAGGGCTC AGCTACATTC AACTCCACCG AGGGGGTCCT TCAGCACCTG
 5551 CTCAGACCCT TGTTCAGAA GAGCAGCATG GGCCCTTCT ACTTGGGTG
 5601 CCAACTGATC TCCCTCAGGC CTGAGAAGGA TGGGGCAGCC ACTGGTGTGG
 5651 ACACCACCTG CACCTACCAC CCTGACCCTG TGGGCCCCGG GCTGGACATA
 5701 CAGCAGCTTT ACTGGGAGCT GAGTCAGCTG ACCCATGGTG TCACCCAAT
 5751 GGGCTTCTAT GTCCTGGACA GGGATAGCCT CTCATCAAT GGCTATGCAC
 5801 CCCAGAATTT ATCAATCCGG GCGAGTACC AGATAAATTT CCACATTGTC
 5851 AACTGGAACC TCAGTAATCC AGACCCACA TCCTCAGAGT ACATCACCTT
 5901 GCTGAGGGAC ATCCAGGACA AGGTCACCAC ACTCTACAAA GGCAGTCAAC
 5951 TACATGACAC ATTCCGCTTC TGCCTGGTCA CCAACTTGAC GATGGACTCC

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125
(SEQ ID NO: 49)

6001 GTGTTGGTCA CTGTCAAGGC ATTGTTCTCC TCCAATTTGG ACCCCAGCCT
6051 GGTGGAGCAA GTCTTTCTAG ATAAGACCCT GAATGCCTCA TTCCATTGGC
6101 TGGGCTCCAC CTACCAAGTTG GTGGACATCC ATGTGACAGA AATGGAGTCA
6151 TCAGTTTATC AACCAACAAG CAGCTCCAGC ACCCAGCACT TCTACCCGAA
6201 TTTCACCATC ACCAACCTAC CATATTCCCA GGACAAAGCC CAGCCAGGCA
6251 CCACCAATTA CCAGAGGAAC AAAAGGAATA TTGAGGATGC GCTCAACCAA
6301 CTCTTCCGAA ACAGCAGCAT CAAGAGTTAT TTTTCTGACT GTCAAGTTTC
6351 AACATTGAGG TCTGTCCCCA ACAGGCACCA CACCGGGGTG GACTCCCTGT
6401 GTAATTCTC GCCACTGGCT CGGAGAGTAG ACAGAGTTGC CATCTATGAG
6451 GAATTTCTGC GGATGACCCG GAATGGTACC CAGCTGCAGA ACTTCACCTT
6501 GGACAGGAGC AGTGTCTTGT TGGATGGGTA TTCTCCCAAC AGAAATGAGC
6551 CCTTAACTGG GAATTCTGAC CTTCCCTTCT GGGCTGTCAT CTTTCATCGGC
6601 TTGGCAGGAC TCCTGGGACT CATCACATGC CTGATCTGCG GTGTCCTGGT
6651 GACCACCCGC CGGCGGAAGA AGGAAGGAGA ATACAACGTC CAGCAACAGT
6701 GCCCAGGCTA CTACCAAGTCA CACCTAGACC TGGAGGATCT GCAATGACTG
6751 GAACTTGCCG GTGCCTGGGG TGCCTTTCCC CCAGCCAGGG TCCAAAGAAG
6801 CTTGGCTGGG GCAGAAATAA ACCATATTGG TCG

TABLE 9

Complete Amino Acid Sequence for 13 Repeats Contiguous with the Carboxy
Terminus of CA125 (SEQ ID NO: 50)

1

ERVLOGLLKP LFRNSSLEYL YSGCRLASLR PEKDSSAMAV DAICTHRPDP

EDLGLDRERL YWELSNLTNG IQELGPYTL D RNSLYVNGFT HRSSMPTTST

PGTSTVDVGT SGT PSSSPSP TTAGPLLMPF TLNFTITNLQ YEEDMRRTGS

2

RKFNTMERVL QGPLSPIFKN SSVGPLYSGC RLTS LRPEKD GAATGMDAVC

LYHPNPKRPG LDREQLYWEL SQLTHNITEL GPYSLDRDSL YVNGFTHQNS

VPTTSTPGTS TVYWATTGTP SSFPGHTEPG PLLIPFTLNF TITNLQYEEN

3

MGHPGSRKFN ITERVLOGLL NPIFKNSSVG PLYSGCRLTS LRPEKDGAAT

GMDAVCLYHP NPKRPGLDRE QLYCELSQLT HNITELGPYS LDRDSLYVNG

FTHQNSVPTT STPGTSTVYW ATTGTPSSFP GHTEPGPLLI PFTLNFTITN

4

LQYEEDMRRT GSRKFNTMER VLQGLLKPLF KSTSVGPLYG GCRLTLLRPE

KHGAATGVDA ICTLRDPTG PGLDRERLYW ELSQLTNSVT ELGPYTLDRD

SLYVNGFTHR SSVPTTSIPG TSAVHLETSG TPASLPGHATA PGPLLVPFTL

NFTITNLQYE EDMRHPGSRK FNTTERVLQ LKPLFKSTS VGPLYSGCRL

5

TLLRPEKRG A TGVDITICHT RLDPLNPGLD REQLYWELSK LTRGIIELGP

YLLDRGSLYV NGFTHRNFVP ITSTPGTSTV HLGTS ETPSS LPRPIVPGPL

LIPFTLNFTI TNLQYEENMG HPGSRKFNT ERVLOGLLKP LFRNSSLEYL

6

YSGCRLASLR PEKDSSAMAV DAICTHRPDP EDLGLDRERL YWELSNLTNG

IQELGPYTL D RNSLYVNGFT HRSSMPTTST PGTSTVDVGT SGT PSSSPSP

TTAGPLLMPF TLNFTITNLQ YEEDMRRTGS RKFNTMESVL QGLLKPLFKN

7

TSVGPLYSGC RLTLRPPKD GAATGVDAIC THRLDPKSPG LNREQLYWEL

SKLTNDIEEV GPYTLDRNSL YVNGFTHRSF VAPTSTLGTS TVDLGTS GTP

SSLPSPTTG V PLLIPFTLNF TITNLQYEEN MGHPGSRKFN IMERVLOGLL

8

SPIFKNSSVG SLYSGCRLTL LRPEKDGAAT RVDVCTHRP DPKSPGLDRE

RLYWKLSQLT HGIIELGPYT LDRHSFYVNG FTHQSSMTT RTPDTSTMHL

ATSRTPASLS GPTTASPLLV LFTINFTITN QRYEENMHHP GSRKFNTTER

TABLE 9-continued

Complete Amino Acid Sequence for 13 Repeats Contiguous with the Carboxy
Terminus of CA125 (SEQ ID NO: 50)

9

VLQGLLRPVF KNTSVGPLY GCRLTLLRPK KDGAATKVDA ICTYRPDPKS
 PGLDREQLYW ELSQLTHSIT ELGPYTQDRD SLVNGFTHR SSVPTTSIPG
 TSAVHLETSG TPASLPGPSA ASPLLVLFTL NFTITNLRYE ENMQHPGSRK
 10
 ENTTERVLQG LLRSLEFKSTS VGPLYSGCRL TLLRPEKDGT ATGVDAICTH
 HPDPKSPRLD REQLYWELSQ LTHNITELGH YALDNDSLFV NGFTHRSSVS
 TTSTPGTPTV YLGASKTPAS IFGPSAASHL LILFTLNFTI TNLRYEENMW
 11
 PGRKFNTE RVLQGLLRPL FKNTSVGPLY SGSRLTLLRP EKDGEATGVD
AICTHRPDPT GPGLDREQLY LELSQLTHSI TELGPYTLDR DSLVNGFTH
 RSSVPTTSTG VVSEEPFTLN FTINNLRMA DMGQPGSLKF NITDNVMKHL
 12
 LSPLFQRSSL GARYTGCRVI ALRSVKNGAE TRVDLLCTYL QPLSGPGLPI
 KQVFHELSQQ THGITRLGPY SLDKDSLYLN GYNEPGLDEP PTPKPATTF
 LPPLSEATTA MGYHLKTLTL NFTISNLQYS PDMGKSATF NSTEGLVQHL
 13
 LRPLFQKSSM GPFYLGCOLI SLRPEKDGA TGVDTTCTYH PDPVGPGLDI
 QQLYWELSQL THGVTQLGFY VLDKDSLFIN GYAPQNLIR GEYQINFHIV
 NWNLSNPDPPT SSEYITLLRD IQDKVTTLYK GSQLHDTFRF CLVTNLTMDL
 VLVTVKALFS SNLDPSLVEQ VFLDKTLNAS FHWLGSTYQL VDIHVTEMES
 SVYQPTSSSS TQHFYLNFTI TNLPSQDKA QPGTTNYQRN KRNIEDALNQ
 LFRNSSIKSY FSDCQVSTFR SVPNRHHTGV DSLCNFSPLA RRVDRAIYE
 EFLRMTRNGT QLQNFSLDRS SVLVDGYSPN RNEPLTGNSD LPFWAVILIG
 LAGLLGLITC LICGVLVTTR RRRKEGEYNV QQCPGGYQS HLDLEDLQ

TABLE 10A

5' Primer Sequence for End of the Open Reading Frame for Contig #32 of Chromosome 19 Cosmid AC008734 (SEQ ID NO: 51), Primer Sequence from within the Repeat Region (SEQ ID NO: 52, 3 Primer Sets Synthesized to Piece Together Entire Open Reading Frame in Contig #32 (SEQ ID NOS: 53 thru 58), Primers to Cosmid No. AC008734 for Contig #32 (SEQ ID NOS: 59 and 60), Sense Primer Sequence (supplied by Ambion) (SEQ ID NO: 61), Anti-Sense Primer Sequence for CA125 (SEQ ID NO: 62), and 5' Sense Primer Sequence (from Ambion) (SEQ ID NO: 63) and Anti-Sense Primer Specific to CA125 (SEQ ID NO: 64)

(SEQ ID NO: 51) (5'-CAGCAGAGACCAGCACGAGTACTC-3')

(SEQ ID NO: 52) (5'-TCCACTGCCATGGCTGAGCT-3')

Primer Sets

(SEQ ID NO: 53) (Set 1) 5'-CCAGCACAGCTCTTCCCAGGAC-3'
 (SEQ ID NO: 54) 5'-GGAATGGCTGAGCTGACGTCTG-3')

(SEQ ID NO: 55) (Set 2) 5'-CTTCCCAGGACAACCTCAAGG-3'
 (SEQ ID NO: 56) 5'-GCAGGATGAGTGAGCCACGTG-3')

(SEQ ID NO: 57) (Set 3) 5'-GTCAGATCTGGTGACCTCACTG-3'
 (SEQ ID NO: 58) 5'-GAGGCACTGGAAAGCCCAGAG-3')

(SEQ ID NO: 59) 5'-CTGATGGCATTATGGAACACATCAC-3'
 (SEQ ID NO: 60) 5'-CCCAGAACGAGAGACCAGTGAG-3')

(SEQ ID NO: 61) 5'-GCTGATGGCGATGAATGAACACTG-3'

(SEQ ID NO: 62) 5'-CCCAGAACGAGAGACCAGTGAG-3'

(SEQ ID NO: 63) 5'-CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG-3'
 (SEQ ID NO: 64) 5'-CCTCTGTGTGCTGCTTCATTGGG-3'

TABLE 10B

Sense and Anti-Sense Primers Used to Order the CA125 Carboxy Terminal Domain
(SEQ. ID NO: 303 and SEQ ID NO: 304, respectively)

(SEQ ID NO: 303) 5'-GGACAAGGTCACCACACTCTAC-3'
(SEQ ID NO: 304) 5'-GCAGATCCTCCAGGTCTAGGTGTG-3'

TABLE 10C

Sense and Anti-Sense Primers Used to Amplify Overlapping Sequences
in the Repeat Domain
(SEQ ID NO: 305 and SEQ ID NO: 306, respectively)

(SEQ ID NO: 305) 5' GTC TCT ATG TCA ATG GTT TCA CCC-3'
(SEQ ID NO: 306) 5'-TAG CTG CTC TCT GTC CAG TCC-3'

TABLE 11

5' Sense Primer 1 Sequence and 3' Antisense Primer 2
(SEQ ID NO: 65 and SEQ ID NO: 66, respectively), and
Nucleotide and Amino Acid Sequences of the CA125 Repeat Expressed in *E. coli*
(SEQ ID NO: 67 and SEQ ID NO: 68, respectively)

(SEQ ID NO: 65) 5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3'

(SEQ ID NO: 66) 5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC -3'

(SEQ ID NO: 67)

```

1  ATGAGAGGAT CGCATCACCA TCACCATCAC GGATCCATGG GCCACACAGA
51  GCCTGGCCCT CTCCTGATAC CATTCACTTT CAACTTTACC ATCACCAACC
101  TGCATTATGA GGAAAACATG CAACACCCTG GTTCCAGGAA GTTCAACACC
151  ACGGAGAGGG TTCTGCAGGG TCTGCTCAAG CCCTTGTTCA AGAACACCAG
201  TGTGAGCCCT CTGTACTCTG GCTGCAGACT GACCTTGCTC AGACCTGAGA
251  AGCATGAGGC AGCCACTGGA GTGGACACCA TCTGTACCCA CCGCGTTGAT
301  CCCATCGGAC CTGGACTGGA CAGAGAGCGG CTATACTGGG AGCTGAGCCA
351  GCTGACCAAC AGCATCACAG AGCTGGGACC CTACACCCTG GACAGGGACA
401  GTCTCTATGT CAATGGCTTC AACCCTCGGA GCTCTGTGCC AACCACCAGC
451  ACTCCTGGGA CCTCCACAGT GCACCTGGCA ACCTCTGGGA CTCCATCCTC
501  CCTGCCT

```

(SEQ ID NO: 68)

```

M R G S H H H H H G S M G H T E P G P L L I P F T F N F T I T N L
H Y E E N M Q H P G S R K F N T T E R V L Q G L L K P L F K N T S V
G P L Y S G C R L T L L R P E K H E A A T G V D T I C T H R V D P I
G P G L D R E R L Y W E L S Q L T N S I T E L G P Y T L D R D S L Y
V N G F N P R S S V P T T S T P G T S T V H L A T S G T P S S L P

```

TABLE 12

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 thru SEQ ID NO: 80)

(SEQ ID NO: 69)

ERVLQGLLGP MEKNTSVGLL YSGCRLTLR PKKDGAATKV DAICTYRDPD
 KSPGLDREQL YWELSQLTHS ITELGPYTL DSDLYVNGFT QRSSVPTTSI
 PGTPVDLGT SGTPVSKPGP SAASPLLIPF TINFTITNLR YEENMGHPGS
 RKFNIMERVL QGLLKPLFKN TSVGPLYSGC RLTLRPPKD GAATGVDAIC
 THRLDPKSPG LNREQLYWEL SKLTNDIEEL GPYTLDNRSL YVNGFTHQSS
 VSTTSTPGTS TVDLRTSGTP SSLSSPTIMA AGPLLIPFTI NFTITNLYE
 ENMHHPGSRK FNTMERVLQG LLMPLEKNTS VSSLYSGCRL TLLRPEKDKA
ATRVDAVCTH RDPKSPGLD RERLYWKLSQ LTHGITELGP YTLDNRSLYV
 NGFTHRSSMP TTSTPGTSTV DVGTSCTPSS SPSPTTAGPL LMPFTLNFTI
 TNLQYEEDMR RTGSRKFNTM ERVLQGLLKP LEKSTSVGPL YSGCRLTLR
PEKHGAATGV DAICTRLRDP TGPGLDRERL YWELSQLTNS VTELGPYTL
 RSDLYVNGFT HRSSVPTTSI PGTSVHLET SGTPASLPKH TAPGPLLIPF
 TLNFTITNLH YEENMQHPGS RKFNTMERVL QGCLVPCSRN TNVGLLYSGC
RLTLRXEKX XAATXVDXXC XXXXDPXXPG LDREXLYWEL SXLTXIXEL
 GPYTLDNRSL YVNGFTHRSS VAPTSTPGTS TVDLGTSGTP SSLPSPTTVP
 LLVPFTLNFT ITNLQGEDM RHPGSRKFNT TERVLQGLLG PLFKNSSVGP
LYSGCRLISL RSEKDGAATG VDAICTHHLN PQSPGLDREQ LYWQLSQVTN
 GIKELGPYTL DRNSLYVNGF THRSSGLTTS TPWTSTVDLG TSGTPSPVPS
 PTTAGPLLI

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 70)

QGLLGPMFKN TSVGLLYSGC RLTLLRPEKR GAATGVD TIC THR L D P L N P G
 LDREQLYWEL SKLTRGIIEI GPYLLDRGSL YVNGFTHRNF VPITSTPGTS
 TVHLGTSETP SSLPRPIVPG PLLVPFTLNF TITNLQYEEA MRHPGSRKFN
 TTERVLQGLL RPLFKNTSVS SLYSGCRLTL LRPEKDGAAT RVDAACTYRP
 DPKSPGLDRE QLYWELSQLT HSITELGPYT LDRVSLYVNG FNPRSSVPTT
 STPGTSTVHL ATSGTPSSLP GHTAPVPLLI PFTLNFTITN LQYEEDMRHP
 GSRKFNTMER VLQGLLRPLF KNTSIGPLYS SCRLTLLRPE KDKAATRVDA
ICTHHPDPOS PGLNREQLYW ELSQLTHGIT ELGPYTLDRD SLYVDGFTHW
 SPIPTTSTPG TSIVNLGTSG IPPSLPETTA TGPLLIPFTP NFTITNLQYE
 EDMRRTGSRK FNTMERVLQG LLSPIFKNSS VGPLYSGCRL TSLRPEKDGA
ATGMDAVCLY HPNPKRPGLD REQLY

(SEQ ID NO: 71)

ERVLQGLLKP LFKSTSVGPI YSGCRLTLR PEKDG VATRV DAICTHRPDP
 KIPGLDRQQL YWELSQTLS ITELGPYTLD RDSLYVNGFT QRSSVPTTST
 PGTFTVQPET SETPSSLPGP TATGPVLLPF TLNFTIINLQ YEEDMHRPGS
 RKFNTERVL QGLLMPLFKN TSVGPLYSGC RLTLLRPEKQ EAATGVD TIC
 THRLDPSEPG LDREQLYWEL SQLTNSITEL GPYTLD RDSL YVNGFTHSGV
 LCPPPSILGI FTVQPETFET PSSLPGTAT GPVLLPFTLN FTIINLQYEE
 DMHRPGSRKF NTERVLQGL LTPLFKNTSV GPLYSGCRLT LLRPEKQEAA
TGVD TIC THR VDPGPGGLDR ERLYWELSQT TNSITELGPY TLD RDSL YVN
 GENPWSSVPT TSTPGTSTVH LATSGTPSSL PGHTAPVPLL IPFTLNFTIT

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

NLHYEENMQH PGSRKFNTE RVLQGLLKPL FKSTSVGPLY SGCRLTLLRP
EKHGAATGVD AICTHRLDPK SPGVDREQLY WELSQLTNGI KELGPYTLDR
 NSLYVNGFTH WIPVPTSSTP GTSTVDLGSG TPSSLPSPTT AGPL

(SEQ ID NO: 72)

TSVGPLYSGC RLTLLRSEKD GAATGVDAIY THRLDPKSPG VDREQLYWEL
 SQLTNGIKEL GPYTLDRNSL YVNGETHQTS APNTSTPGTS TVDLGTSGTP
 SSLPSPTSAG PLLIPFTINF TITNLRYEEN MHPGSRKFN TMERVLOGLL
 KPLFKSTSVG PLYSGCRLTL LRPEKDG VAT RVDAICTHRP DPKIPGLDRQ
 QLYWELSQLT HSITELGPYT LDRDSLYVNG FTQRSSVPTT STPGTFTVQP
 ETSETPSSLP GPTATGPVLL PFTLNFTIIN LQYEEDMHRP GSRKENTTER
 VLQGLLKPLF KSTSVGPLY GCRLTLLRPE KHGAATGVDA ICTLRDPTG
 PGLDRERLYW ELSQLTNSIT ELGPYTLDRD SLYVNGFNPW SSVPTTSTPG
 TSTVHLATSG TPSSLPGHTA PVPL

(SEQ ID NO: 73)

ERVLQGLLKPL LFKSTSVGPL YSGCRLTLLR PEKRGAAATGV DTICTHRLDP
 LNPGLDREQL YWELSKLTRG IIELGPYLLD RDSLYVNGFT HRSSVPTTSI
 PGTSVHLET SGTPASLP GH TAPGPLLVPF TLNFTITNLQ YEEDMRHGPS
 RKFNTERVL QGLLKPLFKS TSVGPLYSGC RLTLLRPEKR GAATGVD TIC
 THRLDPLNPG LDREQLYWEL SKLTRGIIEI GPYLLDRGSL YVNGFTHRNF
 VPITSTPGTS TVHLGTSETP SSLPRPIVPG PLLIPF

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 74)

ERVLOGLLRP VFKNTSVGFL YSGCRLTLR PKKDGAATKV DAICTYRPDP
KSPGLDREQL YWELSQLTHS ITELGPYTL DRSLYVNGFT QRSSVPTTSI
PGTPTVDLGT SGTPVSKPGP SAASPLLVPF TLNFTITNLQ YEEDMHRPGS
RKFNATERVL QGLLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGMDAVC
LYHPNPKRPG LDREQLYWEL SQLTHNITEL GPYSLDRDSL YVNGFTHQSS
MTTTRTPDTS TMHLATS RTP ASLSGPTTAS PLLIPF

(SEQ ID NO: 75)

ERVLOGLLKP LFKSTSVGFL YSGCRLTLR PEKRGAAATGV DTICTHRLDP
LNPGLDREQL YWELSKLTRG IIELGPYLLD RGSLYVNGFS RQSSMTTTRT
PDTSTMHLAT SRTPASLSGP TTASPLLIPF TLNFTITNLQ YEENMGHPGS
RKFNIMERVL QGLLNPIFKN SSVGPLYSGC RLTSLKPEKD GAATGMDAVC
LYHPNPKRPG LDREQLYWEL SQLTHGIKEL GPYTLDNRSL YVNGFTHRSS
VAPTSTPGTS TVDLGTSGTP SSLPSPTTAV PLLIPF

(SEQ ID NO: 76)

ERVLOGLLKP LFRNSSLEYL YSGCRLASLR PEKDSSAMAV DAICTHRPDP
EDLGLDRERL YWELSNLTNG IQELGPYTL DRSLYVNGFT HRSSGLTST
PWTSTVDLGT SGTPSPVPSP TTAGPLLIPF TLNFTITNLQ YEENMGHPGS
RKFNIMERVL QGLLMPLFKN TSVSSLYSGC RLTLRPEKD GAATRVDAVC
TQRPDPKSPG LDRERLYWKL SQLTHGITEL GPYTLDRHSL YVNGLTHQSS
MTTTRTPDTS TMHLATS RTP ASLSGPTTAS PLLIPF

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 77)

ERVLQGLLSP ISKNSSVGPL YSGCRLTSLR PEKDGAATGM DAVCLYHPNP
 KRPGLDREQL YWELSQLTHN ITELGPYSLD RDSLYVNGFT HQNSVPTTST
 PGTSTVYWAT TGTSSFPFGH TEPGPLLIPF TVNFTITNLR YEENMHHPGS
 RKFNTERVL QGLLRPVFKN TSVGPLYSGC RLTLLRPKKD GAATKVDAIC
 TYRDPKSPG LDREQLYWEL SKLTNDIEEL GPYTLDRNSL YVNGFTHQSS
 VSTTSTPGTS TVDLRTSGTP SSLSSEPTIMA AGPLLIPF

(SEQ ID NO: 78)

ERVLHGLLTP LFKNTRVGPL YSGCRLTLR PEKQEAATGV DTICTHRVDP
 IGPGLDRERL YWELSQLTNS ITELGPYTL D RDSLYVNGFN PWSSVPTTST
 PGTSTVHLAT SGTSSSLPGH TAPVPLLIPF TLNFTITNLH YEENMQHPGS
 RKFNTERVL QGLLKPLFKN TSVGPLYSGC RLTLFKPEKH EAATGVDAIC
 TLRLDPTGPG LDRQLYWELS QLTNSVTELG PYTLDRDSLY VNGFTHRSSV
 PTTIPGTSA VHLETSGTPA SLPGHTAPGP LLIPFTLNFT ITNLQYEEDM
 RRTGSRKENT MERVLOGLLK PLFKSTSVGP LYSGCRLTLL RPEKRGAAATG
VDTICTHRLD PLNPGLDREQ LYWELSKLTR GIIELGPYLL DRGSLYVNGF
 THRNFPVITS TPGTSTVHLG TSETPSSLPR PIVPGPLLIP FTINFTITNL
 RYEENMHHPG SRKFNIMERV LQLLGPLFK NSSVGPLYSG CRLISLRSEK
DGAATGVDAI CTHHLNPQSP GLDREQLYWQ LSQMTNGIKE LGPYTLDRNS
 LYVNGFTHRS SGLTTSTPWT STVDLGTSGT PSPVPSPTTA GPLLIPF

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 79)

GPLYSGCRLT SLRPEKDGA TGM DAVCLYH PNPKRPG LDR EQLYWELSQL
 THNITELGPY SLDRDSLYVN GFTHQNSVPT TSTPGTSTVY WATTGTPSSF
 PGHTEPGPLL IPFTLNFTIT NLQYEENMGH PGSRKFNITE SVLQGLLTPL
 FKNSSVGPLY SGCRLISLRS EKDGAATGVD AICTHHLNPQ SPGLDREQLY
 WQLSQMTNGI KELGPYTLD RSLYVNGFTH RSLGLTTSTP WTSTVDLGTS
 GTPSPVPSPT TAGPLLIPT LNFTITNLQY EENMGHPGSR KFNIMERVLQ
 GLLRPVFKNT SVGPLYSGCR LTLRPKKDG AATKVDAICT YRPDPKSPGL
 DREQLYWELS QLTHSITELG PYTLDRDSLY VNGFTQRSSV PTTSIPGTPT
 VDLGTSGTPV SKPGPSAASP

(SEQ ID NO: 80)

QLYWELSKLT NDIEELGPYT LDRNSLYVNG FTHQSSVSTT STPGTSTVDL
 RTSGTPSSL SPTIMAAGPL LIPFTLNFTI TNLQYEENMG HPGSRKFNIM
 ERVLQGLLGP MFKNTSVGLL YSGCRLTLR PEKNGAATGM DAICSHRLDP
 KSPGLNREQL YWELSQLTHG IKELGPYTLD RNSLYVNGFT HRSSVAPTST
 PGTSTVDLGT SGTPSSLPS TTA VPLLIPF TLNFTITNLK YEEDMHCPGS
 RKFNTERVL QSLFGPMFKN TSVGPLYSGC RLTLRSEKD GAATGVDAIC
 THRLDPKSLG VDREQLYWEL SQLTNGIKEL GPYTLD RNSL YVNGFTHQTS
 APNTSTPGTS TVDLGTSGTP SSLPSPTSAG PLLVPFTLNF TITNLQYEED
 MRRTGSRKFN TMESVLQGLL KPLFKNTSVG PLYSGCRLTL LRPEKDGAAT
 GVDAICTHRL DPKSPGLNRE QLYWELSKL

TABLE 13

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

1 CAGAGAGCGT TGAGCTGGGA ACAGTGACAA GTGCTTATCA AGTTCCTTCA
51 CTCTCAACAC GGTGACAAG AACTGATGGC ATTATGGAAC ACATCACAAA
101 AATACCCAAT GAAGCAGCAC ACAGAGGTAC CATAAGACCA GTCAAAGGCC
151 CTCAGACATC CACTTCGCCT GCCAGTCCTA AAGGACTACA CACAGGAGGG
201 ACAAAAAGAA TGGAGACCAC CACCACAGCT TTGAAGACCA CCACCACAGC
251 TTTGAAGACC ACTTCCAGAG CCACCTTGAC CACCAGTGTC TATACTCCCA
301 CTTTGGGAAC ACTGACTCCC CTCAATGCAT CAAGGCAAAT GGCCAGCACA
351 ATCCTCACAG AAATGATGAT CACAACCCCA TATGTTTTCC CTGATGTTCC
401 AGAAACGACA TCCTCATTGG CTACCAGCCT GGGAGCAGAA ACCAGCACAG
451 CTCTTCCCAG GACAACCCCA TCTGTTCTCA ATAGAGAATC AGAGACCACA
501 GCCTCACTGG TCTCTCGTTC TGGGGCAGAG AGAAGTCCGG TTATTCAAAC
551 TCTAGATGTT TCTTCTAGTG AGCCAGATAC AACAGCTTCA TGGGTTATCC
601 ATCCTGCAGA GACCATCCCA ACTGTTTCCA AGACAACCCC CAATTTTTTC
651 CACAGTGAAT TAGACACTGT ATCTTCCACA GCCACCAGTC ATGGGGCAGA
701 CGTCAGCTCA GCCATTCCAA CAAATATCTC ACCTAGTGAA CTAGATGCAC
751 TGACCCCACT GGTCACTATT TCGGGGACAG ATACTAGTAC AACATTCCCA
801 AACTGACTA AGTCCCCACA TGAAACAGAG ACAAGAACCA CATGGCTCAC
851 TCATCCTGCA GAGACCAGCT CAACTATTCC CAGAACAATC CCCAATTTTT
901 CTCATCATGA ATCAGATGCC ACACCTTCAA TAGCCACCAG TCCTGGGGCA
951 GAAACCAGTT CAGCTATTCC AATTATGACT GTCTCACCTG GTGCAGAAGA

TABLE 13-continued

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

1001	TCTGGTGACC	TCACAGGTCA	CTAGTTCTGG	GACAGACAGA	AATATGACTA
1051	TTCCAAC TTT	GACTCTTTCT	CCTGGTGAAC	CAAAGACGAT	AGCCTCATTA
1101	GTCACCCATC	CTGAAGCACA	GACAAGTTCTG	GCCATTCCAA	CTTCAACTAT
1151	CTCGCCTGCT	GTATCACGGT	TGGTGACCTC	AATGGTCACC	AGTTTGGCGG
1201	CAAAGACAAG	TACAACTAAT	CGAGCTCTGA	CAAAC TCCCC	TGGTGAACCA
1251	GCTACAACAG	TTTCATTGGT	CACGCATCCT	GCACAGACCA	GCCCAACAGT
1301	TCCCTGGACA	ACTTCCATTT	TTTTCCATAG	TAAATCAGAC	ACCACACCTT
1351	CAATGACCAC	CAGTCATGGG	GCAGAATCCA	G TTCAGCTGT	TCCAAC TCCA
1401	ACTGTTTCAA	CTGAGGTACC	AGGAGTAGTG	ACCCCTTTGG	TCACCAGTTC
1451	TAGGGCAGTG	ATCAGTACAA	CTATTCCAAT	TCTGACTCTT	TCTCCTGGTG
1501	AACCAGAGAC	CACACCTTCA	ATGGCCACCA	GTCATGGGGA	AGAAGCCAGT
1551	TCTGCTATTC	CAACTCCAAC	TGTTTCACCT	GGGGTACCAG	GAGTGGTGAC
1601	CTCTCTGGTC	ACTAGTTCTA	GGGCAGTGAC	TAGTACA ACT	ATTCCAATTC
1651	TGACTTTTTTC	TCTTGGTGAA	CCAGAGACCA	CACCTTCAAT	GGCCACCAGT
1701	CATGGGACAG	AAGCTGGCTC	AGCTGTTCCA	ACTGTTTTAC	CTGAGGTACC
1751	AGGAATGGTG	ACCTCTCTGG	TTGCTAGTTC	TAGGGCAGTA	ACCAGTACAA
1801	CTCTTCCAAC	TCTGACTCTT	TCTCCTGGTG	AACCAGAGAC	CACACCTTCA
1851	ATGGCCACCA	GTCATGGGGC	AGAAGCCAGC	TCAACTGTTC	CAACTGTTTC
1901	ACCTGAGGTA	CCAGGAGTGG	TGACCTCTCT	GGTCACTAGT	TCTAGTGGAG
1951	TAAACAGTAC	AAGTATTCCA	ACTCTGATTC	TTTCTCCTGG	TGAACTAGAA

TABLE 13-continued

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

2001 ACCACACCTT CAATGGCCAC CAGTCATGGG GCAGAAGCCA GCTCAGCTGT
2051 TCCAACCTCCA ACTGTTTCAC CTGGGGTATC AGGAGTGGTG ACCCCTCTGG
2101 TCACTAGTTC CAGGGCAGTG ACCAGTACAA CTATTCCAAT TCTAACTCTT
2151 TCTTCTAGTG AGCCAGAGAC CACACCTTCA ATGGCCACCA GTCATGGGGT
2201 AGAAGCCAGC TCAGCTGTTC TAACTGTTTC ACCTGAGGTA CCAGGAATGG
2251 TGACCTCTCT GGTCAGTAGT TCTAGAGCAG TAACCAGTAC AACTATTCCA
2301 ACTCTGACTA TTTCTTCTGA TGAACCAGAG ACCACAACCT CATTGGTCAC
2351 CCATTCTGAG GCAAAGATGA TTTCAGCCAT TCCAACCTTA GCTGTCTCCC
2401 CTAAGTGACA AGGGCTGGTG ACTTCACTGG TCACTAGTTC TGGGTCAGAG
2451 ACCAGTGCCT TTTCAAATCT AACTGTTGCC TCAAGTCAAC CAGAGACCAT
2501 AGACTCATGG GTCGCTCATC CTGGGACAGA AGCAAGTTCT GTTGTTCCTA
2551 CTTTGACTGT CTCCACTGGT GAGCCGTTTA CAAATATCTC ATTGGTCACC
2601 CATCCTGCAG AGAGTAGCTC AACTCTTCCC AGGACAACCT CAAGGTTTTT
2651 CCACAGTGAA TTAGACACTA TGCCTTCTAC AGTCACCAGT CCTGAGGCAG
2701 AATCCAGCTC AGCCATTTCA ACTACTATTT CACCTGGTAT ACCAGGTGTG
2751 CTGACATCAC TGGTCACTAG CTCTGGGAGA GACATCAGTG CAACTTTTCC
2801 AACAGTGCCT GAGTCCCCAC ATGAATCAGA GGCAACAGCC TCATGGGGTTA
2851 CTCATCCTGC AGTCACCAGC ACAACAGTTC CCAGGACAAC CCCTAATTAT
2901 TCTCATAGTG AACCAGACAC CACACCATCA ATAGCCACCA GTCCTGGGGC
2951 AGAAGCCACT TCAGATTTTC CAACAATAAC TGTCTCACCT GATGTACCAG

TABLE 13-continued

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

3001	ATATGGTAAC	CTCACAGGTC	ACTAGTTCTG	GGACAGACAC	CAGTATAACT
3051	ATTCCAACCTC	TGACTCTTTC	TTCTGGTGAG	CCAGAGACCA	CAACCTCATT
3101	TATCACCTAT	TCTGAGACAC	ACACAAGTTC	AGCCATTCCA	ACTCTCCCTG
3151	TCTCCCCTGG	TGCATCAAAG	ATGCTGACCT	CACTGGTCAT	CAGTTCTGGG
3201	ACAGACAGCA	CTACAACTTT	CCCAACACTG	ACGGAGACCC	CATATGAACC
3251	AGAGACAACA	GCCATACAGC	TCATTCATCC	TGCAGAGACC	AACACAATGG
3301	TTCCCAAGAC	AACTCCCAAG	TTTCCCATA	GTAAGTCAGA	CACCACACTC
3351	CCAGTAGCCA	TCACCAGTCC	TGGGCCAGAA	GCCAGTTCAG	CTGTTTCAAC
3401	GACAACTATC	TCACCTGATA	TGTCAGATCT	GGTGACCTCA	CTGGTCCCTA
3451	GTTCTGGGAC	AGACACCAGT	ACAACCTTCC	CAACATTGAG	TGAGACCCCA
3501	TATGAACCAG	AGACTACAGT	CACGTGGCTC	ACTCATCCTG	CAGAAACCAG
3551	CACAACGGTT	TCTGGGACAA	TTCCCAACTT	TTCCCATAGG	GGATCAGACA
3601	CTGCACCCTC	AATGGTCACC	AGTCCTGGAG	TAGACACGAG	GTCAGGTGTT
3651	CCAACTACAA	CCATCCCACC	CAGTATACCA	GGGGTAGTGA	CCTCACAGGT
3701	CACTAGTTCT	GCAACAGACA	CTAGTACAGC	TATTCCAACCT	TTGACTCCTT
3751	CTCCTGGTGA	ACCAGAGACC	ACAGCCTCAT	CAGCTACCCA	TCCTGGGACA
3801	CAGACTGGCT	TCACTGTTCC	AATTCGGACT	GTTCCCTCTA	GTGAGCCAGA
3851	TACAATGGCT	TCCTGGGTCA	CTCATCCTCC	ACAGACCAGC	ACACCTGTTT
3901	CCAGAACAAC	CTCCAGTTTT	TCCCATAGTA	GTCCAGATGC	CACACCTGTA
3951	ATGGCCACCA	GTCCTAGGAC	AGAAGCCAGT	TCAGCTGTAC	TGACAACAAT

TABLE 13-continued

Amino Terminal Nucleotide Sequence (SEQ ID NO: 81)					
<hr/>					
4001	CTCACCTGGT	GCACCAGAGA	TGGTGACTTC	ACAGATCACT	AGTTCTGGGG
4051	CAGCAACCAG	TACAACTGTT	CCAACTTTGA	CTCATTCTCC	TGGTATGCCA
4101	GAGACCACAG	CCTTATTGAG	CACCCATCCC	AGAACAGGGA	CAAGTAAAAC
4151	ATTCCTGCT	TCAACTGTGT	TTCCTCAAGT	ATCAGAGACC	ACAGCCTCAC
4201	TCACCATTAG	ACCTGGTGCA	GAGACTAGCA	CAGCTCTCCC	AACTCAGACA
4251	ACATCCTCTC	TCTTCACCCT	ACTTGTA ACT	GGAACCAGCA	GAGTTGATCT
4301	AAGTCCA ACT	GCTTCACCTG	GTGTTTCTGC	AAAAACAGCC	CCACTTTCCA
4351	CCCATCCAGG	GACAGAGACC	AGCACAA TGA	TTCCA ACTTC	AACTCTTTCC
4401	CTTGGTTTAC	TAGAGACTAC	AGGCTTACTG	GCCACCAGCT	CTTCAGCAGA
4451	GACCAGCACG	AGTACTCTAA	CTCTGACTGT	TTCCCCTGCT	GTCTCTGGGC
4501	TTTCCAGTGC	CTCTATAACA	ACTGATAAGC	CCCAA ACTGT	GACCTCCTGG
4551	AACACAGAAA	CCTCACCATC	TGTA ACTTCA	GTTGGACCCC	CAGAATTTTC
4601	CAGGACTGTC	ACAGGCACCA	CTATGACCTT	GATACCATCA	GAGATGCCAA
4651	CACCACCTAA	AACCAGTCAT	GGAGAAGGAG	TGAGTCCAAC	CACTATCTTG
4701	AGAACTACAA	TGGTTGAAGC	CACTAATTTA	GCTACCACAG	GTTCCAGTCC
4751	CACTGTGGCC	AAGACAACAA	CCACCTTCAA	TACACTGGCT	GGAAGCCTCT
4801	TTACTCCTCT	GACCACACCT	GGGATGTCCA	CCTTGGCCTC	TGAGAGTGTG
4851	ACCTCAAGAA	CAAGTTATAA	CCATCGGTCC	TGGATCTCCA	CCACCAGCAG
4901	TTATAACCGT	CGGTACTGGA	CCCCTGCCAC	CAGCACTCCA	GTGACTTCTA
4951	CATTCTCCCC	AGGGATTTC	ACATCCTCCA	TCCCCAGCTC	CACAGCAGCC

TABLE 13-continued

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

5001 ACAGTCCCAT TCATGGTGCC ATTCACCCTC AACTTCACCA TCACCAACCT
5051 GCAGTACGAG GAGGACATGC GGCACCCTGG TTCCAGGAAG TTCAACGCCA
5101 CAGAGAGAGA ACTGCAGGGT CTGCTCAAAC CCTTGTTTCAG GAATAGCAGT
5151 CTGGAATACC TCTATTTCAGG CTGCAGACTA GCCTCACTCA GGCCAGAGAA
5201 GGATAGCTCA GCCATGGCAG TGGATGCCAT CTGCACACAT CGCCCTGACC
5251 CTGAAGACCT CGGACTGGAC AGAGAGCGAC TGTACTGGGA GCTGAGCAAT
5301 CTGACAAATG GCATCCAGGA GCTGGGCCCC TACACCCTGG ACCGGAACAG
5351 TCTCTATGTC AATGGTTTCA CCCATCGAAG CTCTATGCCC ACCACCAGCA
5401 CTCCTGGGAC CTCCACAGTG GATGTGGGAA CCTCAGGGAC TCCATCCTCC
5451 AGCCCCAGCC CCACG

TABLE 14

Amino Terminal Protein Sequence
(SEQ ID NO: 82)

1 ESVLEGTVTS AYQVPSLSTR LTRTDGIMEH ITKIPNEAAH RGTIRPVKGP
51 QTSTSPASPK GLHTGGTKRM ETTTALKTT TTALKTTSRA TLTTSVYTPT
101 LGTLTPLNAS RQMASTILTE MMITTPYVFP DVPETTSSLA TSLGAETSTA
151 LPRTTPSVLN RESETTASLV SRSGAERSPV IQTLDVSSSE PDTTASWVIH
201 PAETIPTVSK TTPNFFHSEL DTVSSTATSH GADVSSAIPT NISPSELDAL
251 TPLVTISGTD TSTTFPTLTK SPHETETRTT WLTHPAETSS TIPRTIPNFS
301 HHESDATPSI ATSPGAETSS AIPIMTVSPG AEDLVTSQVT SSGTDRNMTI
351 PTLTLSPGEP KTIASLVTHP EAQTSSAIPT STISPAVSRL VTSMVTSLAA
401 KTSTTNRALT NSPGEPATTV SLVTHPAQTS PTVPWTSIF FHSKSDTTPS
451 MTTSHGAESS SAVPTPTVST EVPGVVTPLV TSSRAVISTT IPILTLSPGE
501 PETTPSMATS HGEEASSAIP TPTVSPGVPG VVTSLVTSR AVTSTTIPIIL
551 TFSLGEPETT PSMATSHGTE AGSAVPTVLP EVPGMVTSLV ASSRAVTSTT
601 LPILTLSPGE PETTPSMATS HGAEASSTVP TVSPEVPGVV TSLVTSSSGV
651 NSTSIPTLIL SPGELETPS MATSHGAEAS SAVPTPTVSP GVSQVVTPLV
701 TSSRAVTSTT IPILTLSSSE PETTPSMATS HGVEASSAVL TVSPEVPGMV
751 TSLVTSSRAV TSTTIPTLTI SSDEPETTTS LVTHSEAKMI SAIPTLAVSP
801 TVQGLVTSLV TSSGSETSAF SNLTVASSQP ETIDSWVAHP GTEASSVVPT
851 LTVSTGEPFT NISLVTHPAE SSSTLPRTTS RFSHSELDTM PSTVTSPEAE
901 SSSAISTTIS PGIPGVLTSL VTSSGRDISA TFPTVPESPH ESEATASWVT

TABLE 14-continued

Amino Terminal Protein Sequence (SEQ ID NO: 82)					
<hr/>					
951	HPAVTSTTVP	RTTPNYSHSE	PDTTPSIATS	PGAEATSDFP	TITVSPDVDP
1001	MVTSQVTSSG	TDTSITIPTL	TLSSGEPETT	TSFITYSETH	TSSAIPTLPV
1051	SPGASKMLTS	LVISSGTDST	TTFPTLTETP	YEPETTAIQL	IHPAETNTMV
1101	PRTTPKFSS	KSDTTLPVAI	TSPGPEASSA	VSTTTISPDM	SDLVTSLVPS
1151	SGTDTSTTFP	TLSETPYEPE	TTATWLTHPA	ETSTTVSGTI	PNFSHRGSDT
1201	APSMVTSPGV	DTRSGVPTTT	IPPSIPGVVT	SQVTSSATDT	STAIPTLTPS
1251	PGEPELTASS	ATHPGTQTGF	TVPIRTVPSS	EPDTMASWVT	HPPQTSTPVS
1301	RTTSSFSHSS	PDATPVMATS	PRTEASSAVL	TTISPGAPEM	VTSQITSSGA
1351	ATSTTVPTLT	HSPGMPETTA	LLSTHPRTET	SKTFPASTVF	PQVSETTASL
1401	TIRPGAETST	ALPTQTTSSL	FLLVLTGTSR	VDLSPTASPG	VSAKTAPLST
1451	HPGTETSTMI	PTSTLSLGLL	ETTGLLATSS	SAETSTSTLT	LTVSPAUSGL
1501	SSASITTDKP	QTVTSWNTET	SPSVTSVGPP	EFRTVTGTT	MTLIPSEMPT
1551	PPKTSHGEGV	SPTTILRTTM	VEATNLATG	SSPTVAKTTT	TFNTLAGSLF
1601	TPLTTPGMST	LASESVTSRT	SYNHRSWIST	TSSYNRRYWT	PATSTPVTST
		*			
1651	FSPGISTSSI	PSSTAATVPF	MVPFTLNFTI	TNLQYEEDMR	HPGSRKFNAT
1701	ERELQGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP
1751	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSMPTTST
1801	PGTSTVDVGT	SGTPSSSPSP	T		

TABLE 15

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 83)

1 GCCACAGTCC CATTTCATGGT GCCATTTCACC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCGGCACCC TGGTTCAGG AAGTTCAACG
101 CCACAGAGAG AGAACTGCAG GGTCTGCTCA AACCTTGTT CAGGAATAGC
151 AGTCTGGAAT ACCTCTATTC AGGCTGCAGA CTAGCCTCAC TCAGGCCAGA
201 GAAGGATAGC TCAGCCATGG CAGTGGATGC CATCTGCATA CATCGCCCTG
251 ACCCTGAAGA CCTCGGACTG GACAGAGAGC GACTGTACTG GGAGCTGAGC
301 AATCTGACAA ATGGCATCCA GGAGCTGGGC CCCTACACCC TGGACCGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG AAGCTCTATG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGATGTGG GAACCTCAGG GACTCCATCC
451 TCCAGCCCCA GCCCCACG

(SEQ ID NO: 84)

1 GCTGCTGGCC CTCTCCTGAT GCCGTTTCACC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCCTCGCAC TGGCTCCAGG AAGTTCAACA
101 CCATGGAGAG TGTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC
151 AGTGTGGGCC CTCTGTACTC TGGCTGCAGA TTGACCTTGC TCAGGCCCAA
201 GAAAGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGCCTTG
251 ACCCCAAAAG CCCTGGACTC AACAGGGAGC AGCTGTACTG GGAGCTAAGC
301 AAACTGACCA ATGACATTGA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTGTG TCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGATCTCA GAACCTCAGG GACTCCATCC

TABLE 15- continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

451 TCCCTCTCCA GCCCCACAAT TATG

(SEQ ID NO: 85)

1 GCTGCTGGCC CTCTCCTGGT ACCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAT GGGGAGGACA TGGGTCACCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG GGTCTGCAG GGTCTGCTTG GTCCCATATT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCTGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG
251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC GGCTGTACTG GGAGCTGAGC
301 CAACTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC
451 TCCCTCCCAA GCCCCGCA

(SEQ ID NO: 86)

1 ACTGCTGGCC CTCTCCTGGT GCTGTTACCC CTCAACTTCA CCATCACCAA
51 CCTGAAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA
101 CCACTGAGAG GGTCTGCAG ACTCTGCTTG GTCCTATGTT CAAGAACACC
151 AGTGTTGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GATCCCTGTG CCCACCAGCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTCAGGGAC TCCATCCTCC
451 CTCCCCAGCC CCACA

(SEQ ID NO: 87)

1 GCTGCTGGCC CTCTCCTGGT GCCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTGCGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC
451 TCCCTCCCCA GCCCTACA

(SEQ ID NO: 88)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACACC
151 AGTGTGCGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC
451 TCCCTCCCCA GCCCTACA

(SEQ ID NO: 89)

1 TCTGCTGGCC CTCTCCTGGT GCCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
101 CCACGGAGCG GGTCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGAATGGG GCAGCCACTG GAATGGATGC CATCTGCAGC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC AGCTGTACTG GGAGCTGAGC
301 CAGCTGACCC ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTCTGTG GCCCCACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC
451 TCCCTCCCCA GCCCCACA

(SEQ ID NO: 90)

1 ACAGCTGTTC CTCTCCTGGT GCCGTTACCC CTCAACTTTA CCATCACCAA
51 TCTGCAGTAT GGGGAGGACA TGCCTCACCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG GGTCTGCAG GGTCTGCTTG GTCCCTTGTT CAAGAACTCC
151 AGTGTCGGCC CTCTGTACTC TGGCTGCAGA CTGATCTCTC TCAGGTCTGA
201 GAAGGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCACCTTA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

251 ACCCTCAAAG CCCTGGACTG GACAGGGAGC AGCTGTACTG GCAGCTGAGC
301 CAGATGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACCGGAA
351 CAGTCTCTAC GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA
401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 91)

1 ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACA
101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATTTT CAAGAACTCC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCGA
201 GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA
251 ATCCCAAAG ACCTGGACTG GACAGAGAGC AGCTGTACTG GGAGCTAAGC
301 CAGCTGACCC ACAACATCAC TGAGCTGGGC CCCTACAGCC TGGACAGGGA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAACTCTGTG CCCACCACCA
401 GTACTCCTGG GACCTCCACA GTGTACTGGG CAACCACTGG GACTCCATCC
451 TCCTTCCCCG GCCACACA

(SEQ ID NO: 92)

1 GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA
51 CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCGA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA
251 ATCCCAAAG ACCTGGGCTG GACAGAGAGC AGCTGTACTG GGAGCTAAGC
301 CAGCTGACCC ACAACATCAC TGAGCTGGGC CCCTACAGCC TGGACAGGGA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAACTCTGTG CCCACCACCA
401 GTACTCCTGG GACCTCCACA GTGTACTGGG CAACCACTGG GACTCCATCC
451 TCCTTCCCCG GCCACACA

(SEQ ID NO: 93)

1 GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA
51 CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAGCATGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG
251 ATCCCATCGG ACCTGGACTG GACAGGGAGC GGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ACAGCATTAC CGAACTGGGA CCCTACACCC TGGACAGGGA
351 CAGTCTCTAT GTCAATGGCT TCAACCCTCG GAGCTCTGTG CCAACCACCA
401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 94)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACT CTCAACTTTA CCATCACCAA
51 CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAGCATGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG
251 ATCCCATCGG ACCTGGACTG NACAGNGAGC NGCTNCTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 95)

1 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGAATGGG GCAGCCACTG GAATGGATGC CATCTGCAGC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTC GACAGAGAGC AGCTGTACTG GGAGCTGAGC
301 CAGCTGACCC ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTCTGTG GCCCCACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC
451 TCCCTCCCCA GCCCCACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 96)

1 ACAGCTGTTT CTCTCCTGGT GCCGTTTACC CTCAACTTTA CCATCACCAA
51 TCTGCAGTAT GGGGAGGACA TGCCTCACCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCTTGTT CAAGAACTCC
151 AGTGTCGGCC CTCTGTACTC TGGCTGCAGA CTGATCTCTC TCAGGTCTGA
201 GAAGGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCACCTTA
251 ACCCTCAAAG CCCTGGACTG GACAGGGAGC AGCTGTACTG GCAGCTGAGC
301 CAGATGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACCGGAA
351 CAGTCTCTAC GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA
401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 97)

1 ACTGCTGGCC CTCTCCTGGT GCCATTACCC CTAAACTTCA CCATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACG
101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATATT CAAGAACTCC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCCGA
201 GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA
251 ATCCCAAAAG ACCTGGACTG GACAGAGAGC AGCTGTACTG GGAGCTAAGC
301 CAGCTGACCC ACAACATCAC TGAGCTGGGC CCCTACAGCC TGGACAGGGA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTATG ACGACCACCA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

401 GAACTCCTGA TACCTCCACA ATGCACCTGG CAACCTCGAG AACTCCAGCC
451 TCCCTGTCTG GACCTACG

(SEQ ID NO: 98)

1 ACCGCCAGCC CTCTCCTGGT GCTATTCACA ATCAACTGCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCCTCGCAC TGGCTCCAGG AAGTTCAACA
101 CCATGGAGAG TGTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA TTGACCTTGC TCAGGCCCAA
201 GAAAGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGCCTTG
251 ACCCCAAAAG CCCTGGACTC AACAGGGAGC AGCTGTACTG GGAGCTAAGC
301 AAACTGACCA ATGACATTGA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTGTG TCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGATCTCA GAACCTCAGG GACTCCATCC
451 TCCCTCTCCA GCCCCACAAT TATG

(SEQ ID NO: 99)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGAG GGTCTTACAG GGTCTGCTCA GGCCCTTGTT CAAGAACACC
151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGCCTGCACC TACCGCCCTG
251 ATCCCAAAAAG CCCTGGACTG GACAGAGAGC AACTATACTG GGAGCTGAGC
301 CAGCTAACCC ACAGCATCAC TGAGCTGGGA CCCTACACCC TGGACAGGGT

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru 145)

351 CAGTCTCTAT GTCAATGGCT TCAACCCTCG GAGCTCTGTG CCAACCACCA
401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 100)

1 GCCCCTGTCC CTCTCTTGAT ACCATTACCC CTCAACTTTA CCATCACCAA
51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
151 AGCGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG
251 ATCCCACTGG TCCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ACAGCGTTAC AGAGCTGGGC CCCTACACCC TGGACAGGGA
351 CAGTCTCTAT GTCAATGGCT TCACCCAGCG GAGCTCTGTG CCAACCACCA
401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC
451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 101)

1 GCCCCTGGCC CTCTCCTGGT GCCATTACCC CTCAACTTCA CTATCACCAA
51 CCTGCAGTAT GAGGTGGACA TGCCTCACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 AAAACGTGGG GCAGCCACCG GCGTGGACAC CATCTGCACT CACCGCCTTG
251 ACCCTCTAAA CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 AACTGACCC GTGGCATCAT CGAGCTGGGC CCCTACCTCC TGGACAGAGG
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAACTTTGTG CCCATCACCA
401 GCACTCCTGG GACCTCCACA GTACACCTAG GAACCTCTGA AACTCCATCC
451 TCCCTACCTA GACCCATA

(SEQ ID NO: 102)

1 GTGCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
51 CTTGCAGTAT GAGGAGGCCA TGCACACCC TGGCTCCAGG AAGTTCAATA
101 CCACGGAGAG GGTCTACAG GGTCTGCTCA GGCCCTTGTT CAAGAATACC
151 AGTATCGGCC CTCTGTACTC CAGCTGCAGA CTGACCTTGC TCAGGCCAGA
201 GAAGGACAAG GCAGCCACCA GAGTGGATGC CATCTGTACC CACCACCCTG
251 ACCCTCAAAG CCCTGGACTG AACAGAGAGC AGCTGTACTG GGAGCTGAGC
301 CAGCTGACCC ACGGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGGA
351 CAGTCTCTAT GTCGATGGTT TCACTCATTG GAGCCCCATA CCGACCACCA
401 GCACTCCTGG GACCTCCATA GTGAACCTGG GAACCTCTGG GATCCCACCT
451 TCCCTCCCTG AACTACA

(SEQ ID NO: 103)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGAG GGTTCTGCAG GGTCTGCTCA AACCCTTGTT CAGGAATAGC
151 AGTCTGGAAT ACCTCTATTC AGGCTGCAGA CTAGCCTCAC TCAGGCCAGA
201 GAAGGATAGC TCAGCCATGG CAGTGGATGC CATCTGCACA CATCGCCCTG

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru 145)

251 ACCCTGAAGA CCTCGGACTG GACAGAGAGC GACTGTACTG GGAGCTGAGC
 301 AATCTGACAA ATGGCATCCA GGAGCTGGGC CCCTACACCC TGGACCGGAA
 351 CAGTCTCTAC GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA
 401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
 451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 104)

1 ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
 51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGTTCCAGG AGGTTCAACA
 101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC
 151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
 201 GAAGCAAGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG
 251 ATCCCATCGG ACCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
 301 CAGCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA
 351 CAGTCTCTAT GTCAATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA
 401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
 451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 105)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCGA
 51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
 101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
 151 AGCGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG
251 ATCCCACTGG TCCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ACAGCGTTAC AGAGCTGGGC CCCTACACCC TGGACAGGGA
351 CAGTCTCTAT GTCAATGGCT TCACCCATCG GAGCTCTGTG CCAACCACCA
401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC
451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 106)

1 GCCCCTGGCC CTCTCCTGGT GCCATTACCC CTCAACTTCA CTATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCCTCACCC TGGTTCCAGG AAGTTCAGCA
101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC
151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCTG
251 ACCCCAAAAG CCCTGGACTG GACAGAGAGC GGCTGTACTG GAAGCTGAGC
301 CAGCTGACCC ACGGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGCA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTATG ACGACCACCA
401 GAACTCCTGA TACCTCCACA ATGCACCTGG CAACCTCGAG AACTCCAGCC
451 TCCCTGTCTG GACCTACG

(SEQ ID NO: 107)

1 ACCGCCAGCC CTCTCCTGGT GCTATTCACA ATTAAGTTCA CCATCACTAA
51 CCTGCGGTAT GAGGAGAACA TGCATCACCC TGGCTCTAGA AAGTTTAACA
101 CCACGGAGAG AGTCCTTCAG GGTCTGCTCA GGCCTGTGTT CAAGAACACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTGGGCC CTCTGTACTC TGGCTGCAGA CTGACCACGC TCAGGCCCAA
201 GAAGGATGGG GCAGCCACCA AAGTGGATGC CATCTGCACC TACCGCCCTG
251 ATCCCAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC
301 CAGCTAACCC ACAGCATCAC TGAGCTGGGC CCCTACACCC AGGACAGGGA
351 CAGTCTCTAT GTCAATGGCT TCACCCATCG GAGCTCTGTG CCAACCACCA
401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AACCTCTGG GACTCCAGCC
451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 108)

1 GCCCCTGGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CTATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCCTCACCC TGGTTCAGG AAGTTCAACA
101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
151 AGTGTGGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 AAAACGTGGG GCAGCCACCG GCGTGGACAC CATCTGCACT CACCGCCTTG
251 ACCCTCTAAA CCCAGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC
301 AAAGTGACCC GTGGCATCAT CGAGCTGGGC CCCTACCTCC TGGACAGAGG
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC
451 TCCCTCCCAA GCCCCGCA

(SEQ ID NO: 109)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCCT NGGNTCCAGG AAGTTCAACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

101 CCACNGAGAG GGTCTGCAG ACTCTGCTTG GTCCTATGTT CAAGAACACC
151 AGTGTTGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AACTATACTG GGAGCTGAGC
301 CAGCTGACCA ATGGCATTAA AGAACTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGGT TCACCCATTG GATCCCTGTG CCCACCAGCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTGAGGGAC TCCATCCTCC
451 CTCCCCAGCC CCACA

(SEQ ID NO: 110)

1 ACTGCTGGCC CTCTCCTGGT GCCGTTTACC CTCAACTTCA CCATCACCAA
51 CCTGAAGTAC GAGGAGGACA TGCATTGCCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG AGTCCTGCAG AGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC
451 TCCCTCCCCA GCCCTACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 111)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GATCCCTGTG CCCACCAGCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTGAGGGAC TCCATCCTCC
451 CTCCCCAGCC CCACA

(SEQ ID NO: 112)

1 ACTGCTGGCC CTCTCCTGGT GCCGTTACCC CTCAACTTCA CCATCACCAA
51 CCTGAAGTAC GAGGAGGACA TGCATTGCCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG AGTCCTGCAG AGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTGTTG
251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 113)

1 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGAATGGG GCAACCACTG GAATGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 114)

1 NCNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNNGANNACA TGCNNCNCNC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGAG GGTTCTGCAG GGTCTGCTCA AACCCTTGTT CAGGAATAGC
151 AGTCTGGAAT ACCTCTATTC AGGCTGCAGA CTAGCCTCAC TCAGGCCAGA
201 GAAGGATAGC TCAGCCATGG CAGTGGATGC CATCTGCACA CATCGCCCTG
251 ACCCTGAAGA CCTCGGACTG GACAGAGAGC GACTGTACTG GGAGCTGAGC
301 AATCTGACAA ATGGCATCCA GGAGCTGGGC CCCTACACCC TGGACCGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG AAGCTCTATG CCCACCACCA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

401 GCACTCCTGG GACCTCCACA GTGGATGTGG GAACCTCAGG GACTCCATCC
451 TCCAGCCCCA GCCCCACG

(SEQ ID NO: 115)

1 ACTGCTGGCC CTCTCCTGAT ACCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAT GGGGAGGACA TGGGTCACCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCATATT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCTGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG
251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC GGCTGTACTG GGAGCTGAGC
301 CAACTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC
451 TCCCTCCCAA GCCCCGCA

(SEQ ID NO: 116)

1 ACTGCTGGCC CTCTCCTGGT GCTGTTACCC CTCAACTTCA CCATCACCAA
51 CCTGAAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA
101 CCACTGAGAG GGTCCTGCAG ACTCTGCTTG GTCCTATGTT CAAGAACACC
151 AGTGTTGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 117)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGAG AGTCCTTCAG GGTCTGCTCA GGCCTGTGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCCAA
201 GAAGGATGGG GCAGCCACCA AAGTGGATGC CATCTGCACC TACCGCCCTG
251 ATCCCAAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC
301 CAGCTAACCC ACAGCATCAC TGAGCTGGGC CCCTACACCC AGGACAGGGA
351 CAGTCTCTAT GTCAATGGCT TCACCCATCG GAGCTCTGTG CCAACCACCA
401 GTATTCTGG GACCTCTGCA GTGCACCTGG AAACCACTGG GACTCCATCC
451 TCCTTCCCCG GCCACACA

(SEQ ID NO: 118)

1 GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA
51 CCTGCGTTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAGCAGGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru 145)

251 ATCCCATCGG ACCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA
351 CAGTCTCTAT GTCGATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA
401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451 CCCCTGCCTG GCCACACA

(SEQ ID NO: 119)

1 GCCCCTGTCC CTCTCTTGAT ACCATTACCC CTCAACTTTA CCATCACCGA
51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
151 AGCGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG
251 ATCCCACTGG TCCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
301 CAGCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA
351 CAGTCTCTAT GTCAATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA
401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 120)

1 ACTGCTGGCC CTCTCCTGGT GCCGTTACCC CTCAACTTCA CCATCACCAA
51 CCTGAAGTAC GAGGAGGACA TGCATTGCCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG AGTCCTGCAG AGTCTGCATG GTCCCATGTT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 121)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG AAGCTCTATG CCCACCACCA
401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC
451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 122)

1 GCCCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CTATCACCAA
51 CCTGCAGTAT GAGGAGGACA TCGTCACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
 201 AAAACGTGGG GCAGCCACCG GCGTGGACAC CATCTGCACT CACCGCCTTG
 251 ACCCTCTAAA CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
 301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
 351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
 401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
 451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 123)

1 NNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
 51 CCTGCANTAN GNGGANNACA TGCNNCNCN NGGNTCCAGG AAGTTCAACA
 101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNNTNTT CAAGAACNCC
 151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
 201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
 251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
 301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
 351 CAGTCTCTAT GTCAATGGTT TTCACCCTCG GAGCTCTGTG CCAACCACCA
 401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
 451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 124)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA
 51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

101 CCACGGAGCG GGTCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACA
151 AGTGTGGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGAATGGG GCAGCCACTG GAATGGATGC CATCTGCAGC CACCGTCTTG
251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 125)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAACTCTGTG CCCACCACCA
401 GTACTCCTGG GACCTCCACA GTGTACTGGG CAACCACTGG GACTCCATCC
451 TCCTTCCCCG GCCACACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 126)

1 GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA
51 CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC
151 AGTGTGGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAGCAGGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG
251 ATCCCATCGG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 127)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTCTGTG CCAACCACCA
401 GCAGTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 128)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA
51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
151 AGTGTGCGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG
251 ATCCCACTGG TCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 129)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNNGANNACA TGCNNCNCN NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 130)

1 GCCCCTGTCC CTCTCTTGAT ACCATTACCC CTCAACTTTA CCATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACA
101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATTTT CAAGAACTCC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCCGA
201 GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA
251 ATCCCAAAG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 131)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCNTNTT CAAGAACNCC
151 AGTGTTGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GAGCTCTGGG CTCACCACCA
401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 132)

1 ACTGCTGGCC CTCTCCTGGT GCCATTACCC CTAAACTTCA CCATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACG
101 CCACAGAGAG GGTCTGCAG GGTCTGCTTA GTCCCATATT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201 GAAGCAGGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG
251 ATCCCATCGG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 133)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNNTNTT CAAGAACNCC
151 AGTGTTGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTTTGGG CTCACCACCA
401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 134)

1 ACTGCTGGCC CTCTCCTGGT GCCATTACCC CTAAACTTCA CCATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTCCCTTCTAG GGTCTGCTTA CGCCCTTGTT CAGGAACACC
151 AGTGTGAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG
251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 135)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

251 ANCCCAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GATCCCTGTG CCCACCAGCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTCAGGGAC TCCATCCTCC
451 CTCCCCAGCC CCACA

(SEQ ID NO: 136)

1 ACTGCTGGCC CTCTCCTGGT ACCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAT GGGGAGGACA TGGGTCACCC TGGCTCCAGG AAGTTCAACA
101 CCACAGAGAG GGTCTGCAG GGTCTGCTTG GTCCCATATT CAAGAACACC
151 AGTGTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCCGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG
251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCN GCCNCACA

(SEQ ID NO: 137)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTACCC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCNCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCNTNTT CAAGAACNCC
151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTTTGCG CCCAACACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC
451 TCCCTCCCC AGCCCTACA

(SEQ ID NO: 138)

1 TCTGCTGGCC CTCTCCTGGT GCCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
101 CCACGGAGCG GGTCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC
151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGAATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG
251 ACCCAAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 139)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
101 CCACNGAGAG GGTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTTGGCC CTCTGTATTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGGACGGA GTAGCCACCA GAGTGGACGC CATCTGCACC CACCGCCCTG
251 ACCCCAAAAT CCCTGGGCTA GACAGACAGC AGCTATACTG GGAGCTGAGC
301 CAGCTGACCC ACAGCATCAC TGAGCTGGGA CCCTACACCC TGGATAGGGA
351 CAGTCTCTAT GTCAATGGTT TCACCCAGCG GAGCTCTGTG CCCACCACCA
401 GCACTCCTGG GACTTTCACA GTACAGCCGG AACCTCTGA GACTCCATCA
451 TCCCTCCCTG GCCCCACA

(SEQ ID NO: 140)

1 GCCACTGGCC CTGTCCTGCT GCCATTACCC CTCAATTTTA CCATCACTAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA
101 CCACGGAGAG GGTCTTCAG GGTCTGCTTA TGCCCTTGTT CAAGAACACC
151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA
201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG
251 ACCCCAAAAG CCCTGGACTG GACAGAGAGC GGCTGTACTG GAAGCTGAGC
301 CAGCTGACCC ACGGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGCA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTATG ACGACCACCA
401 GAACTCCTGA TACCTCCACA ATGCACCTGG CAACCTCGAG AACTCCAGCC
451 TCCCTGTCTG GACCTACG

(SEQ ID NO: 141)

1 ACCGCCAGCC CTCTCCTGGT GCTATTCACA ATTAATTCA CCATCACTAA
51 CCTGCGGTAT GAGGAGAACA TGCATCACCC TGGCTCTAGA AAGTTTAAACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

101 CCACGGAGAG AGTCCTTCAG GGTCTGCTCA GGCCTGTGTT CAAGAACACC
 151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCCAA
 201 GAAGGATGGG GCAGCCACCA AAGTGGATGC CATCTGCACC TACCGCCCTG
 251 ATCCCAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC
 301 CAGCTAACCC ACAGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGGA
 351 CAGTCTCTAT GTCAATGGTT TCACACAGCG GAGCTCTGTG CCCACCACTA
 401 GCATTCTTGG GACCCCCACA GTGGACCTGG GAACATCTGG GACTCCAGTT
 451 TCTAAACCTG GTCCCTCG

(SEQ ID NO: 142)

1 GCTGCCAGCC CTCTCCTGGT GCTATTCCTT CTCAACTTCA CCATCACCAA
 51 CCTGCGGTAT GAGGAGAACA TGCAGCACCC TGGCTCCAGG AAGTTCAACA
 101 CCACGGAGAG GGTCTTCAG GGCCTGCTCA GGTCCCTGTT CAAGAGCACC
 151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACTTTGC TCAGGCCTGA
 201 AAAGGATGGG ACAGCCACTG GAGTGGATGC CATCTGCACC CACCACCCTG
 251 ACCCAAAG CCCTAGGCTG GACAGAGAGC AGCTGTATTG GGAGCTGAGC
 301 CAGCTGACCC ACAATATCAC TGAGCTGGGC CACTATGCCC TGGACAACGA
 351 CAGCCTCTTT GTCAATGGTT TCACTCATCG GAGCTCTGTG TCCACCACCA
 401 GCACTCCTGG GACCCCCACA GTGTATCTGG GAGCATCTAA GACTCCAGCC
 451 TCGATATTG GCCCTTCA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 143)

1 GCTGCCAGCC ATCTCCTGAT ACTATTCACC CTCAACTTCA CCATCACTAA
51 CCTGCGGTAT GAGGAGAACA TGTGGCCTGG CTCCAGGAAG TTCAACACTA
101 CAGAGAGGGT CCTTCAGGGC CTGCTAAGGC CCTTGTTCAA GAACACCAGT
151 GTTGGCCCTC TGTACTCTGG CTCCAGGCTG ACCTTGCTCA GGCCAGAGAA
201 AGATGGGGAA GCCACCGGAG TGGATGCCAT CTGCACCCAC CGCCCTGACC
251 CCACAGGCCC TGGGCTGGAC AGAGAGCAGC TGTATTTGGA GCTGAGCCAG
301 CTGACCCACA GCATCACTGA GCTGGGCCCC TACACACTGG ACAGGGACAG
351 TCTCTATGTC AATGGTTTCA CCCATCGGAG CTCTGTACCC ACCACCAGC

(SEQ ID NO: 144)

1 ACCGGGGTGG TCAGCGAGGA GCCATTCACA CTGAACTTCA CCATCAACAA
51 CCTGCGCTAC ATGGCGGACA TGGGCCAACC CGGCTCCCTC AAGTTCAACA
101 TCACAGACAA CGTCATGAAG CACCTGCTCA GTCCTTTGTT CCAGAGGAGC
151 AGCCTGGGTG CACGGTACAC AGGCTGCAGG GTCATCGCAC TAAGGTCTGT
201 GAAGAACGGT GCTGAGACAC GGGTGGACCT CCTCTGCACC TACCTGCAGC
251 CCCTCAGCGG CCCAGGTCTG CCTATCAAGC AGGTGTTCCA TGAGCTGAGC
301 CAGCAGACCC ATGGCATCAC CCGGCTGGGC CCCTACTCTC TGGACAAAGA
351 CAGCCTCTAC CTTAACGGTT ACAATGAACC TGGTCTAGAT GAGCCTCCTA
401 CAACTCCCAA GCCAGCCACC ACATTCCTGC CTCCTCTGTC AGAAGCCACA
451 ACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 145)

1 GCCATGGGGT ACCACCTGAA GACCCTCACA CTCAACTTCA CCATCTCCAA
51 TCTCCAGTAT TCACCAGATA TGGGCAAGGG CTCAGCTACA TTCAACTCCA
101 CCGAGGGGGT CCTTCAGCAC CTGCTCAGAC CCTTGTTCCA GAAGAGCAGC
151 ATGGGCCCCT TCTACTTGGG TTGCCAACTG ATCTCCCTCA GGCCTGAGAA
201 GGATGGGGCA GCCACTGGTG TGGACACCAC CTGCACCTAC CACCCTGACC
251 CTGTGGGCCC CGGGCTGGAC ATACAGCAGC TTTACTGGGA GCTGAGTCAG
301 CTGACCCATG GTGTCACCCA ACTGGGCTTC TATGTCCTGG ACAGGGATAG
351 CCTCTTCATC AATGGCTATG CACCCCAGAA TTTATCAATC CGGGGCGAGT
401 ACCAGATAAA TTTCCACATT GTCAACTGGA ACCTCAGTAA TCCAGACCCC
451 ACATCCTCAG AGTAC

**CA125 Repeat Domains
(SEQ ID NO: 146)**

107

CA125 Repeat Domains
(SEQ ID NO: 146)

108

TABLE 17

Carboxy Terminal Nucleotide Sequence
(SEQ ID NO: 147)

1 GCCATGGGGT ACCACCTGAA GACCCTCACA CTCAACTTCA CCATCTCCAA
51 TCTCCAGTAT TCACCAGATA TGGGCAAGGG CTCAGCTACA TTCAACTCCA
101 CCGAGGGGGT CCTTCAGCAC CTGCTCAGAC CCTTGTTCCA GAAGAGCAGC
151 ATGGGCCCCT TCTACTTGGG TTGCCAACTG ATCTCCCTCA GGCCTGAGAA
201 GGATGGGGCA GCCACTGGTG TGGACACCAC CTGCACCTAC CACCCTGACC
251 CTGTGGGGCC CGGGCTGGAC ATACAGCAGC TTTACTGGGA GCTGAGTCAG
301 CTGACCCATG GTGTCACCCA ACTGGGCTTC TATGTCCTGG ACAGGGATAG
351 CCTCTTCATC AATGGCTATG CACCCAGAA TTTATCAATC CGGGGCGAGT
401 ACCAGATAAA TTTCCACATT GTCAACTGGA ACCTCAGTAA TCCAGACCCC
451 ACATCCTCAG AGTACATCAC CCTGCTGAGG GACATCCAGG ACAAGGTCAC
501 CACACTCTAC AAAGGCAGTC AACTACATGA CACATTCCGC TTCTGCCTGG
551 TCACCAACTT GACGATGGAC TCCGTGTTGG TCACTGTCAA GGCATTGTTC
601 TCCTCCAATT TGGACCCCAG CCTGGTGGAG CAAGTCTTTC TAGATAAGAC
651 CCTGAATGCC TCATTCCATT GGCTGGGCTC CACCTACCAG TTGGTGGACA
701 TCCATGTGAC AGAAATGGAG TCATCAGTTT ATCAACCAAC AAGCAGCTCC
751 AGCACCCAGC ACTTCTACCT GAATTTACC ATCACCAACC TACCATATTC
801 CCAGGACAAA GCCCAGCCAG GCACCACCA TTACCAGAGG AACAAAAGGA
851 ATATTGAGGA TGCCTCAAC CAACTCTTCC GAAACAGCAG CATCAAGAGT
901 TATTTTTCTG ACTGTCAAGT TTCAACATTC AGGTCTGTCC CCAACAGGCA

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

TABLE 17-continued

Carboxy Terminal Nucleotide Sequence
(SEQ ID NO: 147)

951 CCACACCGGG GTGGACTCCC TGTGTAACCT CTCGCCACTG GCTCGGAGAG
1001 TAGACAGAGT TGCCATCTAT GAGGAATTTT TCGGATGAC CCGGAATGGT
1051 ACCCAGCTGC AGAACTTCAC CCTGGACAGG AGCAGTGTCC TTGTGGATGG
1101 GTATTCTCCC AACAGAAATG AGCCCTTAAC TGGGAATTCT GACCTTCCCT
1151 TCTGGGCTGT CATCCTCATC GGCTTGGCAG GACTCCTGGG ACTCATCACA
1201 TGCCTGATCT GCGGTGTCCT GGTGACCACC CGCCGGCGGA AGAAGGAAGG
1251 AGAATACAAC GTCCAGCAAC AGTGCCCAGG CTACTACCAG TCACACCTAG
1301 ACCTGGAGGA TCTGCAATGA CTGGAAGTTG CCGGTGCCTG GGGTGCCTTT
1351 CCCCCAGCCA GGGTCCAAAG AAGCTTGGCT GGGGCAGAAA TAAACCATAT
1401 TGGTCGGAAA AAAAAAAAAA AA

TABLE 18

Carboxy Terminal Amino Acid Sequence
(SEQ ID NO: 148)

1 AMGYHLKTLT LNETISNLQY SPD MGKGSAT FNSTEGVLQH LLRPLFQKSS
51 MGP FYLG CQL ISLRPEKDGA ATGVDTTCTY HPDPVGPGLD IQQLYWELSQ
101 LTHGVTQLGF YVLD RDSLFI NGYAPQNLSI RGEYQINFHI VNWNLSNPDP
*
151 TSSEYITLLR DIQDKVTTLY KGSQLHDTFR FCLVTNLTMD SVLVTVKALF
201 SSNLDPSLVE QVFLDKTLNA SFHWLGSTYQ LVDIHVTEME SSVYQPTSSS
251 STQH FYLNFT ITNLPYSQDK AQP GTTNYQR NKRNI EDALN QLF RNSSIKS
301 YFSDCQVSTF RSVPNRHHTG VDSL CNFSPL ARRVD RVAIY EEFLRMTRNG
351 TQLQNFTLDR SSVLVDGYSP NRNEPLTGNS DLPFWAVILI GLAGLLGLIT
401 CLICGVLVTT RRRKKEGEYN VQQQCPGYQ SHLDLEDLQ

TABLE 19A

Serine/Threonine O-glycosylation Pattern Predicted for the
Amino Terminal End of the CA125 Molecule
(SEQ ID NO: 149)

SEQ ID NO: 149 Length: 1799

RTDGIMEHITKIPNEAAHRTGIRPVKGPQTSTSPASPKGLHTGGTKRMETTTTALKTTTALKTTSRATLTTSVYTPTLG	80
TLTPLNASRQMASTILTEMMITTPYVFPDVPETTSLSLATSILGAETSTALPRTTPSVLNRESETTASLVSRSRGAERSFVIO	160
TLDVSSSEPDTTASWVIHPAETIPTVSKTTPNFFHSELDIVSSSTATSHGADVSSAIPTNISPELDTALPLVTISGTDTS	240
TTFTPLTKSPHETETRTTWLTHPAETSSSTIPRTIPNFSHESDATPSIATSPGAETSSAIPIMTVSPGAEDLVTSQVTS	320
GTDRNMTIPTLTLSLPGPEKTIASLVTHPEAQTSSAIPSTISPAVSRLVTSMTVSLAAKTSTTNRALTNSPGEPAITVSL	400
VTHPAQTSPTVPWTTISFFHKSQDTPSMTTSHGAESSAVPTPTVSTEVPGVVPLVTSRAVISTTIPILTLSPGEPE	480
TTPSMATSHGEEASSAIPPTVSPGVPGVVTSLVTSRAVSTTIPILTFSLGEPETTPSMATSHGTEAGSAVPTVLPEV	560
PGMVTSLVASSRAVSTTTLPTLTLSLPGEPETTPSMATSHGAEASSVPTVSPGVPGVVTSLVTSRAVSTTIPILTLSP	640
GELETTPSMATSHGAEASSAVPTPTVSPGVPGVVTPLVTSRAVSTTIPILTLSSSEPETTPSMATSHGVEASSAVLTV	720
SPEVPGMVTSLVTSRAVSTTIPILTLSSDEPETTTSLVTHSEAKMISAIPTLAVSPTVQGLVTSILVTSSEGETSAFSN	800
LTVASSQPETIDSWVAHPGTEASSVVPILTVSTGEPFTNISLVTHPAESSSTLPRTTSRFHSSELDTMPSTVTSPEAESS	880
SAISTTISPGIPGVLTSVLTSSGRDISATFPTVPESPHESEATASWVTHPAVSTTVPRTPPNYHSEPDTPSIATSPG	960
AEATSDFPPTITVSPDVPDMVTSQVTSSEGTDTSTIPTLTLSLPGEPETTTSFITYSEHTSSAIPTLFVSPGASKMLTSLV	1040
ISSGTDSTTTFTPLTETPYEPETTAIQLIHPAETNTMVPRTTPKFSHKSQDITLFAITSPGPEASSAVSTTTISPDMSD	1120
LVTSLVPSSGTDSTTTFTPLSETPYEPETTAIQLIHPAETNTMVPRTTPKFSHKSQDITLFAITSPGPEASSAVSTTTISPDMSD	1200
PSIPGVVTSQVTSSEATDTSTAIPTLTPSPGEPETTASSATHPGTQTGFVPIRTVPSSEPDTMASWVTHPPQTSPTVSR	1280
TSSFHSSPDATFVMASTPRTEASSAVLTTISPGAPEMVTSQITSSGAATSTTVPTLTHSPGMPETTALLSTHPRTEISK	1360
TFPASTVFPQVSETTASLTIRPGAETSTALPTQTSSSLFLLVGTGRVDLSPTASPGVSAKTAPLSTHPGTETSTMIPT	1440
STLSLGLLETTGLLATSSSAETSTSTLHLTVSPAVSGLSSASITTDKQPTVTSWNTETSPSVTSVGPPEFSRTVTGTMT	1520
LIPSEMPTPPKTSHGEGVSPPTILRTTMVEATNLATTGSSPTVAKTTTTFNTLAGSLFTPLTTPGMSTLASEVTSRTSY	1600
NHRSWISTTSSYNRRYWPATSTFVTSFTSPGISTSSIPSSAATVPMVPTLNTITNLQYEDMRHGPSRKFNATER	1680
ELQGLLKPLFRNSSLEYLYSGCRLASLRPEKSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRN	1760
SLYVNGETHRSSMPTTSTPGTSTVDVGTSGTPSSSPSPST	

TABLE 19B

.....T.....TSTS.....TTT...TTTT...TT....TT...T....	80
.....ST.....TT.....	160
....S....T.....T.S.....T.....S.....S.....S.T..S	240
T...T.T.....TSS...T.....S.T.S..TS.....S.....T.....T..TS.	320
.....T.S.....T.S.....TSS...TST.....T.....STT...T.S....TT.S.	400
.T...TS.T...T.....S..T...TTS...SSS...T.T.ST.....T.....T.S....	480
TT.S..T.....SS...T.T.S.....S.....T.....T.S..TS.....S.T....	560
.....T....T.S....TT.S..TS....SST..T.S.....TS.S...T.....	640
....T.S..T.....SS...T.T.S...S.....S.....T.....T.SSS...T.S..TS.....S....	720
S.....S.....STT..T.T.SS....TT.....S.....T.....T.....	800
....S.....SS...T.....T.....SSS...T.....ST.T.....S	880
S...TT.S.....S.....T.....S..T...T...TSTT...TT...S.S...T.S..TS..	960
..TS....T.....T..TS.....T.T.SS....T...T...T.S...T.....	1040
.S..T.STTT..T.T.T.....T.....TT.....S.....S.....SS...TT.....	1120
.....S..T..STT..T.S.T.....TT...T.....ST.....TS.....S....TT..	1200
.S....T...TS..T.TST...T.T.S....TT.SS.T.....T..SS...T.S..T...TST..S.T	1280
TSS.S.SS...T...TS..T.SS....T.S....T...TS...TSTT...T.S.....ST...T..S.	1360
....ST....S.TT..T.....ST..T.TT.S.....T.S...S.....ST...T..ST...T	1440
ST.....T..S..TSTS....T.....S..S..S..T...T.TS..T..S.S.TS.....S.....T	1520

TABLE 19B-continued

Serine/Threonine O-glycosylation Pattern Predicted for the
Amino Terminal End of the CA125 Molecule

...S...T....S.....T.....TT.SS.T.....T...ST..S.....	1600
.....TST..TST.S...STSS..SST.....	1680
.....TTST...ST....TS.T.SSS.S.T	1760

TABLE 20

Nucleotide and Amino Acid Sequences of Recombinant CA125 Repeat Showing Peptides (Underlined 1-4) which are Antigenically Matched for Immune Stimulation of Patients with the HLA-2 Histocompatibility Subtype

CA 125 Recombinant Nucleotide and Amino Acid Sequences
(SEQ ID NO: 151 and SEQ ID NO: 152, respectively)
CA 125 Recombinant Nucleotide (Anti-Sense Strand) Sequence (SEQ ID NO: 153)
Peptide 1 (SEQ ID NO: 154); Peptide 2 (SEQ ID NO: 155);
Peptide 3 (SEQ ID NO: 156) and Peptide 4 (SEQ ID NO: 157)

```

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGGGCCACACAGAGCCTGGCCCT
1  -----+-----+-----+-----+-----+-----+ 60
TACTCTCCTAGCGTAGTGGTAGTGGTAGTGCCTAGGTACCCGGTGTGTCTCGGACCGGGA

M R G S H H H H H G S M G H T E P G P -
                                     ↑
CTCCTGATACCATTCACCTTTCAACTTTACCATCACCAACCTGCATTATGAGGAAAACATG
61 -----+-----+-----+-----+-----+-----+ 120
GAGGACTATGGTAAGTGAAAGTTGAAATGGTAGTGGTGGACGTAATACTCCTTTTGATC

L L I P F T F N F T I T N L H Y E E N M -
CAACACCCTGGTTCAGGAAGTTCAACACCACGGAGAGGGTTCTGCAGGGTCTGCTCAAG
121 -----+-----+-----+-----+-----+-----+ 180
GTTGTGGGACCAAGGTCCTTCAAGTTGTGGTGCCTCTCCCAAGACGTCCAGACGAGTTC

Q H P G S R K F N T T E R V L Q G L L K -
                                     3
CCCTTGTTCAAGAACACCAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACCTTGCTC
181 -----+-----+-----+-----+-----+-----+ 240
GGGAACAAGTTCCTGTGGTCACAACCGGGAGACATGAGACCGACGTCTGACTGGAACGAG

P L F K N T S V G P L Y S G C R L T L L -
AGACCTGAGAAGCATGAGGCAGCCACTGGAGTGGACACCATCTGTACCCACCGCGTTGAT
241 -----+-----+-----+-----+-----+-----+ 300
TCTGGACTCTTCGTACTCCGTCCGTGACCTCACCTGTGGTAGACATGGGTGGCGCAACTA

R P E K H E A A T G V D T I C T H R V D -
CCCATCGGACCTGGACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGCTGACCAAC
301 -----+-----+-----+-----+-----+-----+ 360
GGGTAGCCTGGACCTGACCTGTCTCTCGCGATATGACCCTCGACTCGGTCGACTGGTTG

P I G P G L D R E R L Y W E L 'S Q L T N -
                                     1         4
AGCATCACAGAGCTGGGACCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGCTTC
361 -----+-----+-----+-----+-----+-----+ 420
TCGTAGTGTCTCGACCCTGGGATGTGGGACCTGTCCCTGTCAGAGATACAGTTACCGAAG

```


TABLE 20 (continued)

Nucleotide and Amino Acid Sequences of Recombinant CA125 Repeat Showing Peptides (Underlined 1-4) which are Antigenically Matched for Immune Stimulation of Patients with the HLA-2 Histocompatibility Subtype

CA 125 Recombinant Nucleotide and Amino Acid Sequences
(SEQ ID NO: 151 and SEQ ID NO: 152, respectively)
CA 125 Recombinant Nucleotide (Anti-Sense Strand) Sequence (SEQ ID NO: 153)
Peptide 1 (SEQ ID NO: 154); Peptide 2 (SEQ ID NO: 155);
Peptide 3 (SEQ ID NO: 156) and Peptide 4 (SEQ ID NO: 157)

```

                2
      S  I  T  E  L  G  P  Y  T  L  D  R  D  S  L  Y  V  N  G  F  -
      AACCTCGGAGCTCTGTGCCAACCACCAGCACTCCTGGGACCTCCACAGTGCACCTGGCA
421  -----+-----+-----+-----+-----+-----+ 480
      TTGGGAGCCTCGAGACACGGTTGGTGGTCGTGAGGACCCTGGAGGTGTCACGTGGACCGT

      N  P  R  S  S  V  P  T  T  S  T  P  G  T  S  T  V  H  L  A  -
      ACCTCTGGGACTCCATCCTCCCTGCCT
481  -----+-----+-----+-----+-----+ 507
      TGGAGACCCTGAGGTAGGAGGGACGGA

      T  S  G  T  P  S  S  L  P  -

```

(SEQ ID NO: 154)

Peptide 1 R L Y W E L S Q L

(SEQ ID NO: 155)

Peptide 2 T L D R D S L Y V

(SEQ ID NO: 156)

Peptide 3 V L Q G L L K P L

(SEQ ID NO: 157)

Peptide 4 Q L T N S I T E L

TABLE 21

CA125 Protein Sequence

(SEQ ID NO: 162)

1	MEHITKIPNE	AAHRGTIRPV	KGPQTSTSPA	SPKGLHTGGT	KRMETTTTAL	.
51	KTTTTALKTT	SRATLTTSVY	TPTLGLTLPL	NASRQMASTI	LTEMMITTPY	A
101	VFPDVPETTS	SLATSLGAET	STALPRTTPS	VLNRESETTA	SLVSRSGAER	. m
151	SPVIQTLDVS	SSEPDTTASW	VIHPAETIPT	VSKTTPNFFH	SELDTVSSTA	i
201	TSHGADVSSA	IPTNISPSSEL	DALTPLVTTIS	GTDTSTTFPT	LTKSPHETET	. n
251	RTTWLTHPAE	TSSTIPRTIP	NFSHESDAT	PSIATSPGAE	TSSAIPIMTV	o
301	SPGAEDLVTS	QVTSSGTDNR	MTIPTLTLSL	GEPKTIASLV	THPEAQTS	.
351	IPTSTISPAV	SRLVTSMTVS	LAAKTSTTNR	ALTNSPGGPA	TTVSLVTHPA	
401	QTSPTVPWTT	SIFFHKSDDT	TPSMTTSHGA	ESSAVPTPT	VSTEVPGVVT	. T
451	PLVTSSRAVI	STTIPILTSL	PGEPEPTPSM	ATSHGEEASS	AIPTPTVSPG	e
501	VPGVVTSLVT	SSRAVTSTTI	PILTFSLGEP	ETTPSMATSH	GTEAGSAVPT	. r
551	VLPEVPGMVT	SLVASSRAVT	STTLPTLTSL	PGEPEPTPSM	ATSHGAEASS	m
601	TVPTVSPEVP	GVVTSVLTSS	SGVNSTSIPT	LILSPGELET	TPSMATSHGA	. i
651	EASSAVPTPT	VSPGVSGVVT	PLVTSSRAVT	STTIPILTSL	SSEPETTPSM	n
701	ATSHGVEASS	AVLTVSPEVP	GMVTSVLTSS	RAVTSTTIPT	LTSSDEPET	. a
751	TTSLVTHSEA	KMISAIPTLA	VSPTVQGLVT	SLVTSSGSET	SAFSNLTVAS	l
801	SQPETIDSWV	AHPGTEASSV	VPTLTVSTGE	PFTNISLVTH	PAESSSTLPR	
851	TTSRFSHSEL	DTMPSTVTSP	EAESSAIST	TISPGIPGVL	TSLVTSSGRD	.
901	ISATFPTVPE	SPHESEATAS	WVTHPAVTST	TVPRTTPNYS	HSEPDTTFSI	D
951	ATSPGAEATS	DFPTITVSPD	VPDMVTSQVT	SSGTDTSITI	PTLTLSGSEP	. o
1001	ETTTSFITYS	ETHTSSAAPT	LPVSPGASKM	LTSLVISSGT	DSTTTFPPTLT	m
1051	ETPYEPETTA	IQLIHPAETN	TMVERTTPKF	SHSKSDTTLP	VAITSPGPEA	. a
1101	SSAVSTTTIS	PDMSDLVTS	VPSSGTDST	TFPTLSETPY	EPETTATWLT	i
1151	HPAETSTTVS	GTIPNFSHRG	SDTAPSMVTS	PGVDTRSGVP	TTTIPPSIPG	. n
1201	VVTSQVTSSA	TDTSTAIPTL	TPSPGEPETT	ASSATHPGTQ	TGFTVPIRTV	
1251	PSSEPDTMAS	WVTHPPQTST	PVSRTTSSFS	HSSPDATPVM	ATSPRTEASS	.
1301	AVLTTISPGA	PEMVTSQITS	SGAATSTTV	TLTHSPGMPE	TTALLSTHPR	
1351	TETSKTFPAS	TVFPQVSETT	ASLTIRPGAE	TSTALPTQTT	SSLFTLLVTG	.
1401	TSRVDLSPTA	SPGVSAKTAP	LSTHPGTETS	TMIPTSTLSL	GLLETTGLLA	
1451	TSSSAETSTS	TLTLTVSPAV	SGLSSASITT	DKPQTVTSWN	TETSPSVTSV	.
1501	GPPEFSRTVT	GTTMTLIPSE	MPTPPKTSHG	EGVSPTTILR	TTMVEATNLA	
1551	TTGSSPTVAK	TTTTFNTLAG	SLFTPLTTPG	MSTLASESVT	SRTSYNHRWS	.
1601	ISTTSSYNRR	YWTPATSTPV	TSTFSPGIST	SSIPSSTA		

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

					AT VPFMVPFTLN
1651	FTITNLQYEE	DMRHPGSRKF	NATERELQGL	LKPLFRNSSL	EYLYSGCRLA
1701	SLRPEKDSSA	MAVDAICTHR	PDPEDLGLDR	ERLYWELSNL	TNGIQELGPY
1751	TLDRNSLYVN	GFTHRSSMPT	TSTPGTSTVD	VGTSGLTPSSS	PSPTAAGPLL
1801	MPFTLNFTIT	NLQYEEDMRR	TGSRKFNTME	SVLQGLLKPL	FKNTSVGPLY
1851	SGCRLTLLRP	EKDGAATGVD	AICTHRLDPK	SPGLNREQLY	WELSKLTNDI
1901	EELGPYTLDR	NSLYVNGFTH	QSSVSTTSTP	GTSTVDLRTS	GTPSSLSSPT
1951	IMAAGPLLVP	FTLNFTITNL	QYGEDMGHPG	SRKFNTTERTV	LQGLLGPIFK
2001	NTSVGPLYSG	CRLTSLRSEK	DGAATGVDAI	CIHHLDPKSP	GLNRERLYWE
2051	LSQLTNGIKE	LGPYTLDRNS	LYVNGFTHRT	SVPTSSTPGT	STVDLGTSGT
2101	PFSLPSPATA	GPLLVLFTLN	FTITNLKYEE	DMHRPGSRKF	NTTERTVLQTL
2151	LGPMPKNTSV	GLLYSGCRLT	LLRSEKDGAA	TGVDAICTHR	LDPKSPGLDR
2201	EQLYWELSQL	TNGIKELGPY	TLDRNSLYVN	GFTHWIPVPT	SSTPGTSTVD
2251	LGSGLTPSSLP	SPTAAGPLL	PFTLNFTITN	LQYEEDMHHP	GSRKFNTTER
2301	VLQGLLGPMF	KNTSVGLLYS	GCRLTLLRSE	KDGAATGVDA	ICTHRLDPKS
2351	PGVDREQLYW	ELSQLTNGIK	ELGPYTLDRN	SLYVNGFTHQ	TSAPNTSTPG
2401	TSTVDLGTSG	TPSSLPSP	AGPLLVPFTL	NFTITNLQYE	EDMRHPGSRK
2451	FNTTERTVLQ	LLKPLFKSTS	VGPLYSGCRL	TLLRSEKDGA	ATGVDAICTH
2501	RLDPKSPGVD	REQLYWELSQL	LTNGIKELGP	YTLDNRSLYV	NGFTHQTSAP
2551	NTSTPGTSTV	DLGTSGTPSS	LPSPTSAGPL	LVPFTLNFTI	TNLQYEEDMH
2601	HPGSRKFNTT	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PEKNGAATGM
2651	DAICSHRLDP	KSPGLNREQL	YWELSQLTHG	IKELGPYTL	RNSLYVNGFT
2701	HRSSVAPTST	PGTSTVDLGT	SGTPSSLPSP	TTAVPLLVPF	TLNFTITNLQ
2751	YGEDMRHPGS	RKFNTTERTVL	QGLLGPLFKN	SSVGPLYSGC	RLISLRSEKD
2801	GAATGVDAIC	THHLNPQSPG	LDREQLYWQL	SQMTNGIKEL	GPYTLDRNSL
2851	YVNGFTHRSS	GLTTSTPWTS	TVDLGTSGTP	SPVPSPTTAG	PLLVPFTLN
2901	TITNLQYEED	MHRPGSRKFN	ATERVLQGLL	SPIFKNSSVG	PLYSGCRLTS
2951	LRPEKDGAAT	GMDAVCLYHP	NPKRPGLDRE	QLYWELSQLT	HNITELGPYS
3001	LDNRSLYVNG	FTHQNSVPTT	STPGTSTVYW	ATTGTPSSFP	GHTEPGPLLI
3051	PFTFNFTITN	LHYEENMQHP	GSRKFNTTER	VLQGLLKPLF	KNTSVGPLY
3101	GCRLTSLRPE	KDGAATGMDA	VCLYHPNPKR	PGLDREQLYC	ELSQLTHNIT
3151	ELGPYSLDRD	SLYVNGFTHQ	NSVPTTSTPG	TSTVYWATTG	TPSSFPGHTE
3201	PGPLLIPFTF	NFTITNLHYE	ENMQHPGSRK	FNTTERTVLQ	LLKPLFKNTS
3251	VGPLYSGCRL	TLLRPEKHEA	ATGVDTICTH	RVDPIGPGLD	RERLYWELSQL
3301	LTNSITELGP	YTLDNRSLYV	NGFNPRSSVP	TTSTPGTSTV	HLATSGTPSS
3351	LPGHTAPVPL	LIPFTLNFTI	TNLHYEENMQ	HPGSRKFNTT	ERVLQGLLKP
3401	LKNTSVGPLY	YSGCRLTLLR	PEKHEAATGV	DTICTHRVDP	IGPGLDREXL
3451	YWELSLTX	IXELGPYXLD	RXSLYVNGFX	XXXXXXXXTST	PGTSXVXLXT
3501	SGTPXXXPXX	TSAGPLLVPF	TLNFTITNLQ	YEEDMHHPGS	RKFNTTERTVL
3551	QGLLGPMFKN	TSVGLLYSGC	RLTLLRPEKN	GAATGMDAIC	SHRLDPKSPG
3601	LDREQLYWEL	SQLTHGIKEL	GPYTLDRNSL	YVNGFTHRSS	VAPTSTPGTS

R
e
p
e
a
t

D
o
m
a
i
n

TABLE 21 - continued

CA125 Protein Sequence
(SEQ ID NO: 162)

3651	TVDLGTSGTP	SSLPSPTTAV	PLLVPFTLN	TITNLQYGED	MRHPGSRKFN
3701	TTERVLQGLL	GPLFKNSSVG	PLYSGCRLIS	LRSEKDGAAT	GVDAICTHHL
3751	NPQSPGLDRE	QLYWQLSQMT	NGIKELGPYT	LDRNSLYVNG	FTHRSSGLTT
3801	STPWTSTVDL	GTSGTPSPVP	SPTTAGPLLV	PFTLNFTITN	LQYEEDMHRP
3851	GSRKFNATER	VLOGLLSPIF	KNSSVGPLY	GCRLTSLRPE	KDGAATGMDA
3901	VCLYHPNPKR	PGLDREQLYW	ELSQLTHNIT	ELGPYSLDRD	SLYVNGFTHQ
3951	SSMTTTRTPD	TSTMHLATSR	TPASLSGPTT	ASPLLVLFTI	NCTITNLQYE
4001	EDMRTGSRK	FNTMESVLQ	LLKPLFKNTS	VGPLYSGCRL	TLLRPKKDGA
4051	ATGVDAICTH	RLDPKSPGLN	REQLYWELSK	LTNDIEELGP	YTLDRNSLYV
4101	NGFTHQSSVS	TTSTPGTSTV	DLRTSGTPSS	LSSPTIMXXX	PLLXPFTLN
4151	TITNLXYEEX	MXXPGRKFN	TTERVLQGLL	RPLFKNTSVS	SLYSGCRLTL
4201	LRPEKDGAAT	RVDAACTYRP	DPKSPGLDRE	QLYWELSQLT	HSITELGPYT
4251	LDRVSLYVNG	FNPRSSVPTT	STPGTSTVHL	ATSGTPSSLP	GHTXX XPLL
4301	XPFTLNFTIT	NLXYEEXMX	PGSRKFNTTE	RVLQGLLKPL	FRNSSLEYLY
4351	SGCRLASLRP	EKDSSAMAVD	AICTHRPDPE	DLGLDRERLY	WELSNLTNGI
4401	QELGPYTLDR	NSLYVNGETH	RSSFLTSTP	WTSTVDLGTS	GTPSPVPSPT
4451	TAGPLLVFT	LNFTITNLQY	EEDMHRPGSR	RFNTTERVLQ	GLLTPLFKNT
4501	SVGPLYSGCR	LTLRPEKQE	AATGVDICT	HRVDPIGPGL	DRERLYWELS
4551	QLTNSITELG	PYTLDRLSLY	VNGFNWSSV	PTTSTPGTST	VHLATSGTPS
4601	SLPGHTAPVP	LLIPFTLNFT	ITDLHYEENM	QHPGSRKFNT	TERVLQGLLK
4651	PLFKSTSVGP	LYSGCRLTLL	RPEKHGAATG	VDAICTLRDL	PTGPGLDRE
4701	LYWELSQLTN	SVTELGPYTL	DRDSLTVNGF	THRSSVPTTS	IPGTSVHLE
4751	TSGTPASLPG	HTAPGPLLVP	FTLNFTITNL	QYEEDMRHPG	SRKFSTTERV
4801	LQGLLKPLFK	NTSVSSLYSG	CRLTLRPEK	DGAATRVDV	CTHRPDPKSP
4851	GLDRERLYWK	LSQLTHGITE	LGPYTLDRLS	LYVNGFTHQS	SMTTTRTPDT
4901	STMHLATSRT	PASLSGPTTA	SPLLVLFTIN	FTITNQRYEE	NMHPGSRKF
4951	NTTERVLQGL	LRPVFKNTSV	GPLYSGCRLT	LLRPKKDGAA	TKVDAICTYR
5001	PDPKSPGLDR	EQLYWELSQL	THSITELGPY	TQDRDSLTVN	GFTHRSSVPT
5051	TSIPGTSVH	LETSGTPASL	PGHTAPGPLL	VPFTLNFTIT	NLQYEEDMRH
5101	PGSRKFNTTE	RVLQGLLKPL	FKSTSVGPLY	SGCRLTLR	EKRGAAATGVD
5151	TICTHRLDPL	NPGLDREQLY	WELSKLTRGI	IELGPYLLDR	GSLYVNGFTH
5201	RTSVPTTSTP	GTSTVDLGTS	GTPFSLPSPA	XXXPLLXPFT	LNFTITNLXY
5201	EEEXMXPGSR	KFNTTERVLQ	TLLGPMFKNT	SVGLLYSGCR	LTLRSEKDG
5251	AATGVDAICT	HRLDPKSPGV	DREQLYWELS	QLTNGIKELG	PYTLDRLNSLY
5301	VNGFTHWIPV	PTSSTPGTST	VDLGSPTPSL	PSSPTTAGPL	LVPFTLNFTI
5351	TNLKYEEDMH	CPGSRKFNTT	ERVLSLLGP	MFKNTSVGPL	YSGCRLTLR
5401	SEKDGAATGV	DAICTHRLDP	KSPGVDREQL	YWELSQLTNG	IKELGPYTLD
5451	RNSLYVNGFT	HQTSAPNTST	PGTSTVDLGT	SGTPSSLPSP	TXXXPLLXPF
5501	TLNFTITNLX	YEEXMXPGS	RKFNTTERVL	QGLLXPXFKX	TSVGXLYSGC
5551	RLTLRREKX	XAATXVDXXC	XXXXDPXXPG	LDREXLYWEL	SXLTXIXEL
5601	GPYXLDXSL	YVNGFTHWIP	VPTSSTPGTS	TVDLGSPTPS	SLPSPTTAGP
5651	LLVPFTLNFT	ITNLKYEEDM	HCPGSRKFNT	TERVLQSLLG	PMFKNTSVGP

R
e
p
e
a
t

D
o
m
a
i
n

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

```

5701  LYSGCRLTSL RSEKDGAATG VDAICTHRVD PKSPGVDREQ LYWELSQLTN
5751  GIKELGPYTL DRNSLYVNGF THQTSAPNTS TPGTSTVDLG TSGTPSSLPS
5801  PTSAGPLLVP FTLNFTITNL QYEEDMHHPG SRKFNTTERV LQGLLGPMFK
5851  NTSVGLLYSG CRLTLLRPEK NGAATGMDAI CTHRLDPKSP GLDREXLYWE
5901  LSXLTXIXE LGPYXLDXRS LYVNGFXXXX XXXXTSTPGT SXVXLXTSQT
5951  PXXXPXXTXX XPLLXPFTLN FTITNLXYEE XXXXPGRKF NTTERVLOGL
6001  LKPLFRNSSL EYLYSGCRLA SLRPEKDSSA MAVDAICTHR PDPEDLGLDR
6051  ERLYWELSNL TNGIQELGPY TLDNRSLYVN GFTHRSSMPT TSTPGTSTVD
6101  VGTSGTPSSS PSPTTAGPLL IPFTLNFTIT NLQYGEDMGH PGSRKFNTTE
6151  RVLQGLLGPI FKNTSVGPLY SGCRLTSLRS EKDGAATGVD AICIHLDLPK
6201  SPGLNRERLY WELSQLTNGI KELGPYTLDR NSLYVNGFTH RTSVPTTSTP
6251  GTSTVDLGTS GTPFSLPSPA TAGPLLVLEF LNFTITNLKY EEDMHRPGSR
6301  KFNTTERVLQ TLLGPMFKNT SVGLLYSGCR LTLRSEKDG AATGVDAICT
6351  HRLDPKSPGL DREXLYWELS XLTXXIXELG PYXLDXRSLY VNGFXXXXXX
6401  XXTSTPGTSX VXLXTSQTPX XXPXXTXXXP LLXPFTLNFT ITNLXYEEXM
6451  XXPGRKFNT TERVLQGLR PVFKNTSVGP LYSGCRLTLL RPKKDGAATK
6501  VDAICTYRPD PKSPGLDREQ LYWELSQLTN SITELGPYTQ DRDSLYVNGF
6551  THRSSVPTTS IPGTSVHLE TTGTPSSFPG HTEPGPLLIP FTFNFTITNL
6601  RYEENMQHPG SRKFNTTERV LQGLLTPLFK NTSVGLLYSG CRLTLLRPEK
6651  QEAATGVDTI CTHRVDPIGP GLDRERLYWE LSQLTNSITE LGPYTLDRDS
6701  LYVDGFNPWS SVPTTSTPGT STVHLATSGT PSPLPGHTAP VPLLIPFTLN
6751  FTITDLHYEE NMQHPGRKF NTTERVLOGL LKPLFKSTSV GPLYSGCRLT
6801  LLRPEKHGAA TGVDICTLR LDPTGPGLDR ERLYWELSQ TNSITELGPY
6851  TLDNRSLYVN GFNPWSSVPT TSTPGTSTVH LATSGTPSSL PGHTTAGPLL
6901  VPFTLNFTIT NLKYEEDMHC PGSRKFNTTE RVLQSLHGPM FKNTSVGPLY
6951  SGCRLTLLRS EKDGAATGVD AICTHRLDPK SPGLDREXLY WELSXLTXIX
7001  XELGPYXLDX XSLYVNGFXX XXXXXXTSTP GTSXVXLXTS GTPXXXPXXT
7051  XXXPLLXPFT LNFTITNLXY EEXMXXPGSR KFNTTERVLQ GLLXPXFKXT
7101  SVGXLYSGCR LTLRKEKXX AATXVDXXCX XXXDPXXPGL DREXLYWELS
7151  XLTNSITELG PYTLDRDSLY VNGFTHRSSM PTTSIPGTTA VHLETSGTPA
7201  SLPGHTAPGP LLVPFTLNFT ITNLQYEDM RHPGRKFNT TERVLQGLLK
7251  PLFKSTSVGP LYSGCRLTLL RPEKRGAAATG VDTICTHRLD PLNPGLDREX
7301  LYWELSXLTX XIXELGPYXL DRXSLYVNGF XXXXXXXXTS TPGTSXVXLX
7351  TSGTPXXXPX XTXXPPLLX FTLNFTITNL XYEEXMXXPG SRKFNTTERV
7401  LQGLLXPXFK XTSVGXLYSG CRLTLLRKEK XXAATXVDXX CXXXXDPXXP
7451  GLDREXLYWE LSXLTXIXE LGPYXLDXRS LYVNGFHPRS SVPTTSTPGT
7501  STVHLATSGT PSSLPGHTAP VPLLIPFTLN FTITNLHYEE NMQHPGRKF
7551  NTTERVLOGL LGPMFKNTSV GLLYSGCRLT LLRPEKNGAA TGMDAICSHR
7601  LDPKSPGLDR EXLYWELSXL TXXIXELGPY XLDXSLYVN GFXXXXXXXXX
7651  TSTPGTSXVX LXTSGTPXXX PXXTXXXPLL XPFTLNFTIT NLXYEEXMXX
7701  PGSRKFNTTE RVLQGLLXPX FKXTSVGXLY SGCRLTLLRX EKXXAATXVD
7751  XXCXXXXDPX XPGLDREXLY WELSXLTXIX XELGPYXLDX XSLYVNGFTH

```

R
e
p
e
a
t

D
o
m
a
i
n

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

7801	QNSVPTTSTP	GTSTVYWATT	GTPSSFPGHT	EPGPLLIPFT	FNFTITNLHY
7851	EENMQHPGSR	KFNTTERVLQ	GLLTPLFKNT	SVGPLYSGCR	LTLLRPEKQE
7901	AATGVDTICT	HRVDPIGPGL	DREXLYWELS	XLTXIXELG	PYXLDXSLY
7951	VNGFXXXXXX	XXTSTPGTSX	VXLXTSCTPX	XXPXXTXXXP	LLXPFTLNFT
8001	ITNLXYEEXM	XXPGSRKFNT	TERVLQGLLX	PXFKXTSVGX	LYSGCRLTLL
8051	RXEKXXAATX	VDXXCXXXXD	PXXPGLDREX	LYWELSXLTX	XIXELGPYXL
8101	DRXSLYVNGF	THRSSVPTTS	SPGTSTVHLA	TSGTPSSSLPG	HTAPVPLLIP
8151	FTLNFTITNL	HYEENMQHPG	SRKFNTTERV	LQGLLKPLFK	STSVGPLYSG
8201	CRLTLLRPEK	HGAATGVDAI	CTLRLDPTGP	GLDREXLYWE	LSXLTXXIXE
8251	LGPLYXLDXRS	LYVNGFXXXX	XXXXTSTPGT	SXVXLXTSCT	PXXXPXXTXX
8301	XPLLXPFTLN	FTITNLXYEE	XXXXPGRKFE	NTTERVLQGL	LXPXFKXTSV
8351	GXLYSGCRLT	LLRXEKXXAA	TXVDXXCXXX	XDPXXPGLDR	EXLYWELSXL
8401	TXIXELGPY	XLDRXSLYVN	GFTHRTSVPT	TSTPGTSTVH	LATSGTPSSL
8451	PGHTAPVPLL	IPFTLNFTIT	NLQYEEDMHR	PGSRKFNTTE	RVLQGLLSPI
8501	FKNSSVGPLY	SGCRLTSLRP	EKDGAATGMD	AVCLYHPNPK	RPGLDREQLY
8551	CELSQLTHNI	TELGPSYSLDR	DSLYVNGFTH	QNSVPTTSTP	GTSTVYWATT
8601	GTPSSFPGHT	XXXPLLXPFT	LNFTITNLXY	EEXMXXPGSR	KFNTTERVLQ
8651	GLLXPXFKXT	SVGXLYSGCR	LTLLRXEKXX	AATXVDXXCX	XXXDPXXPGL
8701	DREXLYWELS	XLTXIXELG	PYXLDXSLY	VNGFTHWSSG	LTTSTPWTST
8751	VDLXTSGTPS	PVPSPTTAGP	LLVPFTLNFT	ITNLQYEEDM	HRPGSRKFNA
8801	TERVLQGLLS	PIFKNTSVGP	LYSGCRLTLL	RPEKQEAATG	VDTICTHRVD
8851	PIGPGLDREX	LYWELSXLTX	XLXELGPYXL	DRXSLYVNGF	XXXXXXXXTS
8901	TPGTSXVXLX	TSGTPXXXPX	XTXXXPLLXP	FTLNFTITNL	XYEEXMXXPG
8951	SRKFNTTERV	LQGLLXPXFK	XTSVGXLYSG	CRLTLLRXEK	XXAATXVDXX
9001	CXXXXDPXXP	GLDREXLYWE	LSXLTXXIXE	LGPLYXLDXRS	LYVNGFTHRS
9051	FGLTTSTPWT	STVDLGTSGT	PSPVPSPTTA	GPLLVPFTLN	FTITNLQYEE
9101	DMHRPGSRKF	NTTERVLQGL	LTPLFRNTSV	SSLYSGCRLT	LLRPEKDGA
9151	TRVDAVCTHR	PDPKSPGLDR	EXLYWELSXL	TXIXELGPY	XLDRXSLYVN
9201	GFXXXXXXXXX	TSTPGTSXVX	LXTSGTPXXX	PXXTXXXPLL	XPFTLNFTIT
9251	NLXYEEXMXX	PGSRKFNTTE	RVLQGLLXPX	FKXTSVGXLY	SGCRLTLLRX
9301	EKXXAATXVD	XXCXXXDPX	XPGLDREXLY	WELSXLTXXI	XELGPYXLD
9351	XSLYVNGFTH	WIPVPTSSTP	GTSTVDLGSG	TPSSLPSPPT	AGPLLVPFTL
9401	NFTITNLQYG	EDMGHPGSRK	FNTTERVLQG	LLGPIFKNTS	VGPLYSGCRL
9451	TSLRSEKDGA	ATGVDAICIH	HLDPKSPGLD	REXLYWELS	LTXXIXELGP
9501	YXLDXSLYV	NGFXXXXXXXX	XTSTPGTSXV	XLXTSCTPX	XPXXTXXXPL
9551	LXPFTLNFTI	TNLXYEEXM	XPGSRKFNTT	ERVLQGLLXP	XFKXTSVGXL
9601	YSGCRLTLLR	XEKXXAATXV	DXCXXXXDP	XXPGLDREXL	YWELSXLTX
9651	IXELGPYXLD	RXSLYVNGFT	HQTAPNTST	PGTSTVDLGT	SGTPSSLPSP
9701	TSAGPLLVPF	TLNFTITNLQ	YEEDMHHPGS	RKFNTTERVL	QGLLGPMFKN
9751	TSVGLLYSGC	RLTLLRPEKN	GAATRVDVC	THRPDPKSPG	LDREXLYWEL
9801	SXLTXIXEL	GPYXLDXSL	YVNGFXXXXX	XXXXTSTPGT	XVXLXTSCTP
9851	XXXXPXTAPV	PLLIPFTLN	TITNLHYEEN	MQHPGSRKFN	TTERVLQGLL

R
e
p
e
a
t
D
o
m
a
i
n

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

9901	RPLFKSTSVG	PLYSGCRLTL	LRPEKHGAAT	GVDAICTLRL	DPTGPGLDRE	
9951	RLYWELSOLT	NSVTELGPYT	LDRDSLIVNG	FTQRSSVPTT	SIPGTSVAVHL	
10001	ETSGTPASLP	GHTAPGPLLV	PFTLNFTITN	LQYEVDMRHP	GSRKFNTTER	
10051	VLQGLLKPLF	KSTSVGPLY	GCRLTLLRPE	KRGAATGVDT	ICTHRLDPLN	
10101	PGLDREQLYW	ELSKLTRGII	ELGPYLLDRG	SLYVNGFTHR	NFVPITSTPG	
10151	TSTVHLGTSE	TPSSLPRPIV	PGPLLVPFTL	NFTITNLQYE	EAMRHFGSRK	
10201	FNTTERVLQG	LLRPLFKNTS	IGPLYSSCRL	TLLRPEKDKA	ATRVDAICTH	
10251	HPDPQSPGLN	REQLYWELSQ	LTHGITELGP	YTLDRDSLIV	DGFTHWSPIP	
10301	TTSTPGTSIV	NLGTSGIPPS	LPETTXXXPL	LXPFTLNFTI	TNLXYEEXMX	
10351	XPGSRKFNTT	ERVLOGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKDGVAITRV	
10451	DAICTHRPDP	KIPGLDRQQL	YWELSOLTHS	ITELGPYTLT	RDSLIVNGFT	
10501	QRSSVPTTST	PGTFTVQPET	SETPSSLPGP	TATGPVLLPF	TLNFTITNLQ	
10551	YEEDMHRPGS	RKFNTTERVL	QGLLMPLFKN	TSVSSLYSGC	RLTLLRPEKD	
10601	GAATRVDAVC	THRPDPKSPG	LDRERLYWKL	SQLTHGITEL	GPYTLDRHSL	
10651	YVNGFTHQSS	MTTTRTPDTS	TMHLATSRTP	ASLSGPTTAS	PLLVLEFTINF	
10701	TITNLRYEEN	MHHPGSRKFN	TTERVLQGLL	RPVFKNTSVG	PLYSGCRLTL	
10751	LRPKKDGAAT	KVDAICTYRP	DPKSPGLDRE	QLYWELSOLT	HSITELGPYT	
10801	QDRDSLIVNG	FTQRSSVPTT	SVPGTPTVDL	GTSGTPVSKP	GPSAASPLL	
10851	LFTLNGTITN	LYEENMQHP	GSRKFNTTER	VLQGLLRSLE	KSTSVGPLY	
10901	GCRLTLLRPE	KDGTATGVDA	ICTHHPDPKS	PRLDREQLYW	ELSQLTHNIT	
10951	ELGHYALDND	SLEVNGETHR	SSVSTSTPG	TPTVYLGAASK	TPASIFGPSA	
11001	ASHLLILFTL	NFTITNLRYE	ENMWPGRKF	NTTERVLQGL	LRPLFKNTSV	
11051	GPLYSGSRLT	LLRPEKDGEA	TGVDAICTHR	PDPTGPGGLDR	EQLYLELSQL	
11101	THSITELGPI	TLDRDSLIVN	GFTHRSSVPT	TSTGVVSEEP	FTLNFTINNL	
11151	RYMADMGQPG	SLKFNITDNV	MKHLSPFLQ	RSSLGARYTG	CRVIALRSVK	
11201	NGAETRVDLL	CTYLQPLSGP	GLPIKQVFHE	LSQQTHGITH	LGPYSLDKDS	
11251	LYLNGYNEPG	LDEPPTTPKP	ATTFLPPLSE	ATTAMGYHLK	TLTLNFTISN	
11301	LQYSPDMGKG	SATFNSTEGV	LQHLLRPLFQ	KSSMGPFYLG	CQLISLRPEK	
11351	DGAATGVDTT	CTYHPDPVGP	GLDIQQLYWE	LSQLTHGVTQ	LGIFYVLDLRS	
11401	LFINGYAPQN	LSIRGEYQIN	FHIVNWNLSN	PDPTSSEY		C T D
				IT LLRDIQDKVT		a e o
11451	TLYKGSQDHD	TFRFCLVTNL	TMDSVLVTVK	ALFSSNLDPS	LVEQVFLDKT	r r m
11501	LNASFHWLGS	TYQLVDIHVT	EMESSVYQPT	SSSSTQHFYL	NFTITNLPPS	b m a
11551	QDKAQPGTTN	YQRNKRNIED	ALNQLFRNSS	IKSYFSDCQV	STFRSVPNRH	o i i
11601	HTGVDSLCLNF	SPLARRVDRV	AIYEEFLRMT	RNGTQLQNFT	LDRSSVLVDG	x n n
11651	YSPNRNEPLT	GNSDLPFWAV	ILIGLAGLLG	LITCLICGVL	VTTTRRRKKEG	y a
11701	EYNVQQQCPG	YYQSHLDLED	LQ			l

TABLE 22

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 307)

1 ACTGCTGGCC CTCTCCTGGT GCCATTACCC CTCAACTTCA CCATCACCAA
51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACA
101 CCACAGAGAG GGTCCCTGCAG GGTCTGCTTA GTCCCATATT CAAGAACACC
151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCTGA
201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG
251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC GGCTGTACTG GGAGCTGAGC
301 CGACTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA
401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC
451 TCCCTCCCAA GCCCCGCA

TABLE 23

CA125 Repeat Amino Acid Sequence**(SEQ ID NO: 308)**

1 TAGPLLVPFT LNFTITNLQY EEDMHRPGSR KFNTTERVLQ GLLSPIFKNT
51 SVGPLYSGCR LTSLRSEKDG AATGVDAICI HHLDPKSPGL NRERLYWELS
101 RLNGIKELG PYTLDRNSLY VNGFTHRTSV PTTSTPGTST VDLGTSGTPF
151 SLPSA

Table 24

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

1	AAGCGTTGCA	CAATTCCCCC	AACCTCCATA	CATACGGCAG	CTCTTCTAGA
51	CACAGGTTTT	CCCAGGTCAA	ATGCGGGGAC	CCCAGCCATA	TCTCCCACCC
101	TGAGAAATTT	TGGAGTTTCA	GGGAGCTCAG	AAGCTCTGCA	GAGGCCACCC
151	TCTCTGAGGG	GATTCTTCTT	AGACCTCCAT	CCAGAGGCAA	ATGTTGACCT
201	GTCCATGCTG	AAACCCTCAG	GCCTTCCTGG	GTCATCTTCT	CCCACCCGCT
251	CCTTGATGAC	AGGGAGCAGG	AGCACTAAAG	CCACACCAGA	AATGGATTCA
301	GGACTGACAG	GAGCCACCTT	GTCACCTAAG	ACATCTACAG	GTGCAATCGT
351	GGTGACAGAA	CATACTCTGC	CCTTTACTTC	CCCAGATAAG	ACCTTGGCCA
401	GTCTTACATC	TTCGGTTGTG	GGAAGAACCA	CCCAGTCTTT	GGGGGTGATG
451	TCCTCTGCTC	TCCCTGAGTC	AACCTCTAGA	GGAATGACAC	ACTCCGAGCA
501	AAGAACCAGC	CCATCGCTGA	GTCCCCAGGT	CAATGGAACT	CCCTCTAGGA
551	ACTACCCTGC	TACAAGCATG	GTTTCAGGAT	TGAGTTCCCC	AAGGACCAGG
601	ACCAGTTCCA	CAGAAGGAAA	TTTTACCAAA	GAAGCATCTA	CATACACACT
651	CACTGTAGAG	ACCACAAGTG	GCCCAGTCAC	TGAGAAGTAC	ACAGTCCCCA
701	CTGAGACCTC	AACAAC TGAA	GGTGACAGCA	CAGAGACCCC	CTGGGACACA
751	AGATATATTC	CTGTAAAAAT	CACATCTCCA	ATGAAAACAT	TTGCAGATTC
801	AACTGCATCC	AAGGAAAATG	CCCCAGTGTC	TATGACTCCA	GCTGAGACCA
851	CAGTTACTGA	CTCACATACT	CCAGGAAGGA	CAAACCCATC	ATTGGGACA
901	CTTTATTCTT	CCTTCCTTGA	CCTATCACCT	AAAGGGACCC	CAAATTCCAG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

951	AGGTGAAACA	AGCCTGGAAC	TGATTCTATC	AACCACTGGA	TATCCCTTCT
1001	CCTCTCCTGA	ACCTGGCTCT	GCAGGACACA	GCAGAATAAG	TACCACTGCG
1051	CCTTTGTCAT	CATCTGCTTC	AGTTCTCGAT	AATAAAATAT	CAGAGACCAG
1101	CATATTCTCA	GGCCAGAGTC	TCACCTCCCC	TCTGTCTCCT	GGGGTGCCCG
1151	AGGCCAGAGC	CAGCACAATG	CCCAACTCAG	CTATCCCTTT	TTCCATGACA
1201	CTAAGCAATG	CAGAAACAAG	TGCCGAAAGG	GTCAGAAGCA	CAATTTCTCT
1251	TCTGGGGACT	CCATCAATAT	CCACAAAGCA	GACAGCAGAG	ACTATCCTTA
1301	CCTTCCATGC	CTTCGCTGAG	ACCATGGATA	TACCCAGCAC	CCACATAGCC
1351	AAGACTTTGG	CTTCAGAATG	GTTGGGAAGT	CCAGGTACCC	TTGGTGGCAC
1401	CAGCACTTCA	GCGCTGACAA	CCACATCTCC	ATCTACCACT	TTAGTCTCAG
1451	AGGAGACCAA	CACCCATCAC	TCCACGAGTG	GAAAGGAAAC	AGAAGGAACT
1501	TTGAATACAT	CTATGACTCC	ACTTGAGACC	TCTGCTCCTG	GAGAAGAGTC
1551	CGAAATGACT	GCCACCTTGG	TCCCCACTCT	AGGTTTACA	ACTCTTGACA
1601	GCAAGATCAG	AAGTCCATCT	CAGGTCTCTT	CATCCCACCC	AACAAGAGAG
1651	CTCAGAACCA	CAGGCAGCAC	CTCTGGGAGG	CAGAGTTCCA	GCACAGCTGC
1701	CCACGGGAGC	TCTGACATCC	TGAGGGCAAC	CACTTCCAGC	ACCTCAAAAG
1751	CATCATCATG	GACCAGTGAA	AGCACAGCTC	AGCAATTTAG	TGAACCCAG
1801	CACACACAGT	GGGTGGAGAC	AAGTCCTAGC	ATGAAAACAG	AGAGACCCCC
1851	AGCATCAACC	AGTGTGGCAG	CCCCTATCAC	CACTTCTGTT	CCCTCAGTGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

1901	TCTCTGGCTT	CACCACCCTG	AAGACCAGCT	CCACAAAAGG	GATTTGGCTT
1951	GAGAAACAT	CTGCAGACAC	ACTCATCGGA	GAATCCACAG	CTGGCCCAAC
2001	CACCCATCAG	TTTGCTGTTC	CCACTGGGAT	TTCAATGACA	GGAGGCAGCA
2051	GCACCAGGGG	AAGCCAGGGC	ACAACCCACC	TACTCACCAG	AGCCACAGCA
2101	TCATCTGAGA	CATCCGCAGA	TTTGACTCTG	GCCACGAACG	GTGTCCCACT
2151	CTCCGTGTCT	CCAGCAGTGA	GCAAGACGGC	TGCTGGCTCA	AGTCCTCCAG
2201	GAGGGACAAA	GCCATCATAT	ACAATGGTTT	CTTCTGTCAT	CCCTGAGACA
2251	TCATCTCTAC	AGTCCTCAGC	TTTCAGGGAA	GGAACCAGCC	TGGGACTGAC
2301	TCCATTAAAC	ACTAGACATC	CCTTCTCTTC	CCCTGAACCA	GACTCTGCAG
2351	GACACACCAA	GATAAGCACC	AGCATTCCTC	TGTTGTCATC	TGCTTCAGTT
2401	CTTGAGGATA	AAGTGTGAGC	GACCAGCACA	TTCTCACACC	ACAAAGCCAC
2451	CTCATCTATT	ACCACAGGGA	CTCCTGAAAT	CTCAACAAAG	ACAAAGCCCA
2501	GCTCAGCCGT	TCTTTCCTCC	ATGACCCTAA	GCAATGCAGC	AACAAGTCCT
2551	GAAAGAGTCA	GAAATGCAAC	TTCCCCTCTG	ACTCATCCAT	CTCCATCAGG
2601	GGAAGAGACA	GCAGGGAGTG	TCCTCACTCT	CAGCACCTCT	GCTGAGACTA
2651	CAGACTCACC	TAACATCCAC	CCAACGGGGA	CACTGACTTC	AGAATCGTCA
2701	GAGAGTCCTA	GCACTCTCAG	CCTCCCAAGT	GTCTCTGGAG	TCAAAACCAC
2751	ATTTTCTTCA	TCTACTCCTT	CCACTCATCT	ATTTACTAGT	GGAGAAGAAA
2801	CAGAGGAAAC	TTCGAATCCA	TCTGTGTCTC	AACCTGAGAC	TTCTGTTTCC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

2851	AGAGTAAGGA	CCACCTTGGC	CAGCACCTCT	GTCCCTACCC	CAGTATTCCC
2901	CACCATGGAC	ACCTGGCCTA	CACGTTTCAGC	TCAGTTCTCT	TCATCCCACC
2951	TAGTGAGTGA	GCTCAGAGCT	ACGAGCAGTA	CCTCAGTTAC	AAACTCAACT
3001	GGTTCAGCTC	TTCCTAAAAT	ATCTCACCTC	ACTGGGACGG	CAACAATGTC
3051	ACAGACCAAT	AGAGACACGT	TTAATGACTC	TGCTGCACCC	CAAAGCACAA
3101	CTTGGCCAGA	GACTAGTCCC	AGATTCAAGA	CAGGGTTACC	TTCAGCAACA
3151	ACCACTGTTT	CAACCTCTGC	CACTTCTCTC	TCTGCTACTG	TAATGGTCTC
3201	TAAATTCACT	TCTCCAGCAA	CTAGTTCCAT	GGAAGCAACT	TCTATCAGGG
3251	AACCATCAAC	AACCATCCTC	ACAACAGAGA	CCACGAATGG	CCCAGGCTCT
3301	ATGGCTGTGG	CTTCTACCAA	CATCCCAATT	GGAAAGGGCT	ACATTACTGA
3351	AGGAAGATTG	GACACAAGCC	ATCTGCCCAT	TGGAACCACA	GCTTCCTCTG
3401	AGACATCTAT	GGATTTTACC	ATGGCCAAAG	AAAGTGCTCT	AATGTCAGTA
3451	TCTCCATCTC	AGTCCATGGA	TGCTGCTGGC	TCAAGCACTC	CAGGAAGGAC
3501	AAGCCAATTC	GTTGACACAT	TTTCTGATGA	TGTCTATCAT	TTAACATCCA
3551	GAGAAATTAC	AATACCTAGA	GATGGAACAA	GCTCAGCTCT	GACTCCACAA
3601	ATGACTGCAA	CTCACCTCC	ATCTCCTGAT	CCTGGCTCTG	CTAGAAGCAC
3651	CTGGCTTGGC	ATCTTGTCCT	CATCTCCTTC	TTCTCCTACT	CCCAAAGTCA
3701	CAATGAGCTC	CACATTTTCA	ACTCAGAGAG	TCACCACAAG	CATGATAATG
3751	GACACAGTTG	AAACTAGTCG	GTGGAACATG	CCCAACTTAC	CTTCCACGAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

3801	TTCCCTGACA	CCAAGTAATA	TTCCAACAAG	TGGTGCCATA	GGAAAAAGCA
3851	CCCTGGTTCC	CTTGGACACT	CCATCTCCAG	CCACATCATT	GGAGGCATCA
3901	GAAGGGGGAC	TTCCAACCCT	CAGCACCTAC	CCTGAATCAA	CAAACACACC
3951	CAGCATCCAC	CTCGGAGCAC	ACGCTAGTTC	AGAAAGTCCA	AGCACCATCA
4001	AACTTACCAT	GGCTTCAGTA	GTAAAACCTG	GCTCTTACAC	ACCTCTCACC
4051	TTCCCCTCAA	TAGAGACCCA	CATTCATGTA	TCAACAGCCA	GAATGGCTTA
4101	CTCTTCTGGG	TCTTCACCTG	AGATGACAGC	TCCTGGAGAG	ACTAACACTG
4151	GTAGTACCTG	GGACCCCAAC	ACCTACATCA	CCACTACGGA	TCCTAAGGAT
4201	ACAAGTTCAG	CTCAGGTCTC	TACACCCAC	TCAGTGAGGA	CACTCAGAAC
4251	CACAGAAAAC	CATCCAAAGA	CAGAGTCCGC	CACCCAGCT	GCTTACTCTG
4301	GAAGTCCTAA	AATCTCAAGT	TCACCCAATC	TCACCAGTCC	GGCCACAAAA
4351	GCATGGACCA	TCACAGACAC	AACTGAACAC	TCCAATCAAT	TACATTACAC
4401	AAAATTGGCA	GAAAAATCAT	CTGGATTGTA	GACACAGTCA	GCTCCAGGAC
4451	CTGTCTCTGT	AGTAATCCCT	ACCTCCCCTA	CCATTGGAAG	CAGCACATTG
4501	GAACAACTT	CTGATGTCCC	AGGGGAACCC	CTGGTCCTTG	CTCCCAGTGA
4551	GCAGACCACA	ATCACTCTCC	CCATGGCAAC	ATGGCTGAGT	ACCAAGTTGA
4601	CAGAGGAAAT	GGCTTCAACA	GACCTTGATA	TTTCAAGTCC	AAGTTCACCC
4651	ATGAGTACAT	TTGCTATTTT	TCCACCTATG	TCCACACCTT	CTCATGAACT
4701	TTCAAAGTCA	GAGGCAGATA	CCAGTGCCAT	TAGAAATACA	GATTCAACAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

4751	CGTTGGATCA	GCACCTAGGA	ATCAGGAGTT	TGGGCAGAAC	TGGGGACTTA
4801	ACAACTGTTC	CTATCACCCC	ACTGACAACC	ACGTGGACCA	GTGTGATTGA
4851	ACACTCAACA	CAAGCACAGG	ACACCCTTTC	TGCAACGATG	AGTCCTACTC
4901	ACGTGACACA	GTCACTCAAA	GATCAAACAT	CTATACCAGC	CTCAGCATCC
4951	CCTTCCCATC	TTACTGAAGT	CTACCCTGAG	CTCGGGACAC	AAGGGAGAAG
5001	CTCCTCTGAG	GCAACCACTT	TTTGGAACC	ATCTACAGAC	ACACTGTCCA
5051	GAGAGATTGA	GACTGGCCCA	ACAAACATTC	AATCCACTCC	ACCCATGGAC
5101	AACACAACAA	CAGGGAGCAG	TAGTAGTGGA	GTCACCCTGG	GCATAGCCCA
5151	CCTTCCCATA	GGAACATCCT	CCCCAGCTGA	GACATCCACA	AACATGGCAC
5201	TGGAAAGAAG	AAGTTCTACA	GCCACTGTCT	CTATGGCTGG	GACAATGGGA
5251	CTCCTTGTTA	CTAGTGCTCC	AGGAAGAAGC	ATCAGCCAGT	CATTAGGAAG
5301	AGTTTCCTCT	GTCCTTCTG	AGTCAACTAC	TGAAGGAGTC	ACAGATTCTA
5351	GTAAGGGAAG	CAGCCCAAGG	CTGAACACAC	AGGGAAATAC	AGCTCTCTCC
5401	TCCTCTCTTG	AACCCAGCTA	TGCTGAAGGA	AGCCAGATGA	GCACAAGCAT
5451	CCCTCTAACC	TCATCTCCTA	CAACTCCTGA	TGTGGAATTC	ATAGGGGGCA
5501	GCACATTTTG	GACCAAGGAG	GTCACCACAG	TTATGACCTC	AGACATCTCC
5551	AAGTCTTCAG	CAAGGACAGA	GTCCAGCTCA	GCTACCCTTA	TGTCCACAGC
5601	TTTGGAAGC	ACTGAAAATA	CAGGAAAAGA	AAAACTCAGA	ACTGCCTCTA
5651	TGGATCTTCC	ATCTCCAAC	CCATCAATGG	AGGTGACACC	ATGGATTCTT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

5701	CTCACTCTCA	GTAATGCCCC	CAATACCACA	GATTCATTG	ACCTCAGCCA
5751	TGGGGTGCAC	ACCAGCTCTG	CAGGGACTTT	GGCCACTGAC	AGGTCATTGA
5801	ATACTGGTGT	CACTAGAGCC	TCCAGATTGG	AAAACGGCTC	TGATACCTCT
5851	TCTAAGTCCC	TGTCTATGGG	AAACAGCACT	CACACTTCCA	TGACTGACAC
5901	AGAGAAGAGT	GAAGTGTCTT	CTTCAATCCA	TCCCCGACCT	GAGACCTCAG
5951	CTCCTGGAGC	AGAGACCACT	TTGACTTCCA	CTCCTGGAAA	CAGGGCCATA
6001	AGCTTAACAT	TGCCTTTTTTC	ATCCATTCCA	GTGGAAGAAG	TCATTTCTAC
6051	AGGCATAACC	TCAGGACCAG	ACATCAACTC	AGCACCCATG	ACACATTCTC
6101	CCATCACCCC	ACCAACAATT	GTATGGACCA	GTACAGGCAC	AATTGAACAG
6151	TCCACTCAAC	CACTACATGC	AGTTTCTTCA	GAAAAAGTTT	CTGTGCAGAC
6201	ACAGTCAACT	CCATATGTCA	ACTCTGTGGC	AGTGTCTGCT	TCCCCTACCC
6251	ATGAGAATTC	AGTCTCTTCT	GGAAGCAGCA	CATCCTCTCC	ATATTCTCTA
6301	GCCTCACTTG	AATCCTTGGA	TTCCACAATC	AGTAGGAGGA	ATGCAATCAC
6351	TTCCTGGCTA	TGGGACCTCA	CTACATCTCT	CCCCACTACA	ACTTGGCCAA
6401	GTA CTAGTTT	ATCTGAGGCA	CTGTCCTCAG	GCCATTCTGG	GGTTTCAAAC
6451	CCAAGTTCAA	CTACGACTGA	ATTTCCACTC	TTTTCAGCTG	CATCCACATC
6501	TGCTGCTAAG	CAAAGAAATC	CAGAAACAGA	GACCCATGGT	CCCCAGAATA
6551	CAGCCGCGAG	TACTTTGAAC	ACTGATGCAT	CCTCGGTCAC	AGGTCTTTCT
6601	GAGACTCCTG	TGGGGGCAAG	TATCAGCTCT	GAAGTCCCTC	TTCCAATGGC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

6651	CATAACTTCT	AGATCAGATG	TTTCTGGCCT	TACATCTGAG	AGTACTGCTA
6701	ACCCGAGTTT	AGGCACAGCC	TCTTCAGCAG	GGACCAAATT	AACTAGGACA
6751	ATATCCCTGC	CCACTTCAGA	GTCTTTGGTT	TCCTTTAGAA	TGAACAAGGA
6801	TCCATGGACA	GTGTCAATCC	CTTTGGGGTC	CCATCCAACT	ACTAATACAG
6851	AAACAAGCAT	CCCAGTAAAC	AGCGCAGGTC	CACCTGGCTT	GTCCACAGTA
6901	GCATCAGATG	TAATTGACAC	ACCTTCAGAT	GGGGCTGAGA	GTATTCCCAC
6951	TGTCTCCTTT	TCCCCCTCCC	CTGATACTGA	AGTGACAACT	ATCTCACATT
7001	TCCCAGAAAA	GACAACTCAT	TCATTTAGAA	CCATTTTCATC	TCTCACTCAT
7051	GAGTTGACTT	CAAGAGTGAC	ACCTATTCCCT	GGGGATTGGA	TGAGTTCAGC
7101	TATGTCTACA	AAGCCCACAG	GAGCCAGTCC	CTCCATTACA	CTGGGAGAGA
7151	GAAGGACAAT	CACCTCTGCT	GCTCCAACCA	CTTCCCCCAT	AGTTCTCACT
7201	GCTAGTTTCA	CAGAGACCAG	CACAGTTTCA	CTGGATAATG	AAACTACAGT
7251	AAAAACCTCA	GATATCCTTG	ACGCACGGAA	AACAAATGAG	CTCCCCTCAG
7301	ATAGCAGTTC	TTCTTCTGAT	CTGATCAACA	CCTCCATAGC	TTCTTCAACT
7351	ATGGATGTCA	CTAAAACAGC	CTCCATCAGT	CCCACTAGCA	TCTCAGGAAT
7401	GACAGCAAGT	TCCTCCCCAT	CTCTCTTCTC	TTCAGATAGA	CCCCAGGTTC
7451	CCACATCTAC	AACAGAGACA	AATACAGCCA	CCTCTCCATC	TGTTTCCAGT
7501	AACACCTATT	CTCTTGATGG	GGGCTCCAAT	GTGGGTGGCA	CTCCATCCAC
7551	TTTACCACCC	TTTACAATCA	CCCACCCTGT	CGAGACAAGC	TCGGCCCTAT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

7601	TAGCCTGGTC	TAGACCAGTA	AGAACTTTCA	GCACCATGGT	CAGCACTGAC
7651	ACTGCCTCCG	GAGAAAATCC	TACCTCTAGC	AATTCTGTGG	TGACTTCTGT
7701	TCCAGCACCA	GGTACATGGA	CCAGTGTAGG	CAGTACTACT	GA CTTACCTG
7751	CCATGGGCTT	TCTCAAGACA	AGTCCTGCAG	GAGAGGCACA	CTCACTTCTA
7801	GCATCAACTA	TTGAACCAGC	CACTGCCTTC	ACTCCCCATC	TCTCAGCAGC
7851	AGTGGTCACT	GGATCCAGTG	CTACATCAGA	AGCCAGTCTT	CTCACTACGA
7901	GTGAAAGCAA	AGCCATTTCAT	TCTTCACCAC	AGACCCCAAC	TACACCCACC
7951	TCTGGAGCAA	ACTGGGAAAC	TTCAGCTACT	CCTGAGAGCC	TTTTGGTAGT
8001	CACTGAGACT	TCAGACACAA	CACTTACCTC	AAAGATTTTG	GTCACAGATA
8051	CCATCTTGTT	TTCAACTGTG	TCCACGCCAC	CTTCTAAATT	TCCAAGTACG
8101	GGGACTCTGT	CTGGAGCTTC	CTTCCCTACT	TTACTCCCGG	ACACTCCAGC
8151	CATCCCTCTC	ACTGCCACTG	AGCCAACAAG	TTCATTAGCT	ACATCCTTTG
8201	ATTCCACCCC	ACTGGTGA CT	ATAGCTTCGG	ATAGTCTTGG	CACAGTCCCA
8251	GAGACTACCC	TGACCATGTC	AGAGACCTCA	AATGGTGATG	CACTGGTTCT
8301	TAAGACAGTA	AGTAACCCAG	ATAGGAGCAT	CCCTGGAATC	ACTATCCAAG
8351	GAGTAACAGA	AAGTCCACTC	CATCCTTCTT	CCACTTCCCC	CTCTAAGATT
8401	GTTGCTCCAC	GGAATACAAC	CTATGAAGGT	TCGATCACAG	TGGCACTTTC
8451	TACTTTGCCT	GCGGGA ACTA	CTGGTTCCCT	TGTATTCA GT	CAGAGTTCTG
8501	AAAACTCAGA	GACAACGGCT	TTGGTAGACT	CATCAGCTGG	GCTTGAGAGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

8551	GCATCTGTGA	TGCCACTAAC	CACAGGAAGC	CAGGGTATGG	CTAGCTCTGG
8601	AGGAATCAGA	AGTGGGTCCA	CTCACTCAAC	TGGAACCAAA	ACATTTTCTT
8651	CTCTCCCTCT	GACCATGAAC	CCAGGTGAGG	TTACAGCCAT	GTCTGAAATC
8701	ACCACGAACA	GACTGACAGC	TACTCAATCA	ACAGCACCCA	AAGGGATACC
8751	TGTGAAGCCC	ACCAGTGCTG	AGTCAGGCCT	CCTAACACCT	GTCTCTGCCT
8801	CCTCAAGCCC	ATCAAAGGCC	TTTGCCTCAC	TGACTACAGC	TCCCCCAACT
8851	TGGGGGATCC	CACAGTCTAC	CTTGACATTT	GAGTTTTCTG	AGGTCCCAAG
8901	TTTGGATACT	AAGTCCGCTT	CTTTACCAAC	TCCTGGACAG	TCCCTGAACA
8951	CCATTCCAGA	CTCAGATGCA	AGCACAGCAT	CTTCCTCACT	GTCCAAGTCT
9001	CCAGAAAAAA	ACCCAAGGGC	AAGGATGATG	ACTTCCACAA	AGGCCATAAG
9051	TGCAAGCTCA	TTTCAATCAA	CAGGTTTTAC	TGAAACCCCT	GAGGGATCTG
9101	CCTCCCCTTC	TATGGCAGGG	CATGAACCCA	GAGTCCCCAC	TTCAGGAACA
9151	GGGGACCCTA	GATATGCCTC	AGAGAGCATG	TCTTATCCAG	ACCCAAGCAA
9201	GGCATCATCA	GCTATGACAT	CGACCTCTCT	TGCATCAAAA	CTCACAACCTC
9251	TCTTCAGCAC	AGGTCAAGCA	GCAAGGTCTG	GTTCTAGTTC	CTCTCCCATA
9301	AGCCTATCCA	CTGAGAAAGA	AACAAGCTTC	CTTTCCCCCA	CTGCATCCAC
9351	CTCCAGAAAG	ACTTCACTAT	TTCTTGGGCC	TTCCATGGCA	AGGCAGCCCA
9401	ACATATTGGT	GCATCTTCAG	ACTTCAGCTC	TGACACTTTC	TCCAACATCC
9451	ACTCTAAATA	TGTCCCAGGA	GGAGCCTCCT	GAGTTAACCT	CAAGCCAGAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

9501	CATTGCAGAA	GAAGAGGGAA	CAACAGCTGA	AACACAGACG	TTAACCTTCA
9551	CACCATCTGA	GACCCCAACA	TCCTTGTTAC	CTGTCTCTTC	TCCCACAGAA
9601	CCCACAGCCA	GAAGAAAGAG	TTCTCCAGAA	ACATGGGCAA	GCTCTATTTT
9651	AGTTCCTGCC	AAGACCTCCT	TGGTTGAAAC	AACTGATGGA	ACGCTAGTGA
9701	CCACCATAAA	GATGTCAAGC	CAGGCAGCAC	AAGGAAATTC	CACGTGGCCT
9751	GCCCCAGCAG	AGGAGACGGG	GACCAGTCCA	GCAGGCACAT	CCCCAGGAAG
9801	CCCAGAAATG	TCTACCACTC	TCAAAATCAT	GAGCTCCAAG	GAACCCAGCA
9851	TCAGCCCAGA	GATCAGGTCC	ACTGTGCGAA	ATTCTCCTTG	GAAGACTCCA
9901	GAAACAACCTG	TTCCCATGGA	GACCACAGTG	GAACCAGTCA	CCCTTCAGTC
9951	CACAGCCCTA	GGAAGTGGCA	GCACCAGCAT	CTCTCACCTG	CCCACAGGAA
10001	CCACATCACC	AACCAAGTCA	CCAACAGAAA	ATATGTTGGC	TACAGAAAGG
10051	GTCTCCCTCT	CCCCATCCCC	ACCTGAGGCT	TGGACCAACC	TTTATTCTGG
10101	AACTCCAGGA	GGGACCAGGC	AGTCACTGGC	CACAATGTCC	TCTGTCTCCC
10151	TAGAGTCACC	AACTGCTAGA	AGCATCACAG	GGACTGGTCA	GCAAAGCAGT
10201	CCAGAACTGG	TTTCAAAGAC	AACTGGAATG	GAATTCTCTA	TGTGGCATGG
10251	CTCTACTGGA	GGGACCACAG	GGGACACACA	TGTCTCTCTG	AGCACATCTT
10301	CCAATATCCT	TGAAGACCCT	GTAACCAGCC	CAAACCTCTGT	GAGCTCATTG
10351	ACAGATAAAT	CCAAACATAA	AACCGAGACA	TGGGTAAGCA	CCACAGCCAT
10401	TCCCTCCACT	GTCCTGAATA	ATAAGATAAT	GGCAGCTGAA	CAACAGACAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

10451	GTCGATCTGT	GGATGAGGCT	TATTCATCAA	CTAGTTCTTG	GTCAGATCAG
10501	ACATCTGGGA	GTGACATCAC	CCTTGGTGCA	TCTCCTGATG	TCACAAACAC
10551	ATTATACATC	ACCTCCACAG	CACAAACCAC	CTCACTAGTG	TCTCTGCCCT
10601	CTGGAGACCA	AGGCATTACA	AGCCTCACCA	ATCCCTCAGG	AGGAAAAACA
10651	AGCTCTGCGT	CATCTGTCAC	ATCTCCTTCA	ATAGGGCTTG	AGACTCTGAG
10701	GGCCAATGTA	AGTGCAGTGA	AAAGTGACAT	TGCCCCTACT	GCTGGGCATC
10751	TATCTCAGAC	TTCATCTCCT	GCGGAAGTGA	GCATCCTGGA	CGTAACCACA
10801	GCTCCTACTC	CAGGTATCTC	CACCACCATC	ACCACCATGG	GAACCAACTC
10851	AATCTCAACT	ACCACACCCA	ACCCAGAAGT	GGGTATGAGT	ACCATGGACA
10901	GCACCCCGGC	CACAGAGAGG	CGCACAACTT	CTACAGAACA	CCCTTCCACC
10951	TGGTCTTCCA	CAGCTGCATC	AGATTCCTGG	ACTGTCACAG	ACATGACTTC
11001	AAACTTGAAA	GTTGCAAGAT	CTCCTGGAAC	AATTTCCACA	ATGCATACAA
11051	CTTCATTCTT	AGCCTCAAGC	ACTGAATTAG	ACTCCATGTC	TACTCCCCAT
11101	GGCCGTATAA	CTGTCATTGG	AACCAGCCTG	GTCACTCCAT	CCTCTGATGC
11151	TTCAGCTGTA	AAGACAGAGA	CCAGTACAAG	TGAAAGAACA	TTGAGTCCTT
11201	CAGACACAAC	TGCATCTACT	CCCATCTCAA	CTTTTCTCG	TGTCCAGAGG
11251	ATGAGCATCT	CAGTTCCTGA	CATTTTAAGT	ACAAGTTGGA	CTCCCAGTAG
11301	TACAGAAGCA	GAAGATGTGC	CTGTTTCAAT	GGTTTCTACA	GATCATGCTA
11351	GTACAAAGAC	TGACCCAAAT	ACGCCCCTGT	CCACTTTTCT	GTTTGATTCT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

11401	CTGTCCACTC	TTGACTGGGA	CACTGGGAGA	TCTCTGTCAT	CAGCCACAGC
11451	CACTACCTCA	GCTCCTCAGG	GGGCCACAAC	TCCCCAGGAA	CTCACTTTGG
11501	AAACCATGAT	CAGCCCAGCT	ACCTCACAGT	TGCCCTTCTC	TATAGGGCAC
11551	ATTACAAGTG	CAGTCACACC	AGCTGCAATG	GCAAGGAGCT	CTGGAGTTAC
11601	TTTTTCAAGA	CCAGATCCCA	CAAGCAAAAA	GGCAGAGCAG	ACTTCCACTC
11651	AGCTTCCCAC	CACCACTTCT	GCACATCCAG	GGCAGGTGCC	CAGATCAGCA
11701	GCAACAACCTC	TGGATGTGAT	CCCACACACA	GCAAAAACCTC	CAGATGCAAC
11751	TTTTTCAGAGA	CAAGGGCAGA	CAGCTCTTAC	AACAGAGGCA	AGAGCTACAT
11801	CTGACTCCTG	GAATGAGAAA	GAAAAATCAA	CCCCAAGTGC	ACCTTGGATC
11851	ACTGAGATGA	TGAATTCTGT	CTCAGAAGAT	ACCATCAAGG	AGGTTACCAG
11901	CTCCTCCAGT	GTATTAAAGG	ACCCTGAATA	CGCTGGACAT	AAACTTGGAA
11951	TCTGGGACGA	CTTCATCCCC	AAGTTTGGAA	AAGCAGCCCA	TATGAGAGAG
12001	TTGCCCCCTC	TGAGTCCACC	ACAGGACAAA	GAGGCAATTC	ACCCTTCTAC
12051	AAACACAGTA	GAGACCACAG	GCTGGGTCAC	AAGTCCGAA	CATGCTTCTC
12101	ATTCCACTAT	CCCAGCCCAC	TCAGCGTCAT	CCAAACTCAC	ATCTCCAGTG
12151	GTTACAACCT	CCACCAGGGA	ACAAGCAATA	GTTTCTATGT	CAACAACCAC
12201	ATGGCCAGAG	TCTACAAGGG	CTAGAACAGA	GCCTAATTCC	TTCTTGACTA
12251	TTGAACTGAG	GGACGTCAGC	CCTTACATGG	ACACCAGCTC	AACCACACAA
12301	ACAAGTATTA	TCTCTTCCCC	AGGTTCCACT	GCGATCACCA	AGGGGCCTAG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

12351	AACAGAAATT	ACCTCCTCTA	AGAGAATATC	CAGCTCATTC	CTTGCCCAGT
12401	CTATGAGGTC	GTCAGACAGC	CCCTCAGAAG	CCATCACCAG	GCTGTCTAAC
12451	TTTCCTGCCA	TGACAGAATC	TGGAGGAATG	ATCCTTGCTA	TGCAAACAAG
12501	TCCACCTGGC	GCTACATCAC	TAAGTGCACC	TACTTTGGAT	ACATCAGCCA
12551	CAGCCTCCTG	GACAGGGACT	CCACTGGCTA	CGACTCAGAG	ATTTACATAC
12601	TCAGAGAAGA	CCACTCTCTT	TAGCAAAGGT	CCTGAGGATA	CATCACAGCC
12651	AAGCCCTCCC	TCTGTGGAAG	AAACCAGCTC	TTCCTCTTCC	CTGGTACCTA
12701	TCCATGCTAC	AACCTCGCCT	TCCAATATTT	TGTTGACATC	ACAAGGGCAC
12751	AGTCCCTCCT	CTACTCCACC	TGTGACCTCA	GTTTTCTTGT	CTGAGACCTC
12801	TGGCCTGGGG	AAGACCACAG	ACATGTCGAG	GATAAGCTTG	GAACCTGGCA
12851	CAAGTTTACC	TCCCAATTTG	AGCAGTACAG	CAGGTGAGGC	GTTATCCACT
12901	TATGAAGCCT	CCAGAGATAC	AAAGGCAATT	CATCATTCTG	CAGACACAGC
12951	AGTGACGAAT	ATGGAGGCAA	CCAGTTCTGA	ATATTCTCCT	ATCCCAGGCC
13001	ATACAAAGCC	ATCCAAAGCC	ACATCTCCAT	TGGTTACCTC	CCACATCATG
13051	GGGGACATCA	CTTCTTCCAC	ATCAGTATTT	GGCTCCTCCG	AGACCACAGA
13101	GATTGAGACA	GTGTCCCTCTG	TGAACCAGGG	ACTTCAGGAG	AGAAGCACAT
13151	CCCAGGTGGC	CAGCTCTGCT	ACAGAGACAA	GCACTGTCAT	TACCCATGTG
13201	TCTAGTGGTG	ATGCTACTAC	TCATGTCACC	AAGACACAAG	CCACTTTCTC
13251	TAGCGGAACA	TCCATCTCAA	GCCCTCATCA	GTTTATAACT	TCTACCAACA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

13301	CATTACAGA	TGTGAGCACC	AACCCCTCCA	CCTCTCTGAT	AATGACAGAA
13351	TCTTCAGGAG	TGACCATCAC	CACCCAAACA	GGTCCTACTG	GAGCTGCAAC
13401	ACAGGGTCCA	TATCTCTTGG	ACACATCAAC	CATGCCTTAC	TTGACAGAGA
13451	CTCCATTAGC	TGTGACTCCA	GATTTTATGC	AATCAGAGAA	GACCACTCTC
13501	ATAAGCAAAG	GTCCCAAGGA	TGTGACCTGG	ACAAGCCCTC	CCTCTGTGGC
13551	AGAAACCAGC	TATCCCTCTT	CCCTGACACC	TTTCTTGGTC	ACAACCATAC
13601	CTCCTGCCAC	TTCCACGTTA	CAAGGGCAAC	ATACATCCTC	TCCTGTTTCT
13651	GCGACTTCAG	TTCTTACCTC	TGGACTGGTG	AAGACCACAG	ATATGTTGAA
13701	CACAAGCATG	GAACCTGTGA	CCAATTCACC	TCAAATTTG	AACAATCCAT
13751	CAAATGAGAT	ACTGGCCACT	TTGGCAGCCA	CCACAGATAT	AGAGACTATT
13801	CATCCTTCCA	TAAACAAAGC	AGTGACCAAT	ATGGGGACTG	CCAGTTCAGC
13851	ACATGTACTG	CATTCCACTC	TCCCAGTCAG	CTCAGAACCA	TCTACAGCCA
13901	CATCTCCAAT	GGTTCCTGCC	TCCAGCATGG	GGGACGCTCT	TGCTTCTATA
13951	TCAATACCTG	GTTCTGAGAC	CACAGACATT	GAGGGAGAGC	CAACATCCTC
14001	CCTGACTGCT	GGACGAAAAG	AGAACAGCAC	CCTCCAGGAG	ATGAACTCAA
14051	CTACAGAGTC	AAACATCATC	CTCTCCAATG	TGTCTGTGGG	GGCTATTACT
14101	GAAGCCACAA	AAATGGAAGT	CCCCTCTTTT	GATGCAACAT	TCATACCAAC
14151	TCCTGCTCAG	TCAACAAAGT	TCCCAGATAT	TTTCTCAGTA	GCCAGCAGTA
14201	GACTTTCAAA	CTCTCCTCCC	ATGACAATAT	CTACCCACAT	GACCACCACC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

14251	CAGACAGGGT	CTTCTGGAGC	TACATCAAAG	ATTCCACTTG	CCTTAGACAC
14301	ATCAACCTTG	GAAACCTCAG	CAGGGACTCC	ATCAGTGGTG	ACTGAGGGGT
14351	TTGCCCCACTC	AAAAATAACC	ACTGCAATGA	ACAATGATGT	CAAGGACGTG
14401	TCACAGACAA	ACCCTCCCTT	TCAGGATGAA	GCCAGCTCTC	CCTCTTCTCA
14451	AGCACCTGTC	CTTGTCACAA	CCTTACCTTC	TTCTGTTGCT	TTCACACCGC
14501	AATGGCACAG	TACCTCCTCT	CCTGTTTCTA	TGTCCTCAGT	TCTTACTTCT
14551	TCACTGGTAA	AGACCGCAGG	CAAGGTGGAT	ACAAGCTTAG	AAACAGTGAC
14601	CAGTTCACCT	CAAAGTATGA	GCAACACTTT	GGATGACATA	TCGGTCACTT
14651	CAGCAGCCAC	CACAGATATA	GAGACAACGC	ATCCTTCCAT	AAACACAGTA
14701	GTTACCAATG	TGGGGACCAC	CGGTTCAGCA	TTTGAATCAC	ATTCTACTGT
14751	CTCAGCTTAC	CCAGAGCCAT	CTAAAAGTCA	CATTCTCCCA	ATGTTACCAC
14801	CTCCACCATG	GAAGACACCA	CAATTTCCAC	GATCAATACC	TAAATCCTCT
14851	AAGACTACAA	GAACTGAGAC	TGAGACAACT	TCCTCCCTGA	CTCCTAAACT
14901	GAGGGAGACC	AGCATCTCCC	AGGAGATCAC	CTCGTCCACA	GAGACAAGCA
14951	CTGTTCTTA	CAAAGAGCTC	ACTGGTGCCA	CTACCGAGGT	ATCCAGGACA
15001	GATGTCACTT	CCTCTAGCAG	TACATCCTTC	CCTGGCCCTG	ATCAGTCCAC
15051	AGTGTCACCTA	GACATCTCCA	CAGAAACCAA	CACCAGGCTG	TCTACCTCCC
15101	CAATAATGAC	AGAATCTGCA	GAAATAACCA	TCACCACCCA	AACAGGTCCT
15151	CATGGGGCTA	CATCACAGGA	TACTTTTACC	ATGGACCCAT	CAAATACAAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

15201	CCCCCAGGCA	GGGATCCACT	CAGCTATGAC	TCATGGATTT	TCACAATTGG
15251	ATGTGACCAC	TCTTATGAGC	AGAATTCCAC	AGGATGTATC	ATGGACAAGT
15301	CCTCCCTCTG	TGGATAAAAC	CAGCTCCCCC	TCTTCCTTTC	TGTCCTCACC
15351	TGCAATGACC	ACACCTTCCC	TGATTTCTTC	TACCTTACCA	GAGGATAAGC
15401	TCTCCTCTCC	TATGACTTCA	CTTCTCACCT	CTGGCCTAGT	GAAGATTACA
15451	GACATATTAC	GTACACGCTT	GGAACCTGTG	ACCAGCTCAC	TTCCAAATTT
15501	CAGCAGCACC	TCAGATAAGA	TACTGGCCAC	TTCTAAAGAC	AGTAAAGACA
15551	CAAAGGAAAT	TTTTCCTTCT	ATAAACACAG	AAGAGACCAA	TGTGAAAGCC
15601	AACAACCTCTG	GACATGAATC	CCATTCCCCT	GCACTGGCTG	ACTCAGAGAC
15651	ACCCAAAGCC	ACAAC TCAAA	TGGTTATCAC	CACCACTGTG	GGAGATCCAG
15701	CTCCTTCCAC	ATCAATGCCA	GTGCATGGTT	CCTCTGAGAC	TACAAACATT
15751	AAGAGAGAGC	CAACATATTT	CTTGACTCCT	AGACTGAGAG	AGACCAGTAC
15801	CTCTCAGGAG	TCCAGCTTTC	CCACGGACAC	AAGTTTTCTA	CTTTCCAAAG
15851	TCCCCACTGG	TACTATTACT	GAGGTCTCCA	GTACAGGGGT	CAACTCTTCT
15901	AGCAAAATTT	CCACCCCAGA	CCATGATAAG	TCCACAGTGC	CACCTGACAC
15951	CTTCACAGGA	GAGATCCCCA	GGGTCTTCAC	CTCCTCTATT	AAGACAAAAT
16001	CTGCAGAAAT	GACGATCACC	ACCCAAGCAA	GTCCTCCTGA	GTCTGCATCG
16051	CACAGTACCC	TTCCCTTGGA	CACATCAACC	AACTTTCCC	AGGGAGGGAC
16101	TCATTCAACT	GTGACTCAGG	GATTCCCATA	CTCAGAGGTG	ACCACTCTCA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

16151	TGGGCATGGG	TCCTGGGAAT	GTGTCATGGA	TGACAACTCC	CCCTGTGGAA
16201	GAAACCAGCT	CTGTGTCTTC	CCTGATGTCT	TCACCTGCCA	TGACATCCCC
16251	TTCTCCTGTT	TCCTCCACAT	CACCACAGAG	CATCCCCTCC	TCTCCTCTTC
16301	CTGTGACTGC	ACTTCCTACT	TCTGTTCTGG	TGACAACCAC	AGATGTGTTG
16351	GGCACAACAA	GCCCAGAGTC	TGTAACCACT	TCACCTCCAA	ATTTGAGCAG
16401	CATCACTCAT	GAGAGACCGG	CCACTTACAA	AGACACTGCA	CACACAGAAG
16451	CCGCCATGCA	TCATTCCACA	AACACCGCAG	TGACCAATGT	AGGGACTTCC
16501	GGGTCTGGAC	ATAAATCACA	ATCCTCTGTC	CTAGCTGACT	CAGAGACATC
16551	GAAAGCCACA	CCTCTGATGA	GTACCACCTC	CACCCTGGGG	GACACAAGTG
16601	TTTCCACATC	AACTCCTAAT	ATCTCTCAGA	CTAACCAAAT	TCAAACAGAG
16651	CCAACAGCAT	CCCTGAGCCC	TAGACTGAGG	GAGAGCAGCA	CGTCTGAGAA
16701	GACCAGCTCA	ACAACAGAGA	CAAATACTGC	CTTTTCTTAT	GTGCCCACAG
16751	GTGCTATTAC	TCAGGCCTCC	AGAACAGAAA	TCTCCTCTAG	CAGAACATCC
16801	ATCTCAGACC	TTGATCGGCC	CACAATAGCA	CCCGACATCT	CCACAGGAAT
16851	GATCACCAGG	CTCTTCACCT	CCCCCATCAT	GACAAAATCT	GCAGAAATGA
16901	CCGTCACCAC	TCAAACAACCT	ACTCCTGGGG	CTACATCACA	GGGTATCCTT
16951	CCTTGGGACA	CATCAACCAC	ACTTTTCCAG	GGAGGGACTC	ATTCAACCGT
17001	GTCTCAGGGA	TTCCCACACT	CAGAGATAAC	CACTCTTCGG	AGCAGAACCC
17051	CTGGAGATGT	GTCATGGATG	ACAACTCCCC	CTGTGGAAGA	AACCAGCTCT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

17101	GGGTTTTCCC	TGATGTCACC	TTCCATGACA	TCCCCTTCTC	CTGTTTCCTC
17151	CACATCACCA	GAGAGCATCC	CCTCCTCTCC	TCTCCCTGTG	ACTGCACTTC
17201	TTACTTCTGT	TCTGGTGACA	ACCACCAATG	TATTGGGCAC	AACAAGCCCCA
17251	GAGACCGTAA	CGAGTTCACC	TCCAAATTTA	AGCAGCCCCA	CACAGGAGAG
17301	ACTGACCACT	TACAAAGACA	CTGCGCACAC	AGAAGCCATG	CATGCTTCCA
17351	TGCATACAAA	CACTGCAGTG	GCCAACGTCG	GGACCTCCAT	TTCTGGACAT
17401	GAATCACAAT	CTTCTGTCCC	AGCTGATTCA	CACACATCCA	AAGCCACATC
17451	TCCAATGGGT	ATCACCTTCG	CCATGGGGGA	TACAAGTGTT	TCTACATCAA
17501	CTCCTGCCTT	CTTTGAGACT	AGAATTCAGA	CTGAATCAAC	ATCCTCTTTG
17551	ATTCCTGGAT	TAAGGGACAC	CAGGACGTCT	GAGGAGATCA	ACACTGTGAC
17601	AGAGACCAGC	ACTGTCCTTT	CAGAAGTGCC	CACTACTACT	ACTACTGAGG
17651	TCTCCAGGAC	AGAAGTTATC	ACTTCCAGCA	GAACAACCAT	CTCAGGGCCT
17701	GATCATTTCA	AAATGTCACC	CTACATCTCC	ACAGAAACCA	TCACCAGGCT
17751	CTCCACTTTT	CCTTTTGTA	CAGGATCCAC	AGAAATGGCC	ATCACCAACC
17801	AAACAGGTCC	TATAGGGACT	ATCTCACAGG	CTACCCTTAC	CCTGGACACA
17851	TCAAGCACAG	CTTCCTGGGA	AGGGACTCAC	TCACCTGTGA	CTCAGAGATT
17901	TCCACACTCA	GAGGAGACCA	CTACTATGAG	CAGAAGTACT	AAGGGCGTGT
17951	CATGGCAAAG	CCCTCCCTCT	GTGGAAGAAA	CCAGTTCTCC	TTCTTCCCCA
18001	GTGCCTTTAC	CTGCAATAAC	CTCACATTCA	TCTCTTTATT	CCGCAGTATC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

18051	AGGAAGTAGC	CCCACTTCTG	CTCTCCCTGT	GACTTCCCTT	CTCACCTCTG
18101	GCAGGAGGAA	GACCATAGAC	ATGTTGGACA	CACACTCAGA	ACTTGTGACC
18151	AGCTCCTTAC	CAAGTGCAAG	TAGCTTCTCA	GGTGAGATAC	TCACTTCTGA
18201	AGCCTCCACA	AATACAGAGA	CAATTCACTT	TTCAGAGAAC	ACAGCAGAAA
18251	CCAATATGGG	GACCACCAAT	TCTATGCATA	AACTACATTC	CTCTGTCTCA
18301	ATCCACTCCC	AGCCATCCGG	ACACACACCT	CCAAAGGTTA	CTGGATCTAT
18351	GATGGAGGAC	GCTATTGTTT	CCACATCAAC	ACCTGGTTCT	CCTGAGACTA
18401	AAAATGTTGA	CAGAGACTCA	ACATCCCCTC	TGACTCCTGA	ACTGAAAGAG
18451	GACAGCACCG	CCCTGGTGAT	GAACTCAACT	ACAGAGTCAA	ACACTGTTTT
18501	CTCCAGTGTG	TCCCTGGATG	CTGCTACTGA	GGTCTCCAGG	GCAGAAGTCA
18551	CCTACTATGA	TCCTACATTC	ATGCCAGCTT	CTGCTCAGTC	AACAAAGTCC
18601	CCAGACATTT	CACCTGAAGC	CAGCAGCAGT	CATTCTAACT	CTCCTCCCTT
18651	GACAATATCT	ACACACAAGA	CCATCGCCAC	ACAAACAGGT	CCTTCTGGGG
18701	TGACATCTCT	TGGCCAACTG	ACCCTGGACA	CATCAACCAT	AGCCACCTCA
18751	GCAGGAACTC	CATCAGCCAG	AACTCAGGAT	TTTGTAGATT	CAGAAACAAC
18801	CAGTGTCATG	AACAATGATC	TCAATGATGT	GTTGAAGACA	AGCCCTTTCT
18851	CTGCAGAAGA	AGCCAACTCT	CTCTCTTCTC	AGGCACCTCT	CCTTGTGACA
18901	ACCTCACCTT	CTCCTGTAAC	TTCCACATTG	CAAGAGCACA	GTACCTCCTC
18951	TCTTGTTTCT	GTGACCTCAG	TACCCACCCC	TACACTGGCG	AAGATCACAG

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

19001	ACATGGACAC	AAACTTAGAA	CCTGTGACTC	GTTCACCTCA	AAATTTAAGG
19051	AACACCTTGG	CCACTTCAGA	AGCCACCACA	GATACACACA	CAATGCATCC
19101	TTCTATAAAC	ACAGCAATGG	CCAATGTGGG	GACCACCAGT	TCACCAAATG
19151	AATTCTATTT	TACTGTCTCA	CCTGACTCAG	ACCCATATAA	AGCCACATCC
19201	GCAGTAGTTA	TCACTTCCAC	CTCGGGGGAC	TCAATAGTTT	CCACATCAAT
19251	GCCTAGATCC	TCTGCGATGA	AAAAGATTGA	GTCTGAGACA	ACTTTCTCCC
19301	TGATATTTAG	ACTGAGGGAG	ACTAGCACCT	CCCAGAAAAT	TGGCTCATCC
19351	TCAGACACAA	GCACGGTCTT	TGACAAAGCA	TTCACTGCTG	CTACTACTGA
19401	GGTCTCCAGA	ACAGAACTCA	CCTCCTCTAG	CAGAACATCC	ATCCAAGGCA
19451	CTGAAAAGCC	CACAATGTCA	CCGGACACCT	CCACAAGATC	TGTCACCATG
19501	CTTTCTACTT	TTGCTGGCCT	GACAAAATCC	GAAGAAAGGA	CCATTGCCAC
19551	CCAAACAGGT	CCTCATAGGG	CGACATCACA	GGGTACCCTT	ACCTGGGACA
19601	CATCAATCAC	AACCTCACAG	GCAGGGACCC	ACTCAGCTAT	GACTCATGGA
19651	TTTTCACAAT	TAGATTTGTC	CACTCTTACG	AGTAGAGTTC	CTGAGTACAT
19701	ATCAGGGACA	AGCCCACCCT	CTGTGGAAAA	AACCAGCTCT	TCCTCTTCCC
19751	TTCTGTCTTT	ACCAGCAATA	ACCTCACCGT	CCCCTGTACC	TACTACATTA
19801	CCAGAAAGTA	GGCCGTCTTC	TCCTGTTTAT	CTGACTTCAC	TCCCCACCTC
19851	TGGCCTAGTG	AAGACCACAG	ATATGCTGGC	ATCTGTGGCC	AGTTTACCTC
19901	CAAACCTGGG	CAGCACCTCA	CATAAGATAC	CGACTACTTC	AGAAGACATT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

19951	AAAGATACAG	AGAAAATGTA	TCCTTCCACA	AACATAGCAG	TAACCAATGT
20001	GGGGACCACC	ACTTCTGAAA	AGGAATCTTA	TTCGTCTGTC	CCAGCCTACT
20051	CAGAACCACC	CAAAGTCACC	TCTCCAATGG	TTACCTCTTT	CAACATAAGG
20101	GACACCATTG	TTTCCACATC	CATGCCTGGC	TCCTCTGAGA	TTACAAGGAT
20151	TGAGATGGAG	TCAACATTCT	CCGTGGCTCA	TGGGCTGAAG	GGAACCAGCA
20201	CCTCCCAGGA	CCCCATCGTA	TCCACAGAGA	AAAGTGCTGT	CCTTCACAAG
20251	TTGACCACTG	GTGCTACTGA	GACCTCTAGG	ACAGAAGTTG	CCTCTTCTAG
20301	AAGAACATCC	ATTCCAGGCC	CTGATCATTC	CACAGAGTCA	CCAGACATCT
20351	CCACTGAAGT	GATCCCCAGC	CTGCCTATCT	CCCTTGGCAT	TACAGAATCT
20401	TCAAATATGA	CCATCATCAC	TCGAACAGGT	CCTCCTCTTG	GCTCTACATC
20451	ACAGGGCACA	TTTACCTTGG	ACACACCAAC	TACATCCTCC	AGGGCAGGAA
20501	CACACTCGAT	GGCGACTCAG	GAATTTCCAC	ACTCAGAAAT	GACCACTGTC
20551	ATGAACAAGG	ACCCTGAGAT	TCTATCATGG	ACAATCCCTC	CTTCTATAGA
20601	GAAAACCAGC	TTCTCCTCTT	CCCTGATGCC	TTCACCAGCC	ATGACTTCAC
20651	CTCCTGTTTC	CTCAACATTA	CCAAAGACCA	TTCACACCAC	TCCTTCTCCT
20701	ATGACCTCAC	TGCTCACCCC	TAGCCTAGTG	ATGACCACAG	ACACATTGGG
20751	CACAAGCCCA	GAACCTACAA	CCAGTTCACC	TCCAAATTTG	AGCAGTACCT
20801	CACATGAGAT	ACTGACAACA	GATGAAGACA	CCACAGCTAT	AGAAGCCATG
20851	CATCCTTCCA	CAAGCACAGC	AGCGACTAAT	GTGGAAACCA	CCAGTTCTGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension**(SEQ ID NO: 309)**

20901	ACATGGGTCA	CAATCCTCTG	TCCTAGCTGA	CTCAGAAAAA	ACCAAGGCCA
20951	CAGCTCCAAT	GGATACCACC	TCCACCATGG	GGCATACAAC	TGTTTCCACA
21001	TCAATGTCTG	TTTCCTCTGA	GACTACAAAA	ATTAAGAGAG	AGTCAACATA
21051	TTCTTGACT	CCTGGACTGA	GAGAGACCAG	CATTTCCTCA	AATGCCAGCT
21101	TTTCCACTGA	CACAAGTATT	GTTCTTTCAG	AAGTCCCCAC	TGGTACTACT
21151	GCTGAGGTCT	CCAGGACAGA	AGTCACCTCC	TCTGGTAGAA	CATCCATCCC
21201	TGGCCCTTCT	CAGTCCACAG	TTTTGCCAGA	AATATCCACA	AGAACAATGA
21251	CAAGGCTCTT	TGCCTCGCCC	ACCATGACAG	AATCAGCAGA	AATGACCATC
21301	CCCACTCAAA	CAGGTCCTTC	TGGGTCTACC	TCACAGGATA	CCCTTACCTT
21351	GGACACATCC	ACCACAAAGT	CCCAGGCAAA	GACTCATTCA	ACTTTGACTC
21401	AGAGATTTCC	ACACTCAGAG	ATGACCACTC	TCATGAGCAG	AGGTCCTGGA
21451	GATATGTCAT	GGCAAAGCTC	TCCCTCTCTG	GAAAATCCCA	GCTCTCTCCC
21501	TTCCCTGCTG	TCTTTACCTG	CCACAACCTC	ACCTCCTCCC	ATTTCTCTCA
21551	CATTACCAGT	GACTATCTCC	TCCTCTCCTC	TTCCTGTGAC	TTCACTTCTC
21601	ACCTCTAGCC	CGGTAACGAC	CACAGACATG	TTACACACAA	GCCCAGAACT
21651	TGTAACCAGT	TCACCTCCAA	AGCTGAGCCA	CACTTCAGAT	GAGAGACTGA
21701	CCACTGGCAA	GGACACCACA	AATACAGAAG	CTGTGCATCC	TTCCACAAAC
21751	ACAGCAGCGT	CCAATGTGGA	GATTCCCAGC	TCTGGACATG	AATCCCCTTC
21801	CTCTGCCTTA	GCTGACTCAG	AGACATCCAA	AGCCACATCA	CCAATGTTTA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

21851	TTACCTCCAC	CCAGGAGGAT	ACAACTGTTG	CCATATCAAC	CCCTCACTTC
21901	TTGGAGACTA	GCAGAATTCA	GAAAGAGTCA	ATTCCTCCC	TGAGCCCTAA
21951	ATTGAGGGAG	ACAGGCAGTT	CTGTGGAGAC	AAGCTCAGCC	ATAGAGACAA
22001	GTGCTGTCCT	TTCTGAAGTG	TCCGTTGGTG	CTACTACTGA	GATCTCCAGG
22051	ACAGAAAGTCA	CCTCCTCTAG	CAGAACATCC	ATCTCTGGTT	CTGCTGAGTC
22101	CACAATGTTG	CCAGAAATAT	CCACCACAAG	AAAAATCATT	AAGTTCCTTA
22151	CTTCCCCCAT	CCTGGCAGAA	TCATCAGAAA	TGACCATCAA	GACCCAAACA
22201	AGTCCTCCTG	GGTCTACATC	AGAGAGTACC	TTTACATTAG	ACACATCAAC
22251	CACTCCCTCC	TTGGTAATAA	CCCATTCGAC	TATGACTCAG	AGATTGCCAC
22301	ACTCAGAGAT	AACCACTCTT	GTGAGTAGAG	GTGCTGGGGA	TGTGCCACGG
22351	CCCAGCTCTC	TCCCTGTGGA	AGAAACAAGC	CCTCCATCTT	CCCAGCTGTC
22401	TTTATCTGCC	ATGATCTCAC	CTTCTCCTGT	TTCTTCCACA	TTACCAGCAA
22451	GTAGCCACTC	CTCTTCTGCT	TCTGTGACTT	CACTTCTCAC	ACCAGGCCAA
22501	GTGAAGACTA	CTGAGGTGTT	GGACGCAAGT	GCAGAACCTG	AAACCAGTTC
22551	ACCTCCAAGT	TTGAGCAGCA	CCTCAGTTGA	AATACTGGCC	ACCTCTGAAG
22601	TCACCACAGA	TACGGAGAAA	ATTCATCCTT	TCTCAAACAC	GGCAGTAACC
22651	AAAGTTGGAA	CTTCCAGTTC	TGGACATGAA	TCCCCTTCCT	CTGTCCTACC
22701	TGACTCAGAG	ACAACCAAAG	CCACATCGGC	AATGGGTACC	ATCTCCATTA
22751	TGGGGGATAC	AAGTGTTTCT	ACATTAACTC	CTGCCTTATC	TAACACTAGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

22801	AAAATTCAGT	CAGAGCCAGC	TTCCTCACTG	ACCACCAGAT	TGAGGGAGAC
22851	CAGCACCTCT	GAAGAGACCA	GCTTAGCCAC	AGAAGCAAAC	ACTGTTCTTT
22901	CTAAAGTGTC	CACTGGTGCT	ACTACTGAGG	TCTCCAGGAC	AGAAGCCATC
22951	TCCTTTAGCA	GAACATCCAT	GTCAGGCCCT	GAGCAGTCCA	CAATGTCACA
23001	AGACATCTCC	ATAGGAACCA	TCCCCAGGAT	TTCTGCCTCC	TCTGTCTCTGA
23051	CAGAATCTGC	AAAAATGACC	ATCACAACCC	AAACAGGTCC	TTCGGAGTCT
23101	AACTAGAAA	GTACCCTTAA	TTTGAACACA	GCAACCACAC	CCTCTTGGGT
23151	GGAAACCCAC	TCTATAGTAA	TTCAGGGATT	TCCACACCCA	GAGATGACCA
23201	CTTCCATGGG	CAGAGGTCCT	GGAGGTGTGT	CATGGCCTAG	CCCTCCCTTT
23251	GTGAAAGAAA	CCAGCCCTCC	ATCCTCCCCG	CTGTCTTTAC	CTGCCGTGAC
23301	CTCACCTCAT	CCTGTTTCCA	CCACATTCCT	AGCACATATC	CCCCCTCTC
23351	CCCTTCCTGT	GACTTCACTT	CTCACCTCTG	GCCCGGCGAC	AACCACAGAT
23401	ATCTTGGGTA	CAAGCACAGA	ACCTGGAACC	AGTTCATCTT	CAAGTTTGAG
23451	CACCACCTCC	CATGAGAGAC	TGACCACTTA	CAAAGACACT	GCACATACAG
23501	AAGCCGTGCA	TCCTTCCACA	AACACAGGAG	GGACCAATGT	GGCAACCACC
23551	AGCTCTGGAT	ATAAATCACA	GTCCTCTGTC	CTAGCTGACT	CATCTCCAAT
23601	GTGTACCACC	TCCACCATGG	GGGATACAAG	TGTTCTCACA	TCAACTCCTG
23651	CCTTCCTTGA	GACTAGGAGG	ATTCAGACAG	AGCTAGCTTC	CTCCCTGACC
23701	CCTGGATTGA	GGGAGTCCAG	TGGCTCTGAA	GGGACCAGCT	CAGGCACCAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

23751	GATGAGCACT	GTCCTCTCTA	AAGTGCCCAC	TGGTGCTACT	ACTGAGATCT
23801	CCAAGGAAGA	CGTCACCTCC	ATCCCAGGTC	CCGCTCAATC	CACAATATCA
23851	CCAGACATCT	CCACAAGAAC	CGTCAGCTGG	TTCTCTACAT	CCCCTGTCAT
23901	GACAGAATCA	GCAGAAATAA	CCATGAACAC	CCATACAAGT	CCTTTAGGGG
23951	CCACAACACA	AGGCACCAGT	ACTTTGGCCA	CGTCAAGCAC	AACCTCTTTG
24001	ACAATGACAC	ACTCAACTAT	ATCTCAAGGA	TTTTCACACT	CACAGATGAG
24051	CACTCTTATG	AGGAGGGGTC	CTGAGGATGT	ATCATGGATG	AGCCCTCCCC
24101	TTCTGGAAAA	AACTAGACCT	TCCTTTTCTC	TGATGTCTTC	ACCAGCCACA
24151	ACTTCACCTT	CTCCTGTTTC	CTCCACATTA	CCAGAGAGCA	TCTCTTCCTC
24201	TCCTCTTCCT	GTGACTTCAC	TCCTCACGTC	TGGCTTGGCA	AAAACTACAG
24251	ATATGTTGCA	CAAAAGCTCA	GAACCTGTAA	CCAACTCACC	TGCAAATTTG
24301	AGCAGCACCT	CAGTTGAAAT	ACTGGCCACC	TCTGAAGTCA	CCACAGATAC
24351	AGAGAAAAC	CATCCTTCTT	CAAACAGAAC	AGTGACCGAT	GTGGGGACCT
24401	CCAGTTCTGG	ACATGAATCC	ACTTCCTTTG	TCCTAGCTGA	CTCACAGACA
24451	TCCAAAGTCA	CATCTCCAAT	GGTTATTACC	TCCACCATGG	AGGATACGAG
24501	TGTCTCCACA	TCAACTCCTG	GCTTTTTTTGA	GACTAGCAGA	ATTCAGACAG
24551	AACCAACATC	CTCCCTGACC	CTTGGACTGA	GAAAGACCAG	CAGCTCTGAG
24601	GGGACCAGCT	TAGCCACAGA	GATGAGCACT	GTCCTTTCTG	GAGTGCCCAC
24651	TGGTGCCACT	GCTGAAGTCT	CCAGGACAGA	AGTCACCTCC	TCTAGCAGAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

24701	CATCCATCTC	AGGCTTTGCT	CAGCTCACAG	TGTCACCAGA	GA CTTCACA
24751	GAAACCATCA	CCAGACTCCC	TACCTCCAGC	ATAATGACAG	AATCAGCAGA
24801	AATGATGATC	AAGACACAAA	CAGATCCTCC	TGGGTCTACA	CCAGAGAGTA
24851	CTCATACTGT	GGACATATCA	ACAACACCCA	ACTGGGTAGA	AACCCACTCG
24901	ACTGTGACTC	AGAGATTTTC	ACACTCAGAG	ATGACCACTC	TTGTGAGCAG
24951	AAGCCCTGGT	GATATGTTAT	GGCCTAGTCA	ATCCTCTGTG	GAAGAAACCA
25001	GCTCTGCCTC	TTCCCTGCTG	TCTCTGCCTG	CCACGACCTC	ACCTTCTCCT
25051	GTTTCCTCTA	CATTAGTAGA	GGATTTCCCT	TCCGCTTCTC	TTCCTGTGAC
25101	TTCTCTTCTC	ACCCCTGGCC	TGGTGATAAC	CACAGACAGG	ATGGGCATAA
25151	GCAGAGAACC	TGGAACCAGT	TCCACTTCAA	ATTGAGCAG	CACCTCCCAT
25201	GAGAGACTGA	CCACTTTGGA	AGACACTGTA	GATACAGAAG	ACATGCAGCC
25251	TTCCACACAC	ACAGCAGTGA	CCAACGTGAG	GACCTCCATT	TCTGGACATG
25301	AATCACAATC	TTCTGTCCTA	TCTGACTCAG	AGACACCCAA	AGCCACATCT
25351	CCAATGGGTA	CCACCTACAC	CATGGGGGAA	ACGAGTGTTT	CCATATCCAC
25401	TTCTGACTTC	TTTGAGACCA	GCAGAATTCA	GATAGAACCA	ACATCCTCCC
25451	TGACTTCTGG	ATTGAGGGAG	ACCAGCAGCT	CTGAGAGGAT	CAGCTCAGCC
25501	ACAGAGGGAA	GCACTGTCCT	TTCTGAAGTG	CCCAGTGGTG	CTACCACTGA
25551	GGTCTCCAGG	ACAGAAGTGA	TATCCTCTAG	GGGAACATCC	ATGTCAGGGC
25601	CTGATCAGTT	CACCATATCA	CCAGACATCT	CTACTGAAGC	GATCACCAGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

25651	CTTTCTACTT	CCCCATTAT	GACAGAATCA	GCAGAAAGTG	CCATCACTAT
25701	TGAGACAGGT	TCTCCTGGGG	CTACATCAGA	GGGTACCCTC	ACCTTGGACA
25751	CCTCAACAAC	AACCTTTTGG	TCAGGGACCC	ACTCAACTGC	ATCTCCAGGA
25801	TFTTCACACT	CAGAGATGAC	CACTCTTATG	AGTAGAACTC	CTGGAGATGT
25851	GCCATGGCCG	AGCCTTCCCT	CTGTGGAAGA	AGCCAGCTCT	GTCTCTTCCT
25901	CACTGTCTTC	ACCTGCCATG	ACCTCAACTT	CTTTTTTCTC	CACATTACCA
25951	GAGAGCATCT	CCTCCTCTCC	TCATCCTGTG	ACTGCACTTC	TCACCCCTGG
26001	CCCAGTGAAG	ACCACAGACA	TGTTGCGCAC	AAGCTCAGAA	CCTGAAACCA
26051	GTTACCTCC	AAATTTGAGC	AGCACCTCAG	CTGAAATATT	AGCCACGTCT
26101	GAAGTCACCA	AAGATAGAGA	GAAAATTCAT	CCCTCCTCAA	ACACACCTGT
26151	AGTCAATGTA	GGGACTGTGA	TTTATAAACA	TCTATCCCCT	TCCTCTGTTT
26201	TGGCTGACTT	AGTGACAACA	AAACCCACAT	CTCCAATGGC	TACCACCTCC
26251	ACTCTGGGGA	ATACAAGTGT	TTCCACATCA	ACTCCTGCCT	TCCCAGAAAC
26301	TATGATGACA	CAGCCAACTT	CCTCCCTGAC	TTCTGGATTA	AGGGAGATCA
26351	GTACCTCTCA	AGAGACCAGC	TCAGCAACAG	AGAGAAGTGC	TTCTCTTTCT
26401	GGAATGCCCA	CTGGTGCTAC	TACTAAGGTC	TCCAGAACAG	AAGCCCTCTC
26451	CTTAGGCAGA	ACATCCACCC	CAGGTCCTGC	TCAATCCACA	ATATCACCAG
26501	AAATCTCCAC	GGAAACCATC	ACTAGAATTT	CTACTCCCCT	CACCACGACA
26551	GGATCAGCAG	AAATGACCAT	CACCCCCAAA	ACAGGTCATT	CTGGGGCATC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

26601	CTCACAAGGT	ACCTTTACCT	TGGACACATC	AAGCAGAGCC	TCCTGGCCAG
26651	GAAGTCACTC	AGCTGCAACT	CACAGATCTC	CACACTCAGG	GATGACCACT
26701	CCTATGAGCA	GAGGTCCTGA	GGATGTGTCA	TGGCCAAGCC	GCCCATCAGT
26751	GGAAAAAACT	AGCCCTCCAT	CTTCCCTGGT	GTCTTTATCT	GCAGTAACCT
26801	CACCTTCGCC	ACTTTATTCC	ACACCATCTG	AGAGTAGCCA	CTCATCTCCT
26851	CTCCGGGTGA	CTTCTCTTTT	CACCCCTGTC	ATGATGAAGA	CCACAGACAT
26901	GTTGGACACA	AGCTTGGAAC	CTGTGACCAC	TTCACCTCCC	AGTATGAATA
26951	TCACCTCAGA	TGAGAGTCTG	GCCACTTCTA	AAGCCACCAT	GGAGACAGAG
27001	GCAATTCAGC	TTTCAGAAAA	CACAGCTGTG	ACTCAGATGG	GCACCATCAG
27051	CGCTAGACAA	GAATTCCTATT	CCTCTTATCC	AGGCCTCCCA	GAGCCATCCA
27101	AAGTGACATC	TCCAGTGGTC	ACCTCTTCCA	CCATAAAAGA	CATTGTTTCT
27151	ACAACCATAC	CTGCTTCCTC	TGAGATAACA	AGAATTGAGA	TGGAGTCAAC
27201	ATCCACCCTG	ACCCCCACAC	CAAGGGAGAC	CAGCACCTCC	CAGGAGATCC
27251	ACTCAGCCAC	AAAGCCAAGC	ACTGTTCTCT	ACAAGGCACT	CACTAGTGCC
27301	ACGATTGAGG	ACTCCATGAC	ACAAGTCATG	TCCTCTAGCA	GAGGACCTAG
27351	CCCTGATCAG	TCCACAATGT	CACAAGACAT	ATCCAGTGAA	GTGATCACCA
27401	GGCTCTCTAC	CTCCCCCATC	AAGGCAGAAT	CTACAGAAAT	GACCATTACC
27451	ACCCAAACAG	GTTCTCCTGG	GGCTACATCA	AGGGGTACCC	TTACCTTGGA
27501	CACTTCAACA	ACTTTTATGT	CAGGGACCCA	CTCAACTGCA	TCTCAAGGAT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

27551	TTTCACACTC	ACAGATGACC	GCTCTTATGA	GTAGAACTCC	TGGAGATGTG
27601	CCATGGCTAA	GCCATCCCTC	TGTGGAAGAA	GCCAGCTCTG	CCTCTTTCTC
27651	ACTGTCTTCA	CCTGTCATGA	CCTCATCTTC	TCCCGTTTCT	TCCACATTAC
27701	CAGACAGCAT	CCACTCTTCT	TCGCTTCCTG	TGACATCACT	TCTCACCTCA
27751	GGGCTGGTGA	AGACCACAGA	GCTGTTGGGC	ACAAGCTCAG	AACCTGAAAC
27801	CAGTTCACCC	CCAAATTTGA	GCAGCACCTC	AGCTGAAATA	CTGGCCACCA
27851	CTGAAGTCAC	TACAGATACA	GAGAACTGG	AGATGACCAA	TGTGGTAACC
27901	TCAGGTTATA	CACATGAATC	TCCTTCCTCT	GTCCTAGCTG	ACTCAGTGAC
27951	AACAAAGGCC	ACATCTTCAA	TGGGTATCAC	CTACCCACAC	GGAGATACAA
28001	ATGTTCTCAC	ATCAACCCCT	GCCTTCTCTG	ACACCAGTAG	GATTCAAACA
28051	AAGTCAAAGC	TCTCACTGAC	TCCTGGGTTG	ATGGAGACCA	GCATCTCTGA
28101	AGAGACCAGC	TCTGCCACAG	AAAAAAGCAC	TGTCCTTTCT	AGTGTGCCCA
28151	CTGGTGCTAC	TACTGAGGTC	TCCAGGACAG	AAGCCATCTC	TTCTAGCAGA
28201	ACATCCATCC	CAGGCCCTGC	TCAATCCACA	ATGTCATCAG	ACACCTCCAT
28251	GGAAACCATC	ACTAGAATTT	CTACCCCCCT	CACAAGGAAA	GAATCAACAG
28301	ACATGGCCAT	CACCCCCAAA	ACAGGTCCTT	CTGGGGCTAC	CTCGCAGGGT
28351	ACCTTTACCT	TGGACTCATC	AAGCACAGCC	TCCTGGCCAG	GAACCTCACTC
28401	AGCTACAAC	TAGAGATTTC	CACAGTCAGT	GGTGACAAC	TCTATGAGCA
28451	GAGGTCCTGA	GGATGTGTCA	TGGCCAAGCC	CGCTGTCTGT	GGAAAAAAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension(SEQ ID NO: 309)

28501	AGCCCTCCAT	CTTCCCTGGT	ATCTTCATCT	TCAGTAACCT	CACCTTCGCC
28551	ACTTTATTCC	ACACCATCTG	GGAGTAGCCA	CTCCTCTCCT	GTCCTGTCA
28601	CTTCTCTTTT	CACCTCTATC	ATGATGAAGG	CCACAGACAT	GTTGGATGCA
28651	AGTTTGGAAC	CTGAGACCAC	TTCAGCTCCC	AATATGAATA	TCACCTCAGA
28701	TGAGAGTCTG	GCCGCTTCTA	AAGCCACCAC	GGAGACAGAG	GCAATTCACG
28751	TTTTTGAAAA	TACAGCAGCG	TCCCATGTGG	AAACCACCAG	TGCTACAGAG
28801	GAACTCTATT	CCTCTTCCCC	AGGCTTCTCA	GAGCCAACAA	AAGTGATATC
28851	TCCAGTGGTC	ACCTCTTCCT	CTATAAGAGA	CAACATGGTT	TCCACAACAA
28901	TGCCTGGCTC	CTCTGGCATT	ACAAGGATTG	AGATAGAGTC	AATGTCATCT
28951	CTGACCCCTG	GA CTGAGGGA	GACCAGAACC	TCCCAGGACA	TCACCTCATC
29001	CACAGAGACA	AGCACTGTCC	TTTACAAGAT	GCCCTCTGGT	GCCACTCCTG
29051	AGGTCTCCAG	GACAGAAGTT	ATGCCCTCTA	GCAGAACATC	CATTCTGCG
29101	CCTGCTCAGT	CCACAATGTC	ACTAGACATC	TCCGATGAAG	TTGTCACCAG
29151	GCTGTCTACC	TCTCCCATCA	TGACAGAATC	TGCAGAAATA	ACCATCACCA
29201	CCCAAACAGG	TTATTCTCTG	GCTACATCCC	AGGTTACCCT	TCCCTTGGGC
29251	ACCTCAATGA	CCTTTTTGTC	AGGGACCCAC	TCAACTATGT	CTCAAGGACT
29301	TTCACACTCA	GAGATGACCA	ATCTTATGAG	CAGGGGTCCT	GAAAGTCTGT
29351	CATGGACGAG	CCCTCGCTTT	GTGGAAACAA	CTAGATCTTC	CTCTTCTCTG
29401	ACATCATTAC	CTCTCACGAC	CTCACTTTCT	CCTGTGTCCT	CCACATTACT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

29451	AGACAGTAGC	CCCTCCTCTC	CTCTTCCTGT	GACTTCACTT	ATCCTCCCAG
29501	GCCTGGTGAA	GACTACAGAA	GTGTTGGATA	CAAGCTCAGA	GCCTAAAACC
29551	AGTTCATCTC	CAAATTTGAG	CAGCACCTCA	GTTGAAATAC	CGGCCACCTC
29601	TGAAATCATG	ACAGATACAG	AGAAAATTCA	TCCTTCCTCA	AACACAGCGG
29651	TGGCCAAAGT	GAGGACCTCC	AGTTCTGTTC	ATGAATCTCA	TTCTCTGTCT
29701	CTAGCTGACT	CAGAAACAAC	CATAACCATA	CCTTCAATGG	GTATCACCTC
29751	CGCTGTGGAC	GATACCACTG	TTTTCACATC	AAATCCTGCC	TTCTCTGAGA
29801	CTAGGAGGAT	TCCGACAGAG	CCAACATTCT	CATTGACTCC	TGGATTCAGG
29851	GAGACTAGCA	CCTCTGAAGA	GACCACCTCA	ATCACAGAAA	CAAGTGCAGT
29901	CCTTTATGGA	GTGCCCCTA	GTGCTACTAC	TGAAGTCTCC	ATGACAGAAA
29951	TCATGTCCTC	TAATAGAACA	CACATCCCTG	ACTCTGATCA	GTCCACGATG
30001	TCTCCAGACA	TCATCACTGA	AGTGATCACC	AGGCTCTCTT	CCTCATCCAT
30051	GATGTCAGAA	TCAACACAAA	TGACCATCAC	CACCCAAAAA	AGTTCTCCTG
30101	GGGCTACAGC	ACAGAGTACT	CTTACCTTGG	CCACAACAAC	AGCCCCCTTG
30151	GCAAGGACCC	ACTCAACTGT	TCCTCCTAGA	TTTTTACACT	CAGAGATGAC
30201	AACTCTTATG	AGTAGGAGTC	CTGAAAATCC	ATCATGGAAG	AGCTCTCCCT
30251	TTGTGGAAAA	AACTAGCTCT	TCATCTTCTC	TGTTGTCCTT	ACCTGTCACG
30301	ACCTCACCTT	CTGTTTCTTC	CACATTACCG	CAGAGTATCC	CTTCTCCTC
30351	TTTTTCTGTG	ACTTCACTCC	TCACCCAGG	CATGGTGAAG	ACTACAGACA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

30401	CAAGCACAGA	ACCTGGAACC	AGTTTATCTC	CAAATCTGAG	TGGCACCTCA
30451	GTTGAAATAC	TGGCTGCCTC	TGAAGTCACC	ACAGATACAG	AGAAAATTCA
30501	TCCTTCTTCA	AGCATGGCAG	TGACCAATGT	GGGAACCACC	AGTTCTGGAC
30551	ATGAACTATA	TTCCTCTGTT	TCAATCCACT	CGGAGCCATC	CAAGGCTACA
30601	TACCCAGTGG	GTACTCCCTC	TTCCATGGCT	GAAACCTCTA	TTCCACATC
30651	AATGCCTGCT	AATTTTGAGA	CCACAGGATT	TGAGGCTGAG	CCATTTTCTC
30701	ATTTGACTTC	TGGATTTAGG	AAGACAAACA	TGTCCCTGGA	CACCAGCTCA
30751	GTCACACCAA	CAAATACACC	TTCTTCTCCT	GGGTCCACTC	ACCTTTTACA
30801	GAGTTCCAAG	ACTGATTTC	CCTCTTCTGC	AAAAACATCA	TCCCCAGACT
30851	GGCCTCCAGC	CTCACAGTAT	ACTGAAATTC	CAGTGGACAT	AATCACCCCC
30901	TTTAATGCTT	CTCCATCTAT	TACGGAGTCC	ACTGGGATAA	CCTCCTTCCC
30951	AGAATCCAGG	TTTACTATGT	CTGTAACAGA	AAGTACTCAT	CATCTGAGTA
31001	CAGATTTGCT	GCCTTCAGCT	GAGACTATTT	CCACTGGCAC	AGTGATGCCT
31051	TCTCTATCAG	AGGCCATGAC	TTCATTTGCC	ACCACTGGAG	TTCCACGAGC
31101	CATCTCAGGT	TCAGGTAGTC	CATTCTCTAG	GACAGAGTCA	GGCCCTGGGG
31151	ATGCTACTCT	GTCCACCATT	GCAGAGAGCC	TGCCTTCATC	CACTCCTGTG
31201	CCATTCTCCT	CTTCAACCTT	CACTACCACT	GATTCTTCAA	CCATCCCAGC
31251	CCTCCATGAG	ATAACTTCCT	CTTCAGCTAC	CCCATATAGA	GTGGACACCA
31301	GTCTTGGGAC	AGAGAGCAGC	ACTACTGAAG	GACGCTTGGT	TATGGTCAGT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

31351 ACTTTGGACA CTTCAAGCCA ACCAGGCAGG ACATCTTCAA CACCCATTTT
31401 GGATACCAGA ATGACAGAGA GCGTTGAGCT GGGAACAGTG ACAAGTGCTT
31451 ATCAAGTTCC TTCACTCTCA ACACGGTTGA CAAGAACTGA TGGCATT

Table 25

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

```

1  MLKPSGLPGS  SSPTRSLMTG  SRSTKATPEM  DSGLTGATLS  PKTSTGAIVV
51  TEHTLPFTSP  DKTLASPTSS  VVGRTTQSLG  VMSSALPEST  SRGMTHSEQR
101 TSPSLSPQVN  GTPSRNYPAT  SMVSGLSSPR  TRTSSTEGNF  TKEASTYTLT
151 VETTSGPVTE  KYTVPTETST  TEGDSTETPW  DTRYIPVKIT  SPMKTFADST
201 ASKENAPVSM  TPAETTVTDS  HTPGRTNPSF  GTLYSSFDDL  SPKGTPNSRG
251 ETSLELILST  TGYPFSSPEP  GSAGHSRIST  SAPLSSASV  LDNKISETSI
301 FSGQSLTSPL  SPGVPEARAS  TMPNSAIPFS  MTLNAETSA  ERVRSTISSL
351 GTPSISTKQT  AETILTFHAF  AETMDIPSTH  IAKTLASEWL  GSPGTLGGTS
401 TSALTTTSPS  TTLVSEETNT  HHSTSGKETE  GTLNTSMTPL  ETSAPGEESE
451 MTATLVPTLG  FTTLDSKIRS  PSQVSSHPT  RELRTTGSTS  GRQSSSTAAB
501 GSSDILRATT  SSTSKASSWT  SESTAQQFSE  PQHTQWVETS  PSMKTERPPA
551 STSVAAPITT  SVPSVVGFT  TLKTSSTKGI  WLEETSADTL  IGESTAGPTT
601 HQFAVPTGIS  MTGGSSTRGS  QGTHLLTRA  TASSETSADL  TLATNGVPVS
651 VSPAUSKTAA  GSSPPGGTKP  SYTMVSSVIP  ETSSLQSSAF  REGTSLGLTP
701 LNTRHPFSSP  EPDSAGHTKI  STSIPLLSSA  SVLEDKVSAT  STFSHHKATS
751 SITGTPEIS  TKTKPSSAVL  SSMTLSNAAT  SPERVRNATS  PLTHPSPSGE
801 ETAGSVLTLS  TSAETDSPN  IHPTGTLTSE  SSESPTLSL  PSVSGVKTTF
851 SSSTPSTHLF  TSGEETEETS  NPSVSPQETS  VSRVRTLAS  TSVPTPVFPT

```

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene Protein Sequence)
(SEQ ID NO: 310)

901 MDTWPTRSAQ FSSSHLVSEL RATSSTSVTN STGSALPKIS HLTGTATMSQ
951 TNRDTFNDSA APQSTTWPET SPRFKTGLPS ATTTVSTSAT SLSATVMVSK
1001 FTSPATSSME ATSIREPSTT ILTTETTNGP GSMAVASTNI PIGKGYITEG
1051 RLDTSHLPIG TTASSETSM DFTMAKESVSM SVSPSQSMDA AGSSTPGRTS
1101 QFVDTFSDDV YHLTSREITI PRDGTSSALT PQMTATHPPS PDPGSARSTW
1151 LGILSSSPSS PTPKVTMSST FSTQRVTTSM IMDTVETSRW NMPNLPSTTS
1201 LTPSNIPTSG AIGKSTLVPL DTPSPATSLE ASEGG LPTLS TYPESTNTPS
1251 IHLGAHASSE SPSTINLTMA SVVKPGSYTP LTFPSIETHI HVSTARMAYS
1301 SGSSPEMTAP GETNTGSTWD PTTYITTTDP KDTSSAQVST PHSVRTLRRT
1351 ENHPKTESAT PAAYSGSPKI SSSPNLTSPA TKAWTITDFT EHSTQLHYTK
1401 LAEKSSGFET QSAPGPVSVV IPTSPTIGSS TLELTSDVPG EPLVLAPSEQ
1451 TTITLPMATW LSTSLTEEMA STDLDISSPS SPMSTFAIFP PMSTPSHEL
1501 KSEADTSAIR NTDSTTLDQH LGIRSLGRTG DLTTVPITPL TTTWTSVIEH
1551 STQAQDTLSA TMSPTHVTQS LKDQTSIPAS ASPSHLTEVY PELGTQGRSS
1601 SEATTFWKPS TDTLREIET GPTNIQSTPP MDNTTTGSSS SGVTLGIAHL
1651 PIGTSSPAET STNMALEERS STATVSMAGT MGLLVTSAPG RSISQSLGRV
1701 SSVLSESTTE GVTDSSKGSS PRLNTQGNTA LSSSLEPSYA EGSQMSTSIP
1751 LTSSPTTPDV EFIGGSTFWT KEVTTVMTSD ISKSSARTES SSATLMSTAL

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

1801	GSTENTGKEK	LRTASMDLPS	PTPSMEVTPW	ISLTLSNAPN	TTDSLDSLHG
1851	VHTSSAGTLA	TDRSLNTGVT	RASRLENGSD	TSSKSLSMGN	STHTSMTDTE
1901	KSEVSSSIHP	RPETSAPGAE	TTLTSTPGNR	AISLTLPFSS	IPVEEVISTG
1951	ITSGPDINSA	PMTHSPITPP	TIVWTSTGTI	EQSTQPLHAV	SSEKVSVQTQ
2001	STPYVNSVAV	SASPTHENS	SSGSSTSSPY	SSASLESlds	TISRRAITS
2051	WLWDLTTS	TTTWPSTSL	EALSSGHSG	SNPSSTTTE	PLFSAASTSA
2101	AKQRNPETET	HGPQNTAAST	LNTDASSVTG	LSETPVGASI	SSEVPLPMAI
2151	TSRSDVSGLT	SESTANPSLG	TASSAGTKLT	RTISLPTSES	LVSFRMNKDP
2201	WTVSIPLGSH	PTTNTETSIP	VNSAGPPGLS	TVASDVIDTP	SDGAESIPTV
2251	SFSPSPDTEV	TTISHFPEKT	THSFRTISSL	THELTSRVTP	IPGDWMSSAM
2301	STKPTGASPS	ITLGERRTIT	SAAPTTSPIV	LTASFTETST	VSLDNETTVK
2351	TSDILDARKT	NELPSDSSSS	SDLINTSIAS	STMDVTKTAS	ISPTSISGMT
2401	ASSSPSLFSS	DRPQVPTSTT	ETNTATSPSV	SSNTYSLDGG	SNVGGTPSTL
2451	PPFTITHPVE	TSSALLAWSR	PVRTFSTMVS	TDASGENPT	SSNSVVTSVP
2501	APGTWTSVGS	TTDLPAMGFL	KTSPAGEAHS	LLASTIEPAT	AFTPHLSAAV
2551	VTGSSATSEA	SLTTSESKA	IHSSPQTPTT	PTSGANWETS	ATPESLLVVT
2601	ETSDTTLTSK	ILVTDILFS	TVSTPPSKFP	STGTLGASF	PTLLPDTPAI
2651	PLTATEPTSS	LATSFDS	TPLVTIASDSL	GTVPETTLT	MSETSNGDALVLK

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

2701 TVSNPDRSIP GITIQGVTES PLHPSS~~T~~SPS KIVAPRNTTY EGSITVALST
2751 LPAGTTGSLV FSQSSENSET TALVDSSAGL ERASVMPLTT GSQGMASGG
2801 IRSGSTHSTG TKTFSSLPLT MNPGEVTAMS EITTNRLTAT QSTAPKGIPV
2851 KPTSAESGLL TPVSASSSPS KAFASLTAP PTWGIPQSTL TFEFSEVPSL
2901 DTKSASLPTP GQSLNTIPDS DASTASSLS KSPEKNPRAR MMTSTKAISA
2951 SSFQSTGFTE TPEGASPSM AGHEPRVPTS GTGDPYASE SMSYPDPKA
3001 SSAMTSTSLA SKLTTLFSTG QAARSGSSSS PISLSTEKET SFLSPTASTS
3051 RKTSFLGPS MARQPNILVH LQTSALTLSPT TSTLNMSQEE PPELTSSQTI
3101 AEEEGTTAET QTLTFTPSET PTSLLPVSSP TEPTARRKSS PETWASSISV
3151 PAKTSLVETT DGLVTTIKM SSQAAQGNST QPAPAEETGT SPAGTSPGSP
3201 EMSTTLKIMS SKEPSISPEI RSTVRNSPWK TPETTVPMET TVEPVTLQST
3251 ALGSGSTSSIS HLPTGTTSPS KSPTENMLAT ERVSLSPSP EAWTNLYSGT
3301 PGGTRQSLAT MSSVSLESPT ARSITGTGQQ SSPELVSKTT GMEFSMWHGS
3351 TGGTTGDTHV SLSTSSNILE DPVTSPNSVS SLTDKSKHKT ETWVSTTAIP
3401 STVLNNKIMA AEQQT~~S~~RSVD EAYSSTSSWS DQTSGSDITL GASPDVTNTL
3451 YITSTAQTTS LVSLPSGDQG ITS~~L~~TNPSSG KTSSASSVTS PSIGLETLRA
3501 NVSAVKSDIA PTAGHLSQTS SPAEVSILDV TTAPTPGIST TITTMGTNSI
3551 STTTPNPEVG MSTMDSTPAT ERRTTSTEHP STWSSTAASD SWTVTDMTSN

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

```

3601  LKVARSPGTI STMHTTSFLA SSTEELDSMST PHGRITVIGT SLVTPSSDAS
3651  AVKTETSTSE RTLSPSDTTA STPISTFSRV QRMSISVPDI LSTSWTPSSST
3701  EAEDVPVSMV PTDHASTKTD PNTPLSTFLF DSLSTLDWDG GRSLSSATAT
3751  TSAPOGATTP QELTLETMIS PATSQLPFSI GHITSAVTPA AMARSSGVTF
3801  SRPDPTSKKA EQTSTQLPTT TSAHPGQVPR SAATTLDDVIP HTAKTPDATE
3851  QRQGQTALTT EARATSDSWN EKEKSTPSAP WITEMMNSVS EDITIKEVTSS
3901  SSVLKDPEYA GHKLGWDDF IPKFGKAAHM RELPLLSPQ DKEAIHPSTN
3951  TVETTGWVTS SEHASHSTIP AHSASSKLTS PVVTTSTREQ AIVSMSTTTW
4001  PESTRARTEP NSFLEIELRD VSPYMDTSST TQTSIISSPG STAITKGHRT
4051  EITSYKRISS SFLAQSMRSS DSPSEAITRL SNFPAMTESG GMILAMQTSP
4101  PGATSIASPT LDTSATASWT GTPLATTQRF TYSEKTTLFS KGREDTSQPS
4151  PPCVEETSSS SSVVPIHATT SPSNILLTSQ GHSPSSTPPV TSVFLSETSG
4201  LGKTTDMSRI SLEPGTSLPP NLSSTAGEAL STYEASRDTK AIHHSADTAV
4251  TNMEATSSEY SPIPGHTKPS KATSPLVTSH IMGDITSSTS VFGSSETTEI
4301  ETVSSVNQGL QERSTSQVAS SATETSTVIT HVSSGDATH VTKTQATFSS
4351  GTSISSPHQF ITSTNTFTDV STNPSTSLIM TESSGVTTIT QTGPTGAATQ
4401  GPYLLDTSTM PYLTETPLAV TPDEFMQSEK TLISKGPKDV TWTSPPSVAE
4451  TSYPSLTPF LVTTPPATL TLQGQHTSSP VSATSVLTSG LVKTTDMLNT

```

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

4501 SMEPVTNSPQ NLNNPSNEIL ATLAATTDIE TIHPSINKAV TNMG TASSAH
4551 VLHSTLPVSS EPSTATSPMV PASSMGDALA SISIPGSETT DIEGEPTSSL
4601 TAGRKENSTL QEMNSTTESN IILSNVSVG A ITEATKMEVP SFDATFIPTP
4651 AQSTKFPDIF SVASSRLSNS PPMTISTHMT TTQTGSSGAT SKIPLALDTS
4701 TLETSAGTPS VVTEGFAHSK ITTAMNNDVK DVSQTNPPFQ DEASSPSSQA
4751 PVLVTTLPS VAFTPQWHST SSPVSMSSVL TSSLVKTAGK VDTSLLETVTS
4801 SPQSMSNTLD DISVTS AATT DIETHPSIN TVVTNVGTTG SAFESHSTVS
4851 AYPEPSKSHI LPMLPPPPWK TPQFPRSIPK SSKTTRTETE TTSSLTPKLR
4901 ETSISQEITS STETSTVPYK ELTGATTEVS RTDVTSSSST SFP GPDQSTV
4951 SLDISTETNT RLSTSPIMTE SAEITITTQT GPHGATSQDT FTMDPSNTTP
5001 QAGIHSAMTH GFSQLDVTTL MS RIPQDVSW TSPPSVDKTS SPSSFLSSPA
5051 MTTPSLISST LPEDKLSSPM TSLLTSGLVK ITDILRTRLE PVTSSLPNFS
5101 STSDKILATS KDSKDTKEIF PSINTEETNV KANNSGHESH SPALADSETP
5151 KATTQM VITT TVGDPAPSTS MPVHGSSETT NIKREPTYFL TPR LRETSTS
5201 QESSFPTDTS FLLSKVPTGT ITEVSSTGVI SSSKISTPDH DKSTVPPDTF
5251 TGEIPRVFTS SIKTKSAEMT ITTQASPPES ASHSTLPLDT STTLSQGGTH
5301 STVSQGFPYS EVTTLMGMP GNVSWMTTPP VEETSSVSSL MSSPAMTSPS
5351 PVSSTSPQSI PSSPLPVTAL PTSVLVTTTD VLGTTSPESV TSSPPNLSSI

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

5401 THERPATYKD TAHTAAMHH STNTAVTNVG TSGSGHKSQS SVLADSETSK
5451 ATPLMSTAST LGDTSVSTST PNISQTNQIQ TEPTASLSPR LRESSTSEKT
5501 SSTTETNTAF SYVPTGAIQ ASRTEISSR TSISDLDRST IAPDISTGMI
5551 TRLEFTSPIMT KSAEMTVTTQ TTPGATSQG ILPWDTSTTL FQGGTHSTVS
5601 QGFPHEITT LRSRTPGDVS WMTTPPVEET SSGFSLMSPS MTSPSPVSST
5651 SPESIPSSPL PVTALLTSVL VTTTNVLGTT SPEPVTSSPP NLSSPTQERL
5701 TTYKDTAHE AMHASMHTNT AVANVGTSIS GHESQSSVPA DSHTSKATSP
5751 MGITFAMGDT SVYTSTPAFF ETRIQSESTS SLIPGLRDTR TSEEINTVTE
5801 TSTVLSEVPT TTTTEVSRTE VITSSRTTIS GPDHSMSPY ISTETITRLS
5851 TFPFVTGSTE MAITNQTGPI GTISQATLTL DTSSTASWEG THSPVTQRF
5901 HSEETTTMSR STKGVSWQSP PSVEETSSPS SPVPLPAITS HSSLYSAVSG
5951 SSPTSALPVT SLLTSGRRKT IDMLDTHSEL VTSSLPSASS FSGEILTSEA
6001 STNTETIHFS ENTAETNMGT TNSMHKLHSS VSIHSQPSGH TPPKVTGSMM
6051 EDAIVSTSTP GSPETKNVDR DSTSPLTPEL KEDSTALVMN STTESNTVFS
6101 SVSLDAATEV SRAEVYYDP TFMPSAQST KSPDISPEAS SSHSNSPPLT
6151 ISTHKTIATQ TGPSGVTSLG QLTLDSTIA TSAGTPSART QDFVDSETTS
6201 VMNNDLNDVL KTSFSAEEA NSLSSQAPLL VTTSPSPVTS TLQEHSTSSL
6251 VSVTSVPTPT LAKITDMDTN LEPVTRSPQN LRNTLATSEA TTDTHMHPS

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

6301	INTAMANVGT	TSSPNEFYFT	VSPDSDPYKA	TSVVITSTS	GDSIVSTSMP
6351	RSSAMKKIES	ETTFSLIFRL	RETSTSQKIG	SSSDTSTVFD	KAFTAATTEV
	Contig16				
6401	SRTELTSSSR	TSIQGTEKPT	MSPDTSTRSV	TMLSTFAGLT	KSEERTIATQ
6451	TGPHRATSQG	TLTWDTSIIT	SQAGTHSAMT	HGFSQLDLST	LTSRVPEYIS
6501	GTSPPSVEKT	SSSSLLSLP	AITSPSPVPT	TLPESRPSSP	VHLTSLPTSG
6551	LVKTTDMLAS	VASLPPNLGS	TSHKIPTTSE	DIKDTEKMYP	STNIAVTNVG
6601	TTTSEKESYS	SVPAYSEPPK	VTSPMVTSTN	IRDTIVSTSM	PGSSEITRIE
6651	MESTFSLAHG	LKGTSTSQDP	IVSTEKSAVL	HKLTTGATET	SRTEVASSRR
6701	TSIPGPDHST	ESPDISTEVI	PSLPISLGIT	ESSNMIIITR	TGPPLGSTSQ
6751	GTFTLDTPTT	SSRAGTHSMA	TQEFPHSEMT	TVMNKDPEIL	SWTIPPSIEK
6801	TSFSSSLMPS	PAMTSPPVSS	TLPKTIHTTP	SPMTSLLTPS	LVMTTDTLGT
6851	SPEPTTSSPP	NLSSTSEIL	TTDEDTTAE	AMHPSTSTAA	TNVETTSSGH
6901	GSQSSVLADS	EKTATAPMD	TTSTMGHTTV	STSMVSSET	TKIKRESTYS
6951	LTPGLRETSI	SQNASFSTD	SIVLSEVPTG	TTAEVSRTEV	TSSGRTSIPG
7001	PSQSTVLPEI	STRMTLRLFA	SPTMTESAEM	TIPTQTGPSG	STSQDTLLTD
7051	TSTTKSQAKT	HSTLTQRFP	SEMTLMSRG	PGDMSWQSSP	SLENPSSLPS
7101	LLSLPATTSP	PPISSTLPVT	ISSSPLPVT	LLTSSPVTTT	DMLHTSPELV
7151	TSSPPKLSHT	SDERLTGKD	TTNTEAVHPS	TNTAASNVEI	PSSGHESPSS

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

7201 ALADSETSKA TSPMFITSTQ EDTTVAISTP HFLETSRIQK ESISSLSPKL
Contig10

7251 RETGSSVETS SAIETSAVLS EVSVGATTEI SRTEVTSSSR TSISGSAIST

7301 MLPEISTTRK IIKFPTSPIL AISSEMTIKT QTSPPGSTSE STFTLDTSTT

7351 PSLVITHSTM TQRLPHSEIT TLVSRGAGDV PRPSSLPVEE TSPSSQLSL

7401 SAMISPSPVS STLPASSHSS SASVTSLLTP GQVKTEVLD ASAEPETSSP

7451 PSLSSTSVEI LATSEVTTDT EKIHPFSNTA VTKVGTSSSG HESPSSVLDP

7501 SETTKATSAM GTISIMGDTs VSTLTPALSM TRKIQSEPAS SLTTRLRETS

7551 TSEETSLATE ANTVLSKVST GATTEVSRTE AISFSRTSMS GPEQSTMSQD

7601 ISIGTIPRIS ASSVLTESAK MTITTQTGPS ESTLESTLNL NTATTPSWVE

7651 THSIVIQGF HPMTTSMGR GPGGVSWPSP PFVKETSPPS SPLSLPAVTS
Contig22

7701 PHPVSTTFLA HIPPSPLPVT SLLTSGPATT TDILGTSTEP GTSSSSSLST

7751 TSHERLTTYK DTAHTEAVHP STNTGGTNVA TTSSGYKSQS SVLADSSPMC

7801 TTSTMGDTSV LTSTPAFLET RRIQTECLASS LTPGLRESSG SEGTSSTGTM

7851 STVLSKVPTG ATTEISKEDV TSIPGPAQST ISPDSTSTRV SWFSTSPVMT

7901 ESAEITMNTN THSPLGATTQG TSTLDTSTT SLTMTHSTIS QGFSSHSQMT

7951 LMRGPEPVS WMSPPLEKT RPSFSLMSSP ATTSPSPVSS TLPESISSSP

8001 LPVTSLLTSG LAKTTDMLHK SSEPVTNSPA NLSSTSVEIL ATSEVTTDTE

8051 KTHPSSNRTV TDVGTSSSGH ESTSFVLADS QTSKVTSPMV ITSTMEDTSV

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

8101	STSTPGFFET	SRIQTEPTSS	LTGLRKTSS	SEGTSLATEM	STVLSGVPTG
8151	ATAEVSRTVEV	TSSSRTSISG	FAQLTVSPET	STETITRLPT	SSIMTESAEM
8201	MIKTQTDPPG	STPESTHTVD	ISTTPNWVET	HSTVTQRFSH	SEMTTLVSR
8251	PGDMLWPSQS	SVEETSSASS	LLSLPATTSP	SPVSSTLVED	FPSASLPVTS
8301	LLTPGLVITT	DRMGISREPG	TSSTSNLSST	SHERLTTLED	TVDTEAMQPS
8351	THTAVTNVRT	SISGHESQSS	VLSDSETPKA	TSSMGTTYTM	GETSVSISTS
8401	DDFETSRVQI	EPTSSLTSG	RETSSSERIS	SATEGSTVLS	EVPSGATTEV
8451	SRTEVISSRG	TSMSGPDQFT	ISPDISTEAI	TRLSTSPIMT	ESAESAITE
8501	TGSPGATSEG	TLTLDSTTT	FWSGTHSTAS	PGFSHSEMTT	LMSRTPGDVP
8551	WPSLPVVEEA	SSVSSSLSSP	AMTSTSFFST	LPESISSSPH	PVTALLTLGP
8601	VKTTDMLRTS	SEPETSSPPN	LSSTSAEILA	TSEVTKDREK	IHPSSNTPVV
8651	NVGTVIYKHL	SPSSVLADLV	TTKPTSPMAT	TSTLGNTSVS	TSTPAFPETM
8701	MTQPTSSLTS	GLREISTSQE	TSSATERSAS	LSGMPTGATT	KVSRTEALSL
8751	GRTSTPGPAQ	STISPEISTE	TITRISTPLT	TTGSAEMTIT	PKTGHSGASS
8801	QGTFTLDTSS	RASWPGTHSA	ATHRSPHSGM	TPMSRGPED	VSWPSRPSVE
8851	KTSPSSLVS	LSAVTSPSPL	YSTPSESSH	SPLRVTSLFT	PVMMKTTDML
8901	DTSLEPVTT	PPSMNITSDE	SLATSKATME	TEAIQLSENT	AVTQMGTTISA
8951	RQEFYSSYPG	LPEPSKVTSP	VVTSSTIKDI	VSTTIPASSE	ITRIEMESTS

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

```

9001  TLTPTPRETS TSQEIHSATK PSTVPYKALT SATIEDSMTQ VMSSSRGPSP
9051  DQSTMSQDIS TEVITRLSTS PIKAESTEMT ITTQTGSPGA TSRGTLTLDL
9101  STTFMSGTHS TASQGFHSQ MTALMSRTPG DVPWLSHPSV EEASSASFSL
9151  SSPVMTSSSP VSSTLPDSIH SSSLPVTSLL TSGLVKTTTEL LGTSSEPETS
9201  SPPNLSSTSA EILATTEVTT DTEKLEMTNV VTSGYTHESP SSVLADSVTT
9251  KATSSMGITY PTGDTNVLTS TPAFSDTSRI QTKSKLSLTP GLMETSISEE
          Contig 36
9301  TSSATEKSTV LSSVPTGATT EVSRTEAISS SRTSIPGPAQ STMSSDTSME
9351  TITRISTPLT RKESTDMAIT PKTGPSGATS QGTFTLDSSS TASWPGTHSA
9401  TTQRFQSVV TTPMSRGPED VSWPSPLSVE KNSPPSSLVS SSSVTSPSP
9451  YSTPSGSSHS SPVPVTSLEFT SIMMKATDML DASLEPETTS APNMNITSDE
9501  SLAASKATTE TEAIHVFENT AASHVETTS TEELYSSSPG FSEPTKVIS
9551  VVTSSSIRDN MVSTTMPGSS GITRIEIESM SSLTPGLRET RTSQDITSST
9601  ETSTVLYKMP SGATPEVSRT EVMPSSRTSI PGPAQSTMSL DISDEVVTRL
9651  STSPIMTESA EITITTQTGY SLATSQVTLP LGTSMTEFLSG THSTMSQGLS
9701  HSEMTNLMSR GPESLSWTSP RFVETTRSSS SLTSLPLTTS LSPVSSTLLD
9751  SSPSSPLPVT SLILPGLVKT TEVLDTSSEP KTSSSPNLSS TSVEIPATSE
9801  IMTDTEKIHP SSNTAVAKVR TSSSVHESHS SVLADSETTI TIPSMGITSA
9851  VDDTTVFSTN PAFSETRRIP TEPTFSLTPG FRETSTSEET TSITETSAVL

```


Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

9901 YGVPTSATTE VSMTEIMSSN RIHIPDSDQS TMSPDIITEV ITRLSSSSMM
9951 SESTQMTITT QKSSPGATAQ STLTWPQQQP PWQGPTQLFL LDFYTSEMTT
10001 LMSRSPENPS WKSSLFVEKT SSSSSLISLP VTTSPSVSST LPQSIPSSSF
10051 SVTSLLLTPGM VKTTDTSTEP GTSLSPNLSG TSVEILAASE VTTDTEKIHP
10101 SSSMAVTNVG TTSSGHELYS SVSIHSEPSK ATYPVGTPSS MAETSISTSM
10151 PANFETTGF E AEPFSLTSG FRKTNMSLD T SSVTPTNTPS SPGSTHLLQS
10201 SKTDFTSSAK TSSPDWPPAS QYTEIPVDII TPFNASPSIT ESTGITSFPE
10251 SRFTMSVTES THHLSTDLLP SAETISTGTV MPSLSEAMTS FATTGVPRAI
10301 SGSGSPFSRT ESGPGDATLS TIAESLPST PVPFSSSTFT TTDSSSTIPAL
10351 HEITSSSATP YRVDTSLGTE SSTTEGRLVM VSTLDTSSQP GRTSSTPILD
10401 TRMTESVELG TVTSAYQVPS LSTRLTRTDG I

Table 26

 Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

contig62

1	MLKPSGLPGS	SSPTRSLMTG	SRSTKATPEM	DSGLTGATLS	PKTSTGAIVV
51	TEHTLPFTSP	DKTLASPTSS	VVGRTTQSLG	VMSSALPEST	SRGMTHSEQR
101	TSPSLSPQVN	GTPSRNYPAT	SMVSGLSSPR	TRTSSTEGNF	TKEASTYTLT
151	VETTSGPVTE	KYTVPTETST	TEGDSTETPW	DTRYIPVKIT	SPMKTFADST
201	ASKENAPVSM	TPAETTVTDS	HTPGRTNPSF	GTLYSSFLDL	SPKGTNPNSRG
251	ETSLELILST	TGYPFSSPEP	GSAGHSRIST	SAPLSSSASV	LDNKISETSI
301	FSGQSLTSPL	SPGVPEARAS	TMPNSAIPFS	MTLSNAETSA	ERVRSTISSL
351	GTPSISTKQT	AETILTFHAF	AETMDIPSTH	IAKTLASEWL	GSPGTLGGTS
401	TSALTTTSPS	TTLVSEETNT	HHSTSGKETE	GTINTSMTPL	ETSAPGEESE
451	MTATLVPTLG	FTTLDKIRS	PSQVSSSHPT	RELRTTGSTS	GRQSSSTAHH
501	GSSDILRATT	SSTSKASSWT	SESTAQQFSE	PQHTQWVETS	PSMKTERPPA
551	STSVAAPITT	SVPSVVSFFT	TLKTSSTKGI	WLEETSADTL	IGESTAGPTT
601	HQFAVPTGIS	MTGGSSTRGS	QGTTHLLTRA	TASSETSADL	TLATNGVPVS
651	VSPAVSKTAA	GSSPPGGTKP	SYTMVSSVIP	ETSSLQSSAF	REGTSLGLTP
701	LNTRHPFSSP	EPDSAGHTKI	STSIPLLSA	SVLEDKVSAT	STFSSHKATS
751	SITTGTPEIS	TKTKPSSAVL	SSMTLSNAAT	SPERVRNATS	PLTHPSPSGE
801	ETAGSVLTLS	TSAETTDSPN	IHPTGTLTSE	SSESPSTLSL	PSVSGVKTTF
851	SSSTPSTHLE	TSGEETEETS	NPSVSQPETS	VSRVRTTLAS	TSVPTPVFPT

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

901	MDTWPTRSAQ	FSSSHLVSEL	RATSSTSVTN	STGSALPKIS	HLTGTATMSQ
	x	oo	o o o	ooo ooo	o
951	TNRDTFNDSA	APQSTTWPET	SPRFKTGLPS	ATTTVSTSAT	SLSATVMVSK
	o o	o oo	oo o	o	
1001	FTSPATSSME	ATSIREPSTT	ILTTETTNGP	GSMVAFASTNI	PIGKGYITEG
	oo			o o o	ooo
1051	RLDTSHLPIG	TTASSETSM	FTMAKESVSM	SVSPSQSMDA	AGSSTPGRTS
			oo o	o o o	
1101	QFVDTFSDDV	YHLTSREITI	PRDGTSSALT	PQMTATHPPS	PDPGSARSTW
	ooo oo	o o ooo	o o		oo o
1151	LGILSSSPSS	PTPKVTMSST	FSTQRVTTSM	IMDTVETSRW	NMPNLPSTTS
	o o	oo	o o o	o o o	oo o
1201	LTPSNIPTSG	AIGKSTLVPL	DTPSPATSLE	ASEGGLPTLS	TYPESTNTPS
	o	oo x			
1251	IHLGAHASSE	SPSTINLTMA	SVVKPGSYTP	LTFPSIETHI	HVSTARMAYS
	o o	o oo	oo oo	o o o	
1301	SGSSPEMTAP	GETNTGSTWD	PTTYITTTDP	KDTSSAQVST	PHSVRTLRTT
	o o o	o o	o x	o o	
1351	ENHPKTESAT	PAAYSGSPKI	SSSPNLTSPA	TKAWTITDDT	EHSTQLHYTK
		o o	o o o		
1401	LAEKSSGFET	QSAPGPVSVV	IPTSPTIGSS	TLELTSDVPG	EPLVLAPSEQ
	o		oo o	oo	oo o
1451	TTITLPMATW	LSTSLTEEMA	STDLDISSPS	SPMSTFAIFP	PMSTPSHEL
				o o	
1501	KSEADTSAIR	NTDSTTLDQH	LGIRSLGRTG	DLTTVPITPL	TTTWTSVIEH
		o o o o	oo o	o	
1551	STQAQDTLSA	TMSPTHVTQS	LKDQTSIPAS	ASPSHLTEVY	PELGTQGRSS
	o		o oo	x oo o	
1601	SEATTFWKPS	TDTLSREIET	GPTNIQSTPP	MDNTTTGSSS	SGVTLGIAHL
	o	o		o	
1651	PIGTSSPAET	STNMALERRS	STATVSMAGT	MGLLVTSAPG	RSISQSLGRV
	o o o			o	oo
1701	SSVLSESTTE	GVTDSKSGSS	PRLNTQGNTA	LSSSLEPSYA	EGSQMSTSIP
	ooo oo			o o o o	o o
1751	LTSSPTTPDV	EFIGGSTFWT	KEVTTVMTSD	ISKSSARTES	SSATIMSTAL

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

1801	GSTENTGKEK	LRTASMDLPS	PTPSMEVTPW	ISLTLSNAPN	TTDSLDSLHG
1851	VHTSSAGTLA	TDRSLNTGVT	RASRLENGSD	TSSKSLSMGN	STHTSMTDTE
1901	KSEVSSSIHP	RPETSAPGAE	TTLTSTPGNR	AISLTLPFSS	IPVEEVISTG
1951	ITSGPDINSA	PMTHSPITPP	TIVWTSTGTI	EQSTQPLHAV	SSEKVSVOQTQ
2001	STPYVNSVAV	SASPTHENSV	SSGSSTSSPY	SSASLESIDS	TISRRNAITS
2051	WLWDLTTSPL	TTTWPSTSL	EALSSGHSV	SNPSTTTEF	PLFSAASTSA
2101	AKQRNPETET	HGPQNTAAST	LNTDASSVTG	LSETPVGASI	SSEVPLPMAI
2151	TSRSDVSGLT	SESTANPSLG	TASSAGTKLT	RTISLPTSES	LVSFRMNKDP
2201	WTVSIPLGSH	PTTNTETSIP	VNSAGPPGLS	TVASDVIDTP	SDGAESIPTV
2251	SFSPSPDTEV	TTISHFPEKT	THSFRTISSL	THELTSRVTP	IPGDWMSSAM
2301	STKPTGASPS	ITLGERRTIT	SAAPTTSPIV	LTASFETETST	VSLDNETTVK
2351	TSDILDARKT	NELPSDSSSS	SDLINTSIAS	STMDVTKTAS	ISPTSISGMT
2401	ASSSPSLFSS	DRPQVPTSTT	ETNTATSPSV	SSNTYSLDGG	SNVGGTPSTL
2451	PPFTITHPVE	TSSALLAWSR	PVRTFTSTMVS	TDASGENPT	SSNSVVTSPV
2501	APGTWTSVGS	TTDLPAMGFL	KTSPAGEAHS	LLASTIEPAT	AFTPHLSAAV
2551	VTGSSATSEA	SLLTTSESKA	IHSSPQTPTT	PTSGANWETS	ATPESLLVVT
2601	ETSDTTLTSK	ILVTDILFS	TVSTPPSKFP	STGTLGASF	PTLLPDTPAI
2651	PLTATEPTSS	LATSFDSTPL	VTIASDSLGT	VPETTLTMSE	TSNGDALVLK

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

2701	TVSNPDRSIP	GITIQQVTES	PLHPSSTSPS	KIVAPRNTTY	EGSITVALST
2751	LPAGTTGSLV	FSQSSENSET	TALVDSSAGL	ERASVMPLTT	GSQGMASGG
2801	IRSGSTHSTG	TKTFSSLPLT	MNPGEVTAMS	EITTNRLTAT	QSTAPKGIPV
2851	KPTSAESGLL	TPVSASSSPS	KAFASLTAP	PTWGIPQSTL	TFEFSEVPSL
2901	DTKSASLPTP	GQSLNTIPDS	DASTASSSLs	KSPEKNPRAR	MMTSTKAISA
2951	SSFQSTGFTE	TPEGSASPSM	AGHEPRVPTS	GTGDPRYASE	SMSYPDPska
3001	SSAMTSTSLA	SKLTTLFSTG	QAARSGSSSS	PISLSTEKET	SFLSPTASTS
3051	RKTSLFLGPS	MARQPNILVH	LQTSALTLSL	TSTLNMSQEE	PELTSSQTI
3101	AEEEGTTAET	QTLTFTPSET	PTSLLPVSSP	TEPTARRKSS	PETWASSISV
3151	PAKTSLVETT	DGTLVTTIKM	SSQAAQGNST	QPAPAEETGT	SPAGTSPGSP
3201	EMSTTLKIMS	SKEPSISPEI	RSTVRNSPWK	TPETTVPMET	TVEPVTLQST
3251	ALGSGSTsis	HLPTGTTSP	KSPTENMLAT	ERVSLSPSP	EAWTNLYSGT
3301	PGGTRQSLAT	MSSVSLESPT	ARSITGTGQQ	SSPELVSKTT	GMEFSMWHGS
3351	TGGTTGDTHV	SLSTSSNILE	DPVTSPNSVS	SLTDKSKHKT	ETWVSTTAIP
3401	STVLNNKIMA	AEQQTSRSVD	EAYSSSTSSWS	DQTS GSDITL	GASPDVTNTL
3451	YITSTAQTTS	LVSLPSGDQG	ITSLTNPSGG	KTSSASSVTS	PSIGLETLRA
3501	NVSAVKSDIA	PTAGHLSQTS	SPA EVSILDV	TTAPT PGIST	TITTMGTNSI
3551	STTPNPEVG	MSTMDSTPAT	ERRTTSTEHP	STWSSTAASD	SWTVTDMTSN

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

3601	LKVARSPGTI	STMHTTSFLA	SSTELDSMST	PHGRITVIGT	SLVTPSSDAS
	o o	o o o o	o o		ooo o ooo
3651	AVKTETSTSE	RTLSPSDTTA	STPISTFSRV	QRMSISVPDI	LSTSWTPSST
	o	o			o o
3701	EAEDVPVSMV	PTDHASTKTD	PNTPLSTFLF	DSLSTLDWDT	GRSLSSATAT
	oo oo			o o	
3751	TSAPQGATTP	QELTLETMIS	PATSQLPFSI	GHITSAVTPA	AMARSSGVTF
	o oo	ooo oo oo			o
3801	SRPDPTSKKA	EQTSTQLPTT	TSAHPGQVPR	SAATTLDVIP	HTAKTPDATEF
	o		oo		o
3851	QRQGQTALT	EARATSDSWN	EKEKSTPSAP	WITEMMNSVS	EDTIKEVTSS
					oo
3901	SSVLKDPEYA	GHKLGIWDDF	IPKFGKAAHM	RELPLLSPPO	DKEAIHPSTN
	o o	oo	o o	o	o
3951	TVETTGWVTS	SEHASHSTIP	AHSASSKLTS	PVVTSTSTREQ	AIVSMSTTTW
	o			o o o oo	
4001	PESTRARTEP	NSFLTIELRD	VSPYMDTSST	TQTSIISSPG	STAITKGHRT
		o			oo
4051	EITSYKRISS	SFLAQSMRSS	DSPSEAITRL	SNFPAMTESG	GMILAMQTSP
	oo o o	o o o o	o		o
4101	PGATISISAPT	LDTSATASWT	GTPLATTQRF	TYSEKTTLFS	KGREDTSQPS
	ooo oo oo		o	o ooo	o o
4151	PPCVEETSSS	SSVVPIHATT	SPSNILLTSQ	GHSPSSTPPV	TSVFLSETSG
		o x o			
4201	LGKTTDMSRI	SLEPGTSLPP	NLSSTAGEAL	STYEASRDTK	AIHHSADTAV
	ooo o	o	o	o	o
4251	TNMEATSSEY	SPIPGHTKPS	KATSPLVTSH	IMGDITSSTS	VFGSSETTEI
		o	o	o o	o o
4301	ETVSSVNQGL	QERSTSQVAS	SATETSTVIT	HVSSGDATTH	VTKTQATFSS
	oo o		oo o o	o oo o oo	o o o
4351	GTSISSPHQF	ITSTNTFTDV	STNPSTSLIM	TESSGVTITT	QTGPTGAATQ
	ooo	o		o	o
4401	GPYLLDTSTM	PYLTTETPLAV	TPDFMQSEKT	TLISKGPKDV	TWTSPPPSVAE
	oo o	oo oo	ooo	o	x
4451	TSYPSSLTPF	LVTTIPPATS	TLQGQHTSSP	VSATSVLTSG	LVKTTDMLNT

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

4501	SMEPVTNSPQ	NLNNPSNEIL	ATLAATTDIE	TIHPSINKAV	TNMGTASSAH
	oo	oo oo	oo		o
4551	VLHSTLPVSS	EPSTATSPMV	PASSMGDALA	SISIPGSETT	DIEGEPTSSL
	x	x	x		o
4601	TAGRKENSTL	QEMNSTTESN	IILSNVSVGA	ITEATKMEVP	SFDATFIPTP
	o	o	oo oo	oo o o	o o
4651	AQSTKFPDIF	SVASSRLSNS	PPMTISTHMT	TTQTGSSGAT	SKIPLALDTS
	o o	o		o	oo o
4701	TLETSAGTPS	VVTEGFAHSK	ITTAMNNDVK	DVSQTNPPFQ	DEASSPSSQA
	o	oo oo	o		o
4751	PVLVTTLPSS	VAFTPQWHST	SSPVSMSSVL	TSSLVKTAGK	VDTSLETVTS
		o o	oo	o	oo o
4801	SPQSMSNTLD	DISVTSAAAT	DIETHPSIN	TVVTNVGTTG	SAFESHSTVS
				o o o	oooo o
4851	AYPEPSKSHI	LPMLPPPPWK	TPQFPRSIPK	SSKTTRTETE	TTSSLTPKLR
	oo oo oo			oooooo o	o
4901	ETSIHQEITS	STETSTVPYK	ELTGATTEVS	RTDVTSSSST	SFPGPDQSTV
	o	o o o	oo	o	o o o
4951	SLDISTETNT	RLSTSPIMTE	SAEITITTQT	GPHGATSQDT	FTMDPSNTTP
				o oo o o oo	
5001	QAGIHSAMTH	GFSQLDVTTL	MSRIPQDVSW	TSPPSVDKTS	SPSSFLSSPA
	oo o o				o x o
5051	MTTPSLISST	LPEDKLSSPM	TSLLTSGLVK	ITDILRTRLE	PVTSSLPNFS
				x	o o
5101	STSDKILATS	KDSKDTKEIF	PSINTEETNV	KANNSGHESH	SPALADSETP
	o oo o	ooo	oo		ooo
5151	KATTQMVIIT	TVGDPAPSTS	MPVHGSSETT	NIKREPTYFL	TPRLRETSTS
	o o	o	oo		oo
5201	QESSFPTDTS	FLLSKVPTGT	ITEVSSTGVI	SSSKISTPDH	DKSTVPPDTF
		o	oo o	o oo	o o
5251	TGEIPRVFTS	SIKTKSAEMT	ITTOASPPES	ASHSTLPLDT	STTLSQGGTH
	o		x oo	oo oo	oo oo o
5301	STVSQGFYPS	EVTTLMGMP	GNVSWMTTPP	VEETSSVSSL	MSSPAMTSPS
	oooo o oo o	o o	o	ooo	ooo x oo
5351	PVSSTSPQSI	PSSPLPTAL	PTSVLVTTTD	VLGTTSPESV	TSSPPNLSSI

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

5401	THERPATYKD	TAHTEAAMHH	STNTAVTNVG	TSGSGHKSQS	SVLADSETSK
	o o	oo oooo	x o	o o	ooo o
5451	ATPLMSTAST	LGDTSVSTST	PNISQTNQIQ	TEPTASLSPR	LRESSTSEKT
	oooo	o	o	oo	o
5501	SSTTETNTAF	SYVPTGAIQ	ASRTEISSSR	TSISDLDRST	IAPDISTGMI
	o o	oo ooo	o		
5551	TRLFTSPIMT	KSAEMTVTTQ	TTTPGATSQG	ILPWDTSTTL	FQGGTHSTVS
		oo	oo o o o	o o ooo	
5601	QGFPHSEITT	LRSRTPGDVS	WMTTPPVEET	SSGFSLMSPS	MTSPSPVSST
	o o oo		oo o	ooo x oo	
5651	SPESIPSSPL	PVTALLTSVL	VTNNVLGTT	SPEPVTSSPP	NLSSPTQERL
				o	oo o
5701	TTYKDTAHE	AMHASMHTNT	AVANVGTSIS	GHEQSSVPA	DSHTSKATSP
		o	o		o
5751	MGITFAMGDT	SVYTSTPAFF	ETRIQSESTS	SLIPGLRDTR	TSEEINTVTE
	oo o o o oo	o	o o	o	o
5801	TSTVLSEVPT	TTTTEVSRT	VITSSRTTIS	GPDHSMSPY	ISTETITRLS
		ox	o	o o o	o
5851	TFPFVTGSTE	MAITNQGP	GTISQATLTL	DTSSTASWEG	THSPVTQRF
		o	ooo o	o	o
5901	HSEETTTMSR	STKGVSWQSP	PSVEETSSPS	SPVPLPAITS	HSSLYSAVSG
	oo oo			o	
5951	SSPTSALPVT	SLLTSGRRKT	IDMLDTHSEL	VTSSLPSASS	FSGEILTSEA
				o	o
6001	STNTETIHFS	ENTAETNMGT	TNSMHKLHSS	VSIHSQPSGH	TPPKVTGSMM
	oooo			x oo	
6051	EDAIVSTSTP	GSPETKNVDR	DSTSPLTPEL	KEDSTALVMN	STTESNTVFS
	o		oo	o o	oo o o
6101	SVSLDAATEV	SRAEVYYDP	TFMPASAQST	KSPDISPEAS	SSHNSNPPLT
		o o	o	oo o o	o
6151	ISTHKTIAQ	TGPGSVTSLG	QLTLDTSTIA	TSAGTPSART	QDFVDSETTS
			o	ooo o oo	ooo
6201	VMNNDLNDVL	KTSPFSAEEA	NSLSSQAPLL	VTTSPSPVTS	TLQEHSTSSL
	o oo o o		o	o	oo o
6251	VSVTSVPTPT	LAKITDMDTN	LEPVTRSPQN	LRNTLATSEA	TTDTHMHPS

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

6301	INTAMANVGT	TSSPNEFYFT	VSPDSDPYKA	TSAAVITSTS	GDSIVSTSMP
		o		ooo	oo
6351	RSSAMKKIES	ETTFSLIFRL	RETSTSQKIG	SSSDTSTVFD	KAFTAATTEV
		oo	o	o	o
6401	SRTELTSSSR	TSIQGTEKPT	MSPDTSTRSV	TMLSTFAGLT	KSEERTIATQ
		oo	o	o	o
6451	TGPHRATSQG	TLTWDTSITT	SQAGTHSAMT	HGFSQLDLST	LTSRVPEYIS
		oo	ooo	o	oo
6501	GTSPPSVEKT	SSSSSLLSLP	AITSPSPVPT	TLPESRPSSP	VHLTSLPTSG
			o	o	
6551	LVKTTDMLAS	VASLPPNLGS	TSHKIPTTSE	DIKDTEKMYP	STNIAVTNVG
		o	o	oo	
6601	TTTSEKESYS	SVPAYSEPPK	VTSPMVTSTFN	IRDTIVSTSM	PGSSEITRIE
				o	o
6651	MESTFSLAHG	LKGTSTSQDP	IVSTEKSAVL	HKLTTGATET	SRTEVASSRR
		oo	oo	x	o
6701	TSIPGPDHST	ESPDISTEVI	PSLPISLGIT	ESSNMTIITR	TGPPLGSTSQ
		o	oo	o	o
6751	GTFTLDTPPT	SSRAGTHSMA	TQEFPHSEMT	TVMNKDPEIL	SWTIPPSIEK
		o	ooo	o	oo
6801	TSFSSSLMPS	PAMTSPPVSS	TLPKTIHTTP	SPMTSLLTPS	LVMTTDTLGT
		o	oooo	x	ooo
6851	SPEPTTSSPP	NLSSTSHEIL	TTDEDTTAIE	AMHPSTSTAA	TNVETTSSGH
			ooo	oo	ooo
6901	GSQSSVLADS	EKTATAPMD	TTSTMGHTTV	STSMSVSSET	TKIKRESTYS
		o	x	o	o
6951	LTPGLRETSI	SQNASFSTD	SIVLSEVPTG	TTAEVSRTEV	TSSGRTSIPG
		oo	oo	o	o
7001	PSQSTVLPEI	STRMTRLFA	SPTMTESAEM	TIPTQTGPSG	STSQDTLTLD
		o	oo	o	o
7051	TSTTKSQAKT	HSTLTQRFPH	SEMTTILMSRG	PGDMSWQSSP	SLENPSSLPS
		o	ooo	ooo	o
7101	LLSLPATTSP	PPISSTLPVT	ISSSPLPVT	LLTSSPVTTT	DMLHTSPELV
		ooo	o	o	o
7151	TSSPPKLSHT	SDERLTTGKD	TTNTEAVHPS	TNTAASNVEI	PSSGHESPSS

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

7201	ALADSETSKA	TSPMFITSTQ	EDTTVAISTP	HFLETSRIQK	ESISSLSPKL
7251	RETGSSVETS	SAIETSAVLS	EVSVGATTEI	SRTEVTSSSR	TSISGSAIST
7301	MLPEISTTRK	IIKFPTSPIL	AISSEMTIKT	QTSPPGSTSE	STFTLDTSTT
7351	PSLVITHSTM	TQRLPHSEIT	TLVSRGAGDV	PRPSSLPVEE	TSPFPSSQLSL
7401	SAMISPPSPVS	STLPASSHSS	SASVTSLTTP	GQVKTTTEVLD	ASAEPETSSP
7451	PSLSSTSVEI	LATSEVTTDT	EKIHPFSNTA	VTKVGTSSSG	HESPSSVLDP
7501	SETTKATSAM	GTISIMGDTS	VSTLTPALSM	TRKIQSEPAS	SLTTRLRETS
7551	TSEETSLATE	ANTVLSKVST	GATTEVSRTE	AISFSRTSMS	GPEQSTMSQD
7601	ISIGTIPRIS	ASSVLTESAK	MTITTTQTGPS	ESTLESTLNL	NTATTPSWVE
7651	THSIVIQGF	HPEMTTSMGR	GPGGVSWPSP	PFVKETSPPS	SPLSLPAVTS
7701	PHPVSTTFLA	HIPPSPLPVT	SLLTSGPATT	TDILGTSTEP	GTSSSSSLST
7751	TSHERLTTYK	DTAHTAVHP	STNTGGTNVA	TTSSGYKSQS	SVLADSSPMC
7801	TTSTMGDTSV	LTSTPAFLET	RRIQTECLASS	LTPGLRESSG	SEGTSSGTMK
7851	STVLSKVPTG	ATTEISKEDV	TSIPGPAQST	ISPDSTSTRV	SWFSTSPVMT
7901	ESAEITMNT	TSPLGATTQG	TSTLDTSSST	SLTMTHSTIS	QGFSHSQMST
7951	LMRRGPEDVS	WMSPPLEKT	RPSFSLMSSP	ATTSPSPVSS	TLPESISSSP
8001	LPVTSLLTSG	LAKTTDMLHK	SSEPVTNSPA	NLSSTSVEIL	ATSEVTTDTE
8051	KTHPSSNRTV	TDVGTSSSGH	ESTSFVLADS	QTSKVTSPMV	ITSTMEDTSV

Table 26 (continued)

 Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

8101	STSTPGFFET	SRIQTEPTSS	LTGLRKTSS	SEGTSLATEM	STVLSGVPTG
	o	o	o	o	o
8151	ATAEVSRTTEV	TSSSRTSISG	FAQLTVSPET	STETITRLPT	SSIMTESAEM
	o	oo	oo	o	o
8201	MIKTQTDPPG	STPESTHTVD	ISTTPNWWET	HSTVTQRFSH	SEMTTLVSR
		o	oo	o	o
8251	PGDMLWPSQS	SVEETSSASS	LLSLPATTSP	SPVSSTLVED	FPSASLPVTS
		o	oo	x	o
8301	LLTPGLVITT	DRMGISREPG	TSSTSNLSST	SHERLTTLED	TVDTEAMQPS
		o	o	o	o
8351	THTAVTNVRT	SISGHESQSS	VLSDSETPKA	TSSMGTTYTM	GETSVSISTS
		o	o	o	o
8401	DEFFETSRVQI	EPTSSLTSGL	RETSSSERIS	SATEGSTVLS	EVPSGATTEV
	o	o	o	o	o
8451	SRTEVISSRG	TMSGPDQFT	ISPDISTEAI	TRLSTSPIMT	ESAESAITE
	o	oo	oo	o	o
8501	TGSPGATSEG	TLTLDTSTTT	FWSGTHSTAS	PGFSHSEMTT	IMSRTPGDVP
		o	oo	o	o
8551	WPSLPSVEEA	SSVSSSLSSP	AMTSTSFST	LPESISSSPH	PVTALLTLGP
	oo	oo	x	oo	o
8601	VKTTDMLRTS	SEPETSSPPN	LSSTSAEILA	TSEVTKDREK	IHPSSNTPVV
			o	o	oo
8651	NVGTVIYKHL	SPSSVLADLV	TTKPTSPMAT	TSTLGNTSVS	TSTPAFPETM
	o	oo	o	o	o
8701	MTQPTSSLTS	GLREISTSQE	TSSATERSAS	LSGMPTGATT	KVSRTALSL
	oo	oo	o	oo	oo
8751	GRTSTPGPAQ	STISPEISTE	TITRISTPLT	TTGSAEMTIT	PKTGHSGASS
		o	o	o	
8801	QGTFTLDTSS	RASWPGTHSA	ATHRSPHSGM	TTPMSRGPED	VSWPSRPSVE
	oo	o	oo	oo	o
8851	KTSPPPSLVS	LSAVTSPSPL	YSTPSESSH	SPLRVTSLEFT	PVMMKTTDML
	o	oo	x	o	o
8901	DTSLEPVTT	PFSMNITSDE	SLATSKATME	TEAIQLSENT	AVTQMGTISA
		o	o	oo	o
8951	RQEFYSSYPG	LPEPSKVTSP	VVTSSTIKDI	VSTTIPASSE	ITRIEMESTS

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

9001	TLTPTPRETS	TSQEIHSA TK	PSTVPYKALT	SATIEDSMTQ	VMSSSRGPSP
9051	DQSTMSQDIS	TEVITRLSTS	PIKAESTEMT	ITTQTGSPGA	TSRGTLTLDT
9101	STTFMSGTHS	TASQGFSHSQ	MTALMSRTPG	DVPWLSHPSV	EEASSASFSL
9151	SSPVMTSSSP	VSTLTPDSIH	SSSLPVTSL	TSGLVKTTTEL	LGTSSEPETS
9201	SPPNLSSTSA	EILATTEVTT	DTEKLEMTNV	VTSGYTHESP	SSVLADSVTT
9251	KATSSMGITY	PTGDTNVLTS	TPAFSDTSRI	QTKSKLSLTP	GLMETSISEE
9301	TSSATEKSTV	LSSVPTGATT	EVSRTAIAIS	SRTSIPGPAQ	STMSSDTSME
9351	TITRISTPLT	RKESTDMAIT	PKTGPSGATS	QGTFTLDSSS	TASWPGTHSA
9401	TTQRFQSVV	TTPMSRGPED	VSWPSPLSVE	KNSPPSSLVS	SSSVTSPSPL
9451	YSTPSGSSHS	SPVPVTSLFT	SIMMKATDML	DASLEPETTS	APNMNITSDE
9501	SLAASKATTE	TEAIHVFENT	AASHVETTS	TEELYSSSPG	FSEPTKVISP
9551	VVTSSSIRDN	MVSTTMPGSS	GITRIEIESM	SSLTPGLRET	RTSQDITSST
9601	ETSTVLYKMP	SGATPEVSRT	EVMPSSRTSI	PGPAQSTMSL	DISDEVVTRL
9651	STSPIMTESA	EITITTQTGY	SLATSQVTLP	LGTSMTFLSG	THSTMSQGLS
9701	HSEMTNLMSR	GPESLSWTSP	RFVETTRSSS	SLTSLPLTTS	LSPVSSTLLD
9751	SSPSSPLPVT	SLILPGLVKT	TEVLDTSSSEP	KTSSSPNLSS	TSVEIPATSE
9801	IMTDTEKIHP	SSNTAVAKVR	TSSSVHESHS	SVLADSETTI	TIPSMGITSA
9851	VDDTTVFETSN	PAFSETTRIP	TEPTFSLTPG	FRETSTSEET	TSITETSAVL

Table 26 (continued)

 Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

9901	YGVPTSATTE	VSMTEIMSSN	RIHIPDSQDS	TMSPDIITEV	ITRLSSSSMM
	o o o				
9951	SESTQMTITT	QKSSPGATAQ	STLTWPQQQP	PWQGPTQLFL	LDFYTSEMTT
	o o o	o o o	o o o	o o o	o o
10001	LMSRSPENPS	WKSSLFVEKT	SSSSSLLSLP	VTTSPSVSST	LPQSIPSSSF
	o	o o	o o x		o
10051	SVTSLLTSGM	VKTDTSTSTEP	GTSLSPNLSG	TSVEILAASE	VTTDTEKIHP
		o	o	o o o	o o o
10101	SSSMAVTNVG	TTSSGHELYS	SVSIHSEPSK	ATYPVGTPTS	MAETSISTSM
			x	o o o o o o o	o o o
10151	PANFETTGF	AEPFSLTSG	FRKTNMSLD	SSVTPTNTPS	SPGSTHLLQS
	o o o	o o o	o	o o o	o o
10201	SKTDFETSSAK	TSSPDWPPAS	QYTEIPVDII	TPFNASPSIT	ESTGITSFPE
	o o o		o o o o	o o	o o
10251	SRFTMSVTES	THHLSTDLLP	SAETISTGT	MPSLSEAMTS	FATTGVPRAI
	o	o	o o o	o o o o o	o o o o
10301	SGSGSPFSRT	ESGPGDATLS	TIAESLPSST	PVPFSSSTFT	TTDSSTIPAL
	o o o o	o o		o	o o o
10351	HEITSSSATP	YRVDTSLGTE	SSTTEGRLVM	VSTLDTSSQP	GRTSSTPILD
	o	o			
10401	TRMTESVELG	TVTSAYQVPS	LSTRLTRTDG	I	

WE CLAIM:

1. A CA125 molecule, comprising:
 - (a) an extracellular amino terminal domain, comprising 5 genomic exons, wherein exon 1 comprises amino acids #1-33 of SEQ ID NO: 299, exon 2 comprises amino acids #34-1593 of SEQ ID NO: 299, exon 3 comprises amino acids #1594-1605 of SEQ ID NO: 299, exon 4 comprises amino acids #1606-1617 of SEQ ID NO: 299, and exon 5 comprises amino acids #1618-1637 of SEQ ID NO: 299;
 - (b) an amino terminal extension, comprising 4 genomic exons, wherein exon 1 comprises amino acids #1-3157 of SEQ ID NO: 310, exon 2 comprises amino acids #3158-3193 of SEQ ID NO: 310, exon 3 comprises amino acids #3194-9277 of SEQ ID NO: 310, and exon 4 comprises amino acids #9278-10,427 of SEQ ID NO: 310;
 - (c) a multiple repeat domain, wherein each repeat unit comprises 5 genomic exons, wherein exon 1 comprises amino acids #1-42 in any of SEQ ID NOS: 164 through 194; exon 2 comprises amino acids #43-65 in any of SEQ ID NOS: 195 through 221; exon 3 comprises amino acids #66-123 in any of SEQ ID NOS: 222 through 249; exon 4 comprises amino acids #124-135 in any of SEQ ID NOS: 250 through 277; and exon 5 comprises amino acids #136-156 in any of SEQ ID NOS: 278 through 298; and
 - (d) a carboxy terminal domain comprising a transmembrane anchor with a short cytoplasmic domain, and further comprising 9 genomic exons, wherein exon 1 comprises amino acids #1-11 of SEQ ID NO: 300; exon 2 comprises amino acids #12-33 of SEQ ID NO: 300; exon 3 comprises amino acids #34-82 of SEQ ID NO: 300; exon 4 comprises amino acids #83-133 of SEQ ID NO: 300; exon 5 comprises amino acids #134-156 of SEQ ID NO: 300; exon 6 comprises amino acids #157-212 of SEQ ID NO: 300; exon 7 comprises amino acids #213-225 of SEQ ID NO: 300; exon 8 comprises amino acids #226-253 of SEQ ID NO: 300; and exon 9 comprises amino acids #254-284 of SEQ ID NO: 300.

2. The CA125 molecule according to claim 1, wherein the N-glycosylation sites of the amino terminal domain marked (x) in Figure 8B are encoded at positions #81, #271, #320, #624, #795, #834, #938, and #1,165 in SEQ ID NO: 299.
3. The CA125 molecule according to claim 1, wherein the serine and threonine O-glycosylation pattern for the amino terminal domain is marked (o) in SEQ ID NO: 299 in Figure 8B.
4. The CA125 molecule according to claim 1, wherein the N-glycosylation sites of the amino terminal extension marked (x) in Table 26 are encoded at positions #139, #434, #787, #930, #957, #1266, #1375, #1633, #1840, #1877, #1890, #2345, #2375, #2737, #3085, #3178, #3501, #4221, #4499, #4607, #4614, #4625, #5048, #5133, #5322, #5396, #5422, #5691, #5865, #6090, #6734, #6861, #6963, #8031, #8057, #8326, #8620, #8686, #8915, #9204, #9495, #9787, #10,077, and #10,175.
5. The CA125 molecule according to claim 1, wherein the serine and threonine O-glycosylation pattern for the amino terminal extension is marked (o) in Table 26.
6. The CA125 molecule according to claim 1, wherein exon 2 in the repeat domain comprises at least 31 different copies; exon 2 comprises at least 27 different copies; exon 3 comprises at least 28 different copies; exon 4 comprises at least 28 different copies, and exon 5 comprises at least 21 different copies.
7. The CA125 molecule according to claim 1, wherein the repeat domain comprises 156 amino acid repeat units which comprise epitope binding sites.
8. The CA125 molecule according to claim 7, wherein the epitope binding sites are located in the C-enclosure at amino acids #59-79 (marked C-C) in SEQ ID NO: 150 in Figure 5.

9. The CA125 molecule according to claim 7, wherein the 156 amino acid repeat unit comprises O-glycosylation sites at positions #128, #129, #132, #133, #134, #135, #139, #145, #146, #148, #150, #151, and #156 in SEQ ID NO: 150 in Figure 5C.

10. The CA125 molecule according to claim 7, wherein the 156 amino acid repeat unit comprises N-glycosylation sites at positions #33 and #49 in SEQ ID NO: 150 in Figure 5C.

11. The CA125 molecule according to claim 7, wherein the 156 amino acid repeat unit comprises at least one conserved methionine (designated M) at position #24 in SEQ ID NO: 150 in Figure 5C.

12. The CA125 molecule according to claim 1, wherein the transmembrane domain of the carboxy terminal domain is located at positions #230-252 (underlined) in SEQ ID NO: 300 of Figure 9B.

13. The CA125 molecule according to claim 1, wherein the cytoplasmic domain of the carboxy terminal domain comprises a highly basic sequence adjacent to the transmembrane at positions #256-260 in SEQ ID NO: 300 of Figure 9B, serine and threonine phosphorylation sites at positions #254, #255, and #276 in SEQ ID NO: 300 in Figure 9B, and tyrosine phosphorylation sites at positions #264, #273, and #274 in SEQ ID NO: 300 of Figure 9B.

14. The CA125 molecule according to claim 7, wherein at least 45 repeat units are present in the repeat domain of the CA125 molecule.

15. A CA125 molecule, comprising an amino terminal domain comprising amino acids #1-1,638 in SEQ ID NO: 162, a repeat domain comprising amino acids #1,643-11,438 in SEQ ID NO: 162, and a carboxy terminal domain comprising amino acids #11,439-11,722 in SEQ ID NO: 162.

16. A repeat domain of the CA125 molecule comprising SEQ ID NO: 146 in Table 16.
17. The repeat domain according to claim 16, further comprising 63 individual repeat units.
18. The repeat domain according to claim 17, wherein each repeat unit comprises at least 156 amino acids.
19. The repeat domain according to claim 18, wherein each repeat unit comprises epitope binding sites located in the C-enclosure at amino acids #59-79 (underlined) in SEQ ID NO: 146.
20. The repeat domain according to claim 18, wherein each repeat unit comprises O-glycosylation sites at positions #128, #129, #132, #133, #134, #135, #139, #145, #146, #148, #150, #151, and #156 in SEQ ID NO: 146.
21. The repeat domain according to claim 18, wherein each repeat unit comprises N-glycosylation sites at positions #33 and #49 in SEQ ID NO: 146.
22. An isolated nucleic acid of the CA125 gene, comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152;
 - (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a);
 - (c) a degenerate variant of any one of (a) to (b); and
 - (d) a fragment of any one of (a) to (c).
23. An isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of:

- (a) the amino acid sequences set forth in SEQ ID NOS: 11-47, 50-80, 82, 146, 148, 149, 151, and 153-158;
 - (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a);
 - (c) a conservative variant of any one of (a) to (b); and
 - (d) a fragment of any one of (a) to (c).
24. A vector comprising the nucleic acid of claim 22.
25. The vector according to claim 24, wherein the vector is a cloning vector, a shuttle vector, or an expression vector.
26. A cultured cell comprising the vector of claim 24.
27. A cultured cell transfected with the vector of claim 24, or a progeny of the cell, wherein the cell expresses the polypeptide.
28. A method of expressing CA125 antigen in a cell, comprising the steps of:
- (a) providing at least one nucleic acid comprising a nucleotide sequence selected from the group consisting of:
 - (i) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152;
 - (ii) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (i);
 - (iii) a degenerate variant of any one of (i) to (ii); and
 - (iv) a fragment of any one of (i) to (iii).
 - (b) providing cells comprising an mRNA encoding the CA125 antigen; and
 - (c) introducing the nucleic acid into the cells, wherein the CA125 antigen is expressed in the cells.

29. A purified polypeptide of the CA125 gene, comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, and 153-158;
- (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a);
- (c) a conservative variant of any one of (a) to (b); and
- (d) a fragment of any one of (a) to (c).

30. A purified antibody that selectively binds to an epitope in the receptor-binding domain of CA125 protein, wherein the epitope is within the amino acid sequence selected from the group consisting of:

- (a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 146, 151, and 153-158;
- (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a);
- (c) a conservative variant of any one of (a) to (b); and
- (d) a fragment of any one of (a) to (c).

31. The antibody according to claim 30 that binds selectively to carcinoma cells selected from the group consisting of the ovaries, colon, liver, and pancreas.

32. A diagnostic for detecting and monitoring the presence of CA125 antigen, comprising recombinant CA125 comprising at least one repeat unit of the CA125 repeat domain including epitope binding sites selected from the group consisting of amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 150, 151, 153-161, and 162 (amino acids #1,643-11,438).

33. The diagnostic according to claim 32, wherein the epitope binding sites are located in the C-enclosure at amino acids #59-79 in SEQ ID NO: 150, and comprise the underlined amino acids in SEQ ID NO: 146 and SEQ ID NO: 162.

34. A therapeutic vaccine to treat mammals with elevated CA125 antigen levels or at risk of developing a disease or disease recurrence associated with elevated CA125 antigen levels, comprising recombinant CA125 repeat domains including epitope binding sites, wherein the repeat domains are selected from the group of amino acid sequences consisting of SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, 153-161, and 162 (amino acids #1,643-11,438), and amino acids #175-284 of SEQ ID NO: 300.

35. The therapeutic vaccine according to claim 34, wherein the mammals include animals and humans.

36. An antisense oligonucleotide that inhibits the expression of CA 125 encoded by:
- (a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150 and 152;
 - (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a);
 - (c) a degenerate variant of any one of (a) to (b); and
 - (d) a fragment of any one of (a) to (c).

1/20

Cyanogen Bromide (CNBr) Cleavage

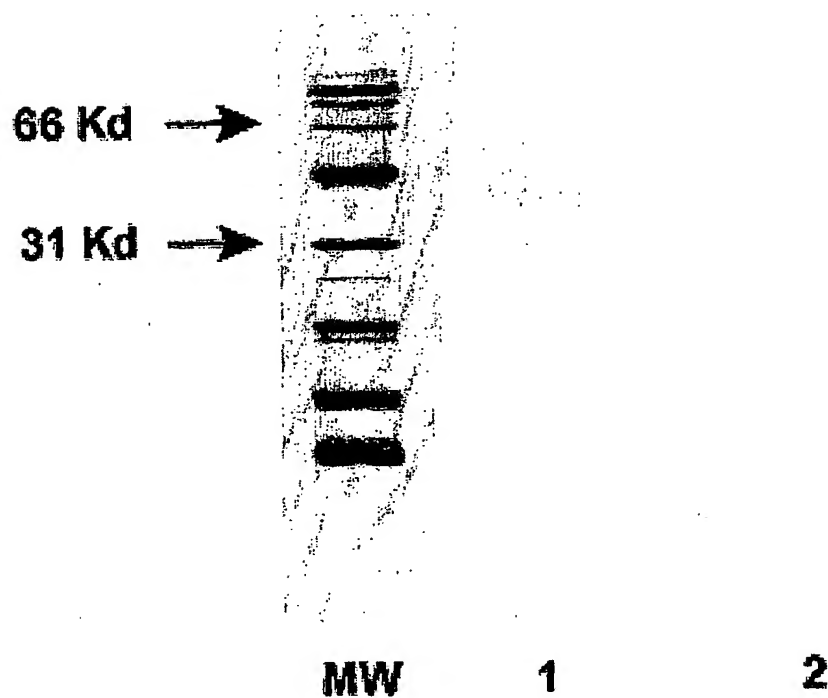
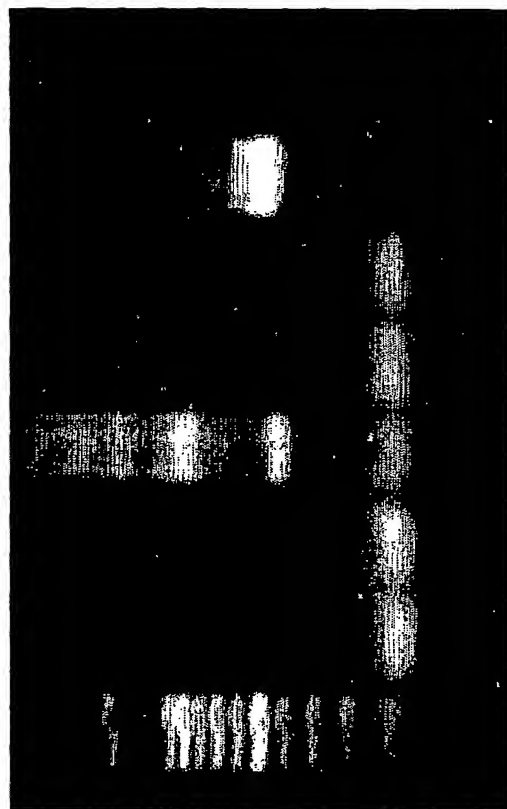


Figure 1

2/20

A

1 2 3 4 5 6



500 bases

B

1 2 3 4 5 6 7 8 9 10 11 12



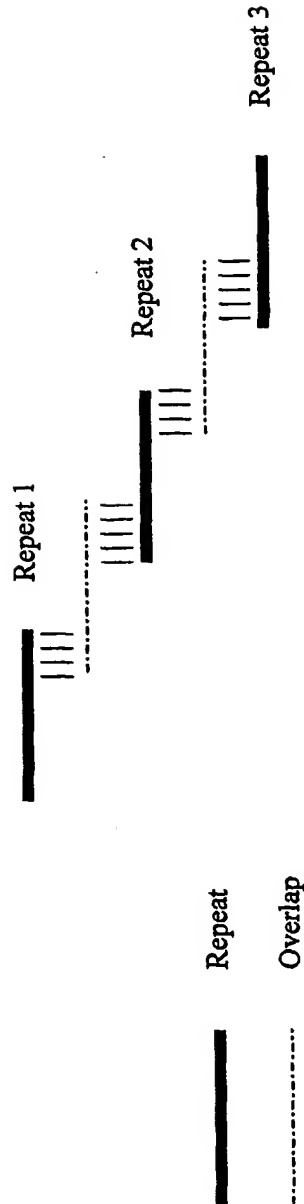
CA125



β-Tubulin

Figure 2

A Strategy for Placing Repeat Sequences in Contiguous Order Using Overlap Sequence Alignment



(SEQ ID NO: 158)

156 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKKNATERVLOGLLKLPLFNKSSGLYVSGCRILSLRPEKOSMAVDACITHRPDPEDLDLDRHLYNELNLNGIQELGPLYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTPSSSPSPT
157 TAGPPLVPEFTLNTFTINLQYEDMHRHTGSRKNTMESVLOGLLKLPLFNKTSVGPVSGCRITLLRPEKOGAATGVDAICTHRLDPKSPGLNREQLYWEIASKRLNDEELGPLYTLDRNSLYVNGFTHHOSVSVTSTPGTSTVDLRTSGTPSSLSPTIM
470 TAGPPLVPEFTLNTFTINLQYEDMGHHPGSRKNTTERVLOGLLGLPLFNKTSVGPVSGCRITLLRPEKOGAATGVDAICTHRLDPKSPGLNREQLYWEISQLNGIKELGPLYTLDRNSLYVNGFTHHIVPSTSTPGTSTVDLGTSGTPSSLPSPA
625 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLGLPLFNKTSVGPVSGCRITLLRPEKOGAATGVDAICTHRLDPKSPGLNREQLYWEISQLNGIKELGPLYTLDRNSLYVNGFTHHIVPSTSTPGTSTVDLG. SGTPESSLPSP
781 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLGLPMFNKTSVGLLYSGCRITLLRSEKOGAATGVDAICTHRLDPKSPGVDRQLYWEISQLNGIKELGPLYTLDRNSLYVNGFTHQTSAPNTSTPGTSTVDLGTSGTPSSLPSPST

(SEQ ID NO: 159)

156 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLGLPMFNKTSVGLLYSGCRITLLRPEKNGAATGMDAICSHRLDPKSPGLNREQLYWEISQLTHGIKELGPLYTLDRNSLYVNGFTHRSSVAPSTPGTSTVDLGTSGTPSSLPSPST
312 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLGLPLFNKSSVGPVSGCRILSLRSEKOGAATGVDAICTHPLNPGPGLDRQLYWEISQLNGIKELGPLYTLDRNSLYVNGFTHHOSVSVLTSTPGTSTVDLGTSGTPSPVPST
468 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLGLPLFNKTSVGPVSGCRITLLRPEKOGAATGMDAVCLYHNPKNPGLDRQLYWEISQLTHHILGELGPLYTLDRNSLYVNGFTHHOSVSVTSTPGTSTVWYATGTSPSSPEFGHT
624 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLKLPLFNKTSVGPVSGCRITLLRPEKOGAATGMDAVCLYHNPKNPGLDRQLYWEISQLTHHITELGPLYTLDRNSLYVNGFTHHOSVSVTSTPGTSTVWYATGTSPSSPEFGHT
780 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLKLPLFNKTSVGPVSGCRITLLRPEKHEAATGVDTICTHRVDPDIPGGLDRERLYWEISQLNWSITELGPLYTLDRSLYVNGFNPRSSVPTSTPGTSTVHLATSGTPSSLPSPST

(SEQ ID NO: 160)

156 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLTLPLFNKTSVGPVSGCRITLLRPEKOGAATGVDTICTHRVDPDIPGGLDRERLYWEISQLNWSITELGPLYTLDRSLYVNGFNPRSSVPTSTPGTSTVHLATSGTPSSLPSPST
312 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLKLPLFNKTSVGPVSGCRITLLRPEKUGAATGVDAICTLALDPTGGLDRERLYWEISQLNWSITELGPLYTLDRSLYVNGFTHRSSVPTSTPGTSAVNHLETSGTPASLPST
468 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLKLPLFNKTSVSSLSGCRITLLRPEKOGAATRVDACTHAPDPKSPGLDRERLYWEISQLTHHITELGPLYTLDRHLYVNGFTHHOSMTRTTRTPESTVHRLATSTPASI
624 TAGPPLVLTFTINFTINLQYEDMHRHPGSRKNTTERVLOGLLRLPVFNKTSVGPVSGCRITLLRPEKOGAATRVDAICTHAPDPKSPGLDRQLYWEISQLHSHSITELGPLYTQDRDLSLYVNGFTHRSSVPTSTPGTSAVNHLETSGTPASLPST
469 TAGPPLVLTFTINFTINLQYEDMHRHPGSRKNTTERVLOGLLRLPVFNKTSVGPVSGCRITLLRPEKOGAATRVDAICTHAPDPKSPGLDRERLYWEISQLHSHSITELGPLYTQDRDLSLYVNGFTHHOSMTRTTRTPESTVHRLATSTPASI

(SEQ ID NO: 161)

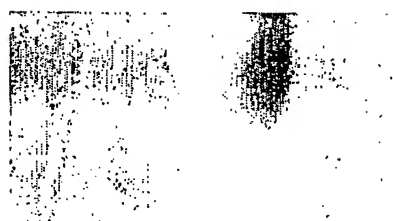
156 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLRLPLFNKTSVSSLSGCRITLLRPEKOGAATRVDACTHAPDPKSPGLDRERLYWEISQLHSHSITELGPLYTQDRDLSLYVNGFTHHOSMTRTTRTPESTVHRLATSTPASI
312 TAGPPLVPEFTLNTFTINLQYEDMHRHPGSRKNTTERVLOGLLRLPLFNKTSVGPVSGCRITLLRPEKOGAATRVDAICTHAPDPKSPGLDRQLYWEISQLHSHSITELGPLYTQDRDLSLYVNGFTHHOSVPTSTPGTSAVNHLETSGTPASLPSPGS
468 TAGPPLVLTFTINFTINLQYEDMHRHPGSRKNTTERVLOGLLRLPVFNKTSVGPVSGCRITLLRPEKOGAATRVDAICTHAPDPKSPGLDRERLYWEISQLHSHSITELGPLYTQDRDLSLYVNGFTHHOSMTRTTRTPESTVHRLATSTPASI
469 TAGPPLVLTFTINFTINLQYEDMHRHPGSRKNTTERVLOGLLRLPVFNKTSVGPVSGCRITLLRPEKOGAATRVDAICTHAPDPKSPGLDRERLYWEISQLHSHSITELGPLYTQDRDLSLYVNGFTHHOSMTRTTRTPESTVHRLATSTPASI

Antibody:M11 OC125 ISOBM 9.2 (Coomassie)

His-CA125
 His-TADG14
 POE-30
 His-CA125
 His-TADG14
 POE-30
 His-CA125
 His-TADG14
 POE-30
 His-CA125
 His-TADG14
 POE-30

4/20

86 →
 43 →
 32 →
 17 →
 7 →



A B C D

Figure 4

5/20

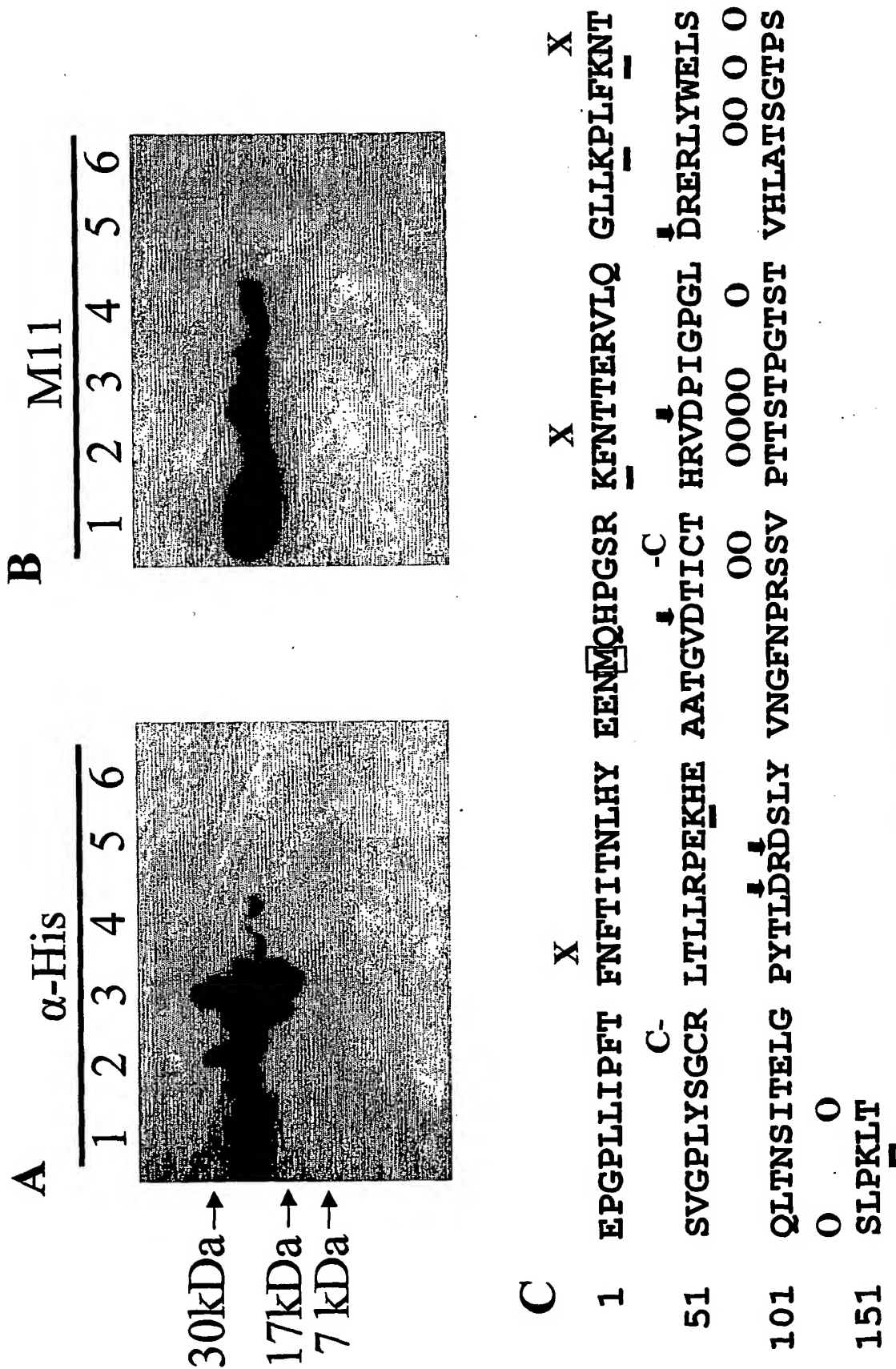


Figure 5 (SEQ ID NO: 150)

6/20

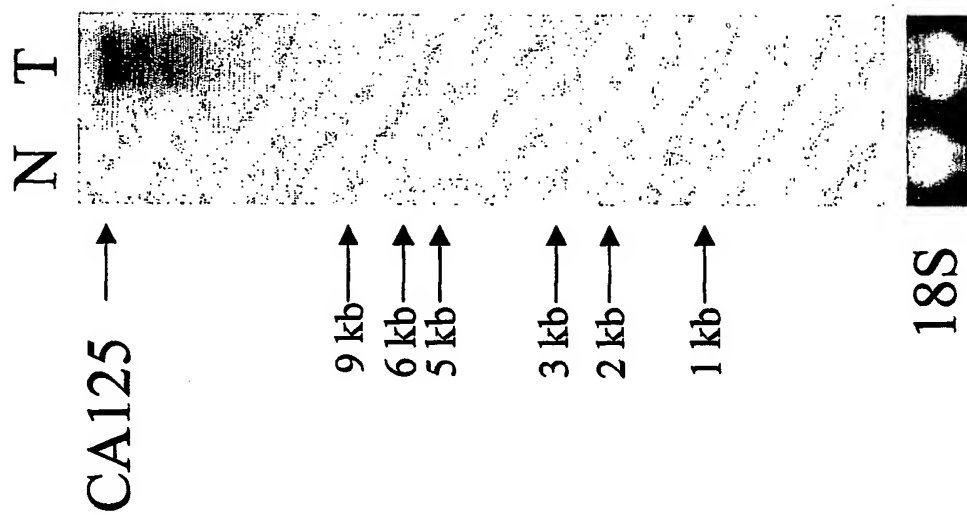


Figure 6

7/20

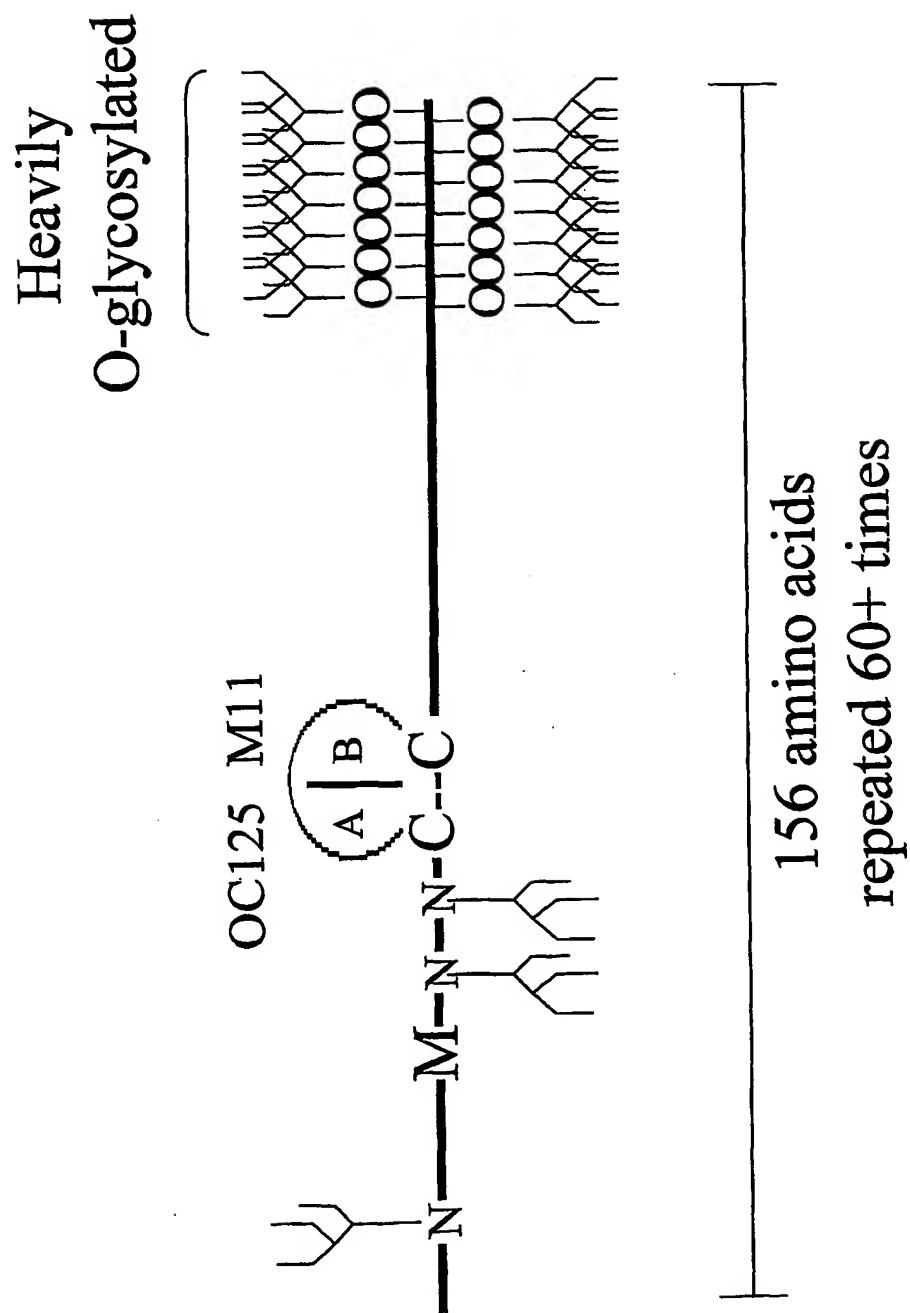


Figure 7A

Genomic Structure of a 156 Amino Acid Repeat Sequence of CA125

← ≈ 1900 bp →

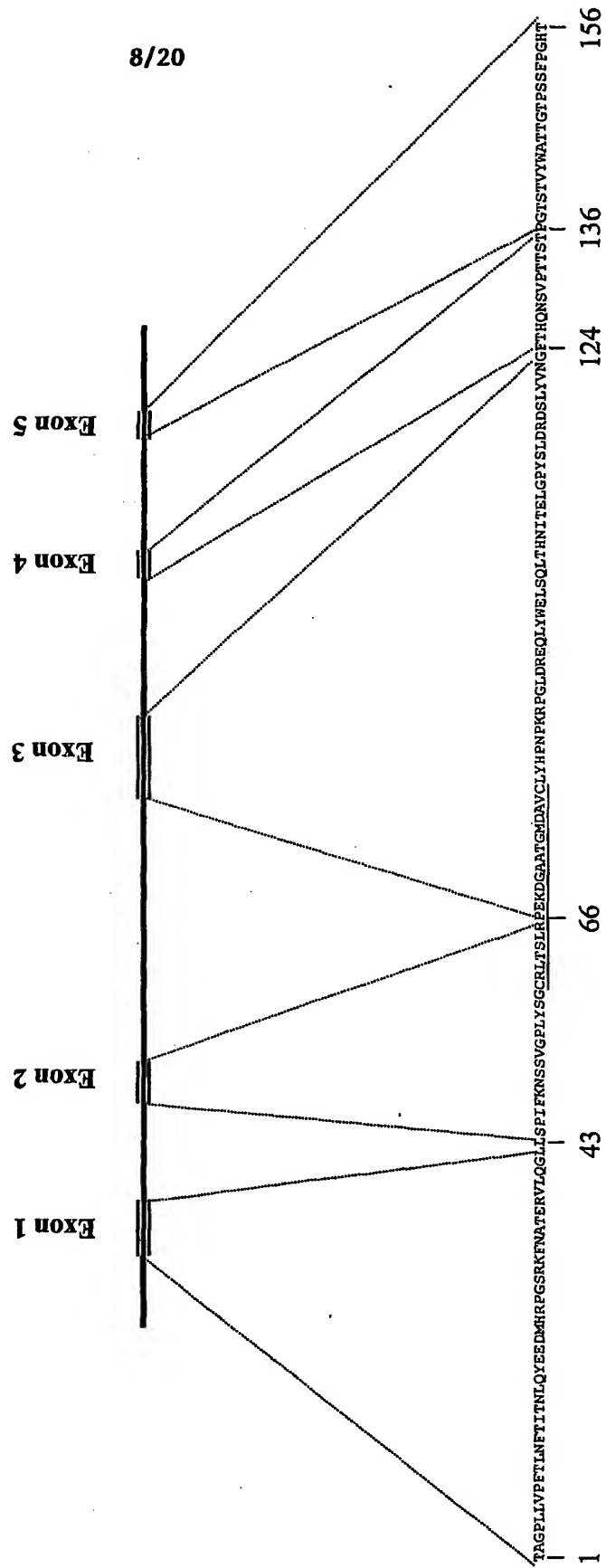


Figure 7B (SEQ ID NO: 163)

9/20

Exon 1

1	42
ATVPFMPFTLNFTITNLQYEDMRHPGSRKFNATERELQGL	(SEQ ID NO: 164)
TAVPLLVPFTLNFTITNLQYGEDMRHPGSRKFNTTTERVLQGL	(SEQ ID NO: 165)
VPGPLLVFTLNFTITNLQYEEAMRHPGSRKFNTTTERVLQGL	(SEQ ID NO: 166)
APGPLLVFTLNFTITNLQYEDMRHPGSRKFSTTTERVLQGL	(SEQ ID NO: 167)
APGPLLVFTLNFTITNLQYEDMRHPGSRKFNTTTERVLQGL	(SEQ ID NO: 168)
APGPLLVFTLNFTITNLQYEDMRHPGSRKFNTTTERVLQGL	(SEQ ID NO: 169)
SAGPLLVPFTLNFTITNLQYEDMRHPGSRKFNTTTERVLQGL	(SEQ ID NO: 170)
AAGPLLMPFTLNFTITNLQYEDMRRTGSRKFNTMESVLQGL	(SEQ ID NO: 171)
TASPLLVLFTINFTITNLQYEDMRRTGSRKFNTMESVLQGL	(SEQ ID NO: 172)
AAGPLLVPFTLNFTITNLQYGEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 173)
TAGPLLIPFTLNFTITNLQYGEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 174)
TAGPLLVPFTLNFTITNLQYGEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 175)
TAGPLLVLFTLNFTITNLQYEDMHRPGSRKFNTTTERVLQGL	(SEQ ID NO: 176)
TAGPLLVPFTLNFTITNLQYEDMHRPGSRKFNATERVLQGL	(SEQ ID NO: 177)
TAGPLLVPFTLNFTITNLQYEDMHRPGSRKFNTTTERVLQGL	(SEQ ID NO: 178)
TAGPLLVPFTLNFTITNLQYEDMHRPGSRKFNTTTERVLQGL	(SEQ ID NO: 179)
APVPLLIPFTLNFTITNLQYEDMHRPGSRKFNTTTERVLQGL	(SEQ ID NO: 180)
ATGPVLLPFTLNFTITNLQYEDMHRPGSRKFNTTTERVLQGL	(SEQ ID NO: 181)
AAGPLLVPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 182)
SAGPLLVPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 183)
TASPLLVLFTINFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 184)
TASPLLVLFTINFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 185)
EPGPLLIPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 186)
EPGPLLIPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 187)
APVPLLIPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 188)
APVPLLIPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 189)
AASPLLVLFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 190)
TAGPLLVPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 191)
AASHLLILFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 192)
TGVVSEEPFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 193)
AMGYHLKTLFTLNFTITNLQYEDMHPGSRKFNTTTERVLQGL	(SEQ ID NO: 194)

Figure 7C

10/20

Exon 2

43	65
LKPLFRNSSLEYLYSGCRLASLR	(SEQ ID NO: 195)
LKPLFKNTSVSSLYSGCRLTLLR	(SEQ ID NO: 196)
LKPLFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 197)
LKPLFKSTSVGPLYSGCRLTLLR	(SEQ ID NO: 198)
LKPLFKSTSVGPLYSSCRLTLLR	(SEQ ID NO: 199)
LKPLFKNTSVGPLYSGCRLTSLR	(SEQ ID NO: 200)
LGPIFKNTSVGPLYSGCRLTSLR	(SEQ ID NO: 201)
LGPMFKNTSVGLLYSGCRLTLLR	(SEQ ID NO: 202)
LGPMFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 203)
LGPMFKNTSVGPLYSGCRLTSLR	(SEQ ID NO: 204)
LGPLFKNSSVGPLYSGCRLISLR	(SEQ ID NO: 205)
LGPLFKNSSVDPLYSGCRLTSLR	(SEQ ID NO: 206)
LSPIFKNSSVGPLYSGCRLTSLR	(SEQ ID NO: 207)
LSPIFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 208)
LSPLFQRSSLGARYTGCRVIALR	(SEQ ID NO: 209)
LRPLFKNTSVSSLYSGCRLTLLR	(SEQ ID NO: 210)
LRPLFKNTSVGPLYSGSRLTLLR	(SEQ ID NO: 211)
LRPLFKNTSIGPLYSSCRLTLLR	(SEQ ID NO: 212)
LRPLFKSTSVGPLYSGCRLTLLR	(SEQ ID NO: 213)
LRPVFKNTSVGLLYSGCRLTLLR	(SEQ ID NO: 214)
LRPVFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 215)
LRSLFKSTSVGPLYSGCRLTLLR	(SEQ ID NO: 216)
LRSLFKSTSVGPLYSGCRLTSLR	(SEQ ID NO: 217)
LTPLFKNTSVGPLYSGCRLTLLR	(SEQ ID NO: 218)
LTPLFRNTSVSSLYSGCRLTLLR	(SEQ ID NO: 219)
LMPLFKNTSVSSLYSGCRLTLLR	(SEQ ID NO: 220)
RPLFQKSSM.GPFYLGQCQLISLR	(SEQ ID NO: 221)

Figure 7C

11/20

Exon 3

66

123

PEKDSSAMAVDAICTHRDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNG (SEQ ID NO: 222)
PEKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 223)
PEKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 224)
PEKDGTATGVDAICTHHPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDLSLEVNG (SEQ ID NO: 225)
PEKDGEATGVDAICTHRDPDTPGGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 226)
PEKDGAATGMDAVCLYHPNPKRPGLDREQLYWELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 227)
PEKDGAATGMDAVCLYHPNPKRPGLDREQLYCELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 228)
PEKDGAATRVDAICTYRDPKSPGLDREQLYWELSQLTHSITELGPYTLDRVSLYVNG (SEQ ID NO: 229)
PEKDGAATKVDAICTYRDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNG (SEQ ID NO: 230)
PEKDGAATKVDAICTYRDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNG (SEQ ID NO: 231)
PEKDGAATRVDAVCTHRDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNG (SEQ ID NO: 232)
PEKDGVATRVDAICTHRDPKIPGLDRQQLYWELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 233)
SEKDGAATGVDAICIHHLDPKSPGLNRERLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 234)
SEKDGAATGVDAICTHRLDPKSPGLDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 235)
SEKDGAATGVDAICTHRLDPKSPGVDRQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 236)
SEKDGAATGVDAICTHRVDPKSPGVDRQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 237)
SEKDGAATGVDAICTHHLNPQSPGLDREQLYWQLSQMTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 238)
PEKRGATGVDTICTHRLDPLNPGLDREQLYWELSKLTRGIIELGPYLLDRGSLYVNG (SEQ ID NO: 239)
PEKNGAATGMDAICSHRLDPKSPGLNREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 240)
PEKNGAATGMDAICSHRLDPKSPGLDREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 241)
PEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSVTELGPYTLDRDSLYVNG (SEQ ID NO: 242)
PEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 243)
PEKHEAATGVDTICTHRVDPGPGGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 244)
PEKQEAATGVDTICTHRVDPGPGGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 245)
PEKQEAATGVDTICTHRVDPGPGGLDRERLYWELSQLTNSITELGPYTLDRDSLYVDG (SEQ ID NO: 246)
PEKDKAATRVDAICTHHPDPQSPGLNREQLYWELSQLTHGITELGPYTLDRDSLYVDG (SEQ ID NO: 247)
SVKNGAETRVDDLCTYLQPLSGPGLPIKQVFHELSQLQTHGITRLGPYSLDKDSLYLNG (SEQ ID NO: 248)
PEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDLDRDSLFINNG (SEQ ID NO: 249)

Figure 7C

12/20

Exon 4

124 135
 FTHRSMPTTST (SEQ ID NO: 250)
 FTHRSMPTTSI (SEQ ID NO: 251)
 FTHRSTVPTSST (SEQ ID NO: 252)
 FTHRSTVPTTST (SEQ ID NO: 253)
 FTHRSSVPTTSS (SEQ ID NO: 254)
 FTHRSSVPTTST (SEQ ID NO: 255)
 FTHRSSVAPTST (SEQ ID NO: 256)
 FTHRSSGLTTST (SEQ ID NO: 257)
 FTHRSEGLTTST (SEQ ID NO: 258)
 FTHRSSFLTST (SEQ ID NO: 259)
 FTHRNEVPITST (SEQ ID NO: 260)
 FTHRSSVPTTSI (SEQ ID NO: 261)
 FTHQSSVPTTST (SEQ ID NO: 262)
 FTHQTSAPNTST (SEQ ID NO: 263)
 FTHQTFAPNTST (SEQ ID NO: 264)
 FTHQNSVPTTST (SEQ ID NO: 265)
 FTHQSSMTTTRT (SEQ ID NO: 266)
 FTHWIPVPTSST (SEQ ID NO: 267)
 FTHWSPITTTST (SEQ ID NO: 268)
 FTHWSSGLTTST (SEQ ID NO: 269)
 FHRSSVPTTST (SEQ ID NO: 270)
 FNRSSVPTTST (SEQ ID NO: 271)
 FNPWSSVPTTST (SEQ ID NO: 272)
 FTQRSSVPTTSI (SEQ ID NO: 273)
 FTQRSSVPTTST (SEQ ID NO: 274)
 FTQRSSVPTTSV (SEQ ID NO: 275)
 YNEPGLDEPPTT (SEQ ID NO: 276)
 YAPQNLSIRGEY (SEQ ID NO: 277)

Exon 5

136 156
 PGTSTVDVGTSGTPSSSPSPT (SEQ ID NO: 278)
 PGTSTVDLRTSGTPSSLSSPTIM (SEQ ID NO: 279)
 PGTSTVDLGTSGTPFSLPSPA (SEQ ID NO: 280)
 PGTSTVDLG.SGTPSSLPSPT (SEQ ID NO: 281)
 PGTSTVDLG.SGTPSLPSPT (SEQ ID NO: 282)
 PGTSTVDLGTSGTPSSLPSPT (SEQ ID NO: 283)
 PGTPTVDLGTSGTPVSKPGPS (SEQ ID NO: 284)
 PWTSTVDLGTSGTPSPVPSPT (SEQ ID NO: 285)
 PGTSTVYWATTGTPSSFPGHT (SEQ ID NO: 286)
 PGTSTVHLATSGTPSSLPGHT (SEQ ID NO: 287)
 PGTSTVHLATSGTPSPLPGHT (SEQ ID NO: 288)
 PDTSTMHLATSRTPASLSGPT (SEQ ID NO: 289)
 PGTSVHLETSCTPASLPGHT (SEQ ID NO: 290)
 PGTSVHLETTGTPSSFPGHT (SEQ ID NO: 291)
 PGTSTVHLGTSETPSSLPRPI (SEQ ID NO: 292)
 PGTSIVNLGTSGIPPSLPETT (SEQ ID NO: 293)
 PGTFTVQPETSETPSSLPGPT (SEQ ID NO: 294)
 PGTPTVDLGTSGTPVSKPGPS (SEQ ID NO: 295)
 PGTPTVYLGASKTPASIFGPS (SEQ ID NO: 296)
 PKPATTFLLPPLSEATT..... (SEQ ID NO: 297)
 QINFHIVNWNLSNPDPTSSEY (SEQ ID NO: 298)

Figure 7C

Structure of Amino Terminal Domain

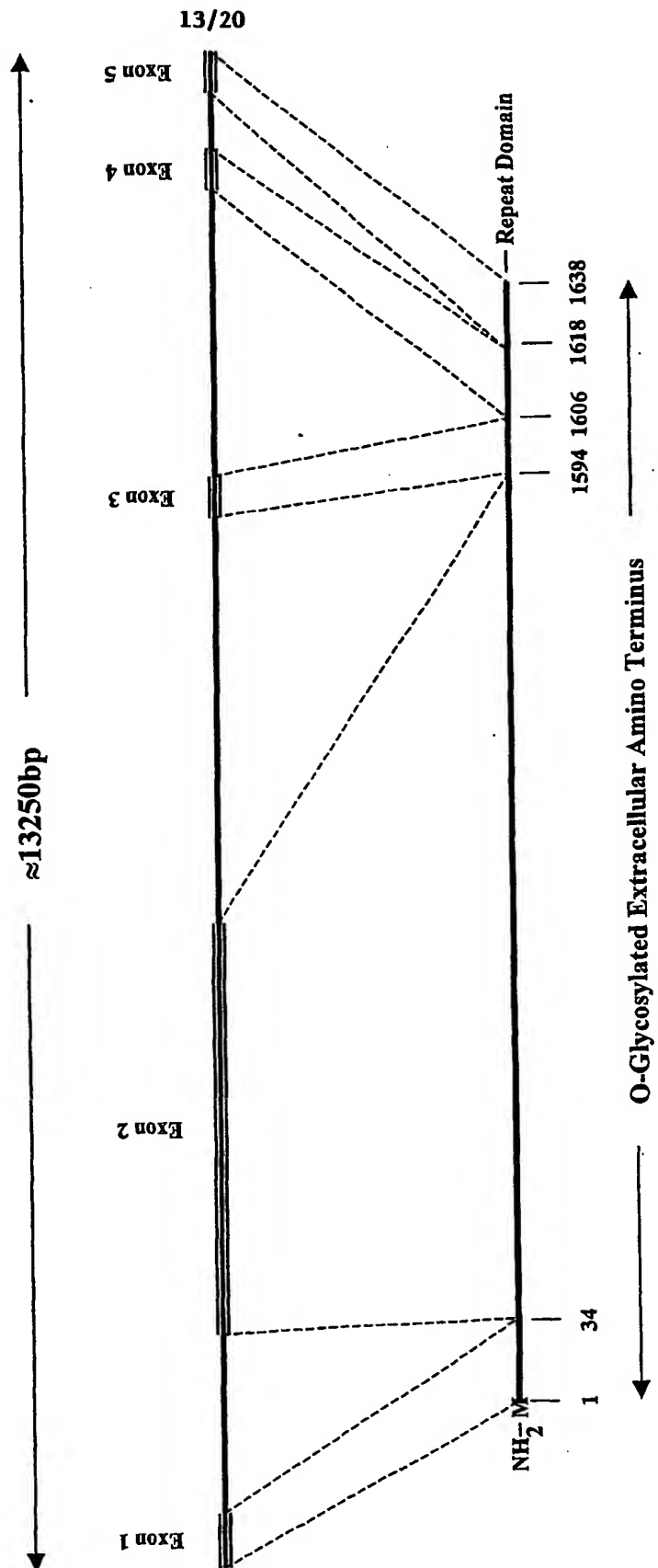


Figure 8A

14/20

1 MEHITKIPNE AHRG⁰⁰⁰⁰IRPV KGPOT⁰⁰⁰⁰STSEFA SPKGLHTGGT KRME⁰⁰⁰⁰TTTTAL
 51 K⁰⁰⁰⁰TTTALK⁰⁰TT SRATL⁰⁰TSVY TP⁰⁰LGLT⁰⁰LPL NASRQMASTI LTEM⁰⁰MITTPY
 101 VPDV⁰⁰PETTS SLAUSLCAET STALPR⁰⁰TTPS VLNRESETTA SLVSRGAER
 151' SPIQ⁰⁰TL⁰⁰DVS SSEP⁰⁰DT⁰⁰ASW VIH⁰⁰PAET⁰⁰TP⁰⁰ VSK⁰⁰TP⁰⁰NFFH SELDT⁰⁰VSSSTA
 201 TSHGAD⁰⁰VSSA IPTN⁰⁰SPSEL DAL⁰⁰TL⁰⁰VTIS G⁰⁰DT⁰⁰ST⁰⁰TP⁰⁰ LTKSPHETET
 251 RTWL⁰⁰THPAE TSST⁰⁰TP⁰⁰RTIP N⁰⁰SHHES⁰⁰DAT P⁰⁰SIAT⁰⁰SPGAE TSSA⁰⁰IPIMIV
 301 SPGAED⁰⁰LVTS QVT⁰⁰SSG⁰⁰TD⁰⁰RN MTI⁰⁰PT⁰⁰L⁰⁰ISP GEPT⁰⁰IAS⁰⁰LV THPEAQ⁰⁰TSSA
 351 IPTST⁰⁰ISPAV SRLV⁰⁰TSMVTS LAAKT⁰⁰ST⁰⁰TNR AL⁰⁰TNS⁰⁰PGEPA TTVSLV⁰⁰THPA
 401 Q⁰⁰SP⁰⁰IVPWT SIF⁰⁰THSKSDT PSM⁰⁰TT⁰⁰SHGA ESS⁰⁰SAVP⁰⁰TP⁰⁰ VSTE⁰⁰VPGVVT
 451 PLVTSSRAVI ST⁰⁰TIPI⁰⁰L⁰⁰TS PGE⁰⁰PE⁰⁰TP⁰⁰SM A⁰⁰SHGEEA⁰⁰SS AIP⁰⁰TP⁰⁰VSPG
 501 VPGV⁰⁰VTSLVT SSR⁰⁰AVTS⁰⁰TI PIL⁰⁰T⁰⁰FS⁰⁰L⁰⁰GEP ET⁰⁰TP⁰⁰SMAT⁰⁰SH GTEAG⁰⁰SAVP⁰⁰TP
 551 VLPEV⁰⁰PGMVT SLVASSRAVT ST⁰⁰TL⁰⁰PT⁰⁰L⁰⁰TS PGE⁰⁰PE⁰⁰TP⁰⁰SM A⁰⁰SHGAE⁰⁰SS
 601 TV⁰⁰PT⁰⁰VSP⁰⁰EV GVTSLV⁰⁰TSS SGV⁰⁰NS⁰⁰TSIPT L⁰⁰ILSPGELET TP⁰⁰SMAT⁰⁰SHGA
 651 EASS⁰⁰AVP⁰⁰TP⁰⁰ VSPGVSGVVT PLVTSSRAVT ST⁰⁰IPIL⁰⁰TS SSEP⁰⁰TP⁰⁰SM
 701 A⁰⁰SHGVEAS⁰⁰ AVLT⁰⁰VSP⁰⁰EV GMVTSLV⁰⁰TSS RAVT⁰⁰ST⁰⁰TIPT⁰⁰ LT⁰⁰ISSDEPET
 751 T⁰⁰SLVTHSEA KMI⁰⁰SAIPTLA VSPTVQGLVT SLV⁰⁰TSSGSET SAFGN⁰⁰LTVA⁰⁰S
 801 SQPETIDSWV AHPGTEA⁰⁰SSV VPTL⁰⁰VSTGE PFTN⁰⁰ISLV⁰⁰TH PAESS⁰⁰TLPR
 851 T⁰⁰SRF⁰⁰SHSEL D⁰⁰TM⁰⁰PT⁰⁰SV⁰⁰ISP EAESS⁰⁰SAIST TP⁰⁰SGIPGVL TSLVTSSGRD
 901 ISAT⁰⁰FP⁰⁰RVPE SPHESE⁰⁰ATAS WVTH⁰⁰PAVTST TP⁰⁰VR⁰⁰TP⁰⁰PNYS HSEP⁰⁰DT⁰⁰PSI
 951 A⁰⁰SPGREA⁰⁰TS DEFT⁰⁰IVSPD VPD⁰⁰MV⁰⁰TSQV⁰⁰ SSGT⁰⁰DT⁰⁰SITI P⁰⁰IL⁰⁰LSGEP
 1001 EFTT⁰⁰ST⁰⁰TS ETH⁰⁰TS⁰⁰SAIPT LPVSPGASKM L⁰⁰SLV⁰⁰ISSGT DST⁰⁰TT⁰⁰FT⁰⁰PLT
 1051 E⁰⁰PPYE⁰⁰ETTA IQLH⁰⁰PAETN TMVPR⁰⁰TP⁰⁰KF SHKS⁰⁰DT⁰⁰TL⁰⁰P VAIT⁰⁰SPGPEA
 1101 S⁰⁰SAVS⁰⁰TTIS PMSDLV⁰⁰TSL VPS⁰⁰SGT⁰⁰DT⁰⁰ST TP⁰⁰FL⁰⁰SE⁰⁰TPY EPE⁰⁰TTATWLT
 1151 HPAET⁰⁰ST⁰⁰VS GTIP⁰⁰N⁰⁰ESH⁰⁰RG SDTAPSMV⁰⁰TS PGVDR⁰⁰SGVP T⁰⁰TI⁰⁰PSIPG
 1201 VV⁰⁰TSQV⁰⁰TS⁰⁰SA TD⁰⁰IS⁰⁰AIPTL TP⁰⁰SPGEP⁰⁰ET⁰⁰ ASSA⁰⁰HPGICQ TGF⁰⁰TVPIRV
 1251 PSSEP⁰⁰DT⁰⁰MA⁰⁰S WVTH⁰⁰PPQ⁰⁰ST PVSR⁰⁰AT⁰⁰SSFS HSSPD⁰⁰AT⁰⁰PVM ATSP⁰⁰RT⁰⁰EA⁰⁰SS
 1301 AVL⁰⁰TI⁰⁰SPGA PEM⁰⁰VT⁰⁰SQ⁰⁰TS SGAAT⁰⁰ST⁰⁰IVP T⁰⁰TH⁰⁰SPGME T⁰⁰TAL⁰⁰STHPR
 1351 TET⁰⁰SKT⁰⁰FPAS TVFPQV⁰⁰SET⁰⁰ ASL⁰⁰IRPGAE TS⁰⁰ALPTQ⁰⁰IT SSL⁰⁰FTLLVTG
 1401 TSRVDLS⁰⁰PTA SPGV⁰⁰SAKTAP LS⁰⁰THPG⁰⁰T⁰⁰TS TMIP⁰⁰TS⁰⁰TL⁰⁰SL GLE⁰⁰TTGLLA
 1451 TSSGAET⁰⁰ST⁰⁰TS TL⁰⁰TL⁰⁰VSPAV SGL⁰⁰SSAS⁰⁰IT⁰⁰ DKPQ⁰⁰TV⁰⁰SMN TET⁰⁰SPSV⁰⁰TSV
 1501 GPPE⁰⁰FSRTVT GTT⁰⁰M⁰⁰LIPSE MP⁰⁰TPK⁰⁰TS⁰⁰HG EGVSP⁰⁰TI⁰⁰LR TTMVEATNLA
 1551 T⁰⁰SGSP⁰⁰TVAK TTTT⁰⁰FN⁰⁰TIAG SLFT⁰⁰PL⁰⁰TPG MST⁰⁰LA⁰⁰SESVT SRTSYN⁰⁰HRSW
 1601 ISTTSSYNRR YWTPA⁰⁰IS⁰⁰TPV TS⁰⁰TS⁰⁰PGIS⁰⁰ SSIP⁰⁰SS⁰⁰TAAT VP⁰⁰FMV⁰⁰FT⁰⁰LN
 1651 FTIT⁰⁰NLQYEE DMRH⁰⁰PGSRAKF NATERE⁰⁰LOGL LKPL⁰⁰FRNSSL EYLYSGCRLA
 1701 SLREEK⁰⁰DSSA MAVDAIC⁰⁰THR PDEPDLGLDR ERLYWE⁰⁰LSNL TNGIQELGPY
 1751 TLD⁰⁰RNSLYN GFTH⁰⁰RSSMP⁰⁰TS⁰⁰TPCT⁰⁰STVD VGT⁰⁰SG⁰⁰TPSS⁰⁰ PSP⁰⁰

Figure 8B (SEQ ID NO: 299)

15/20

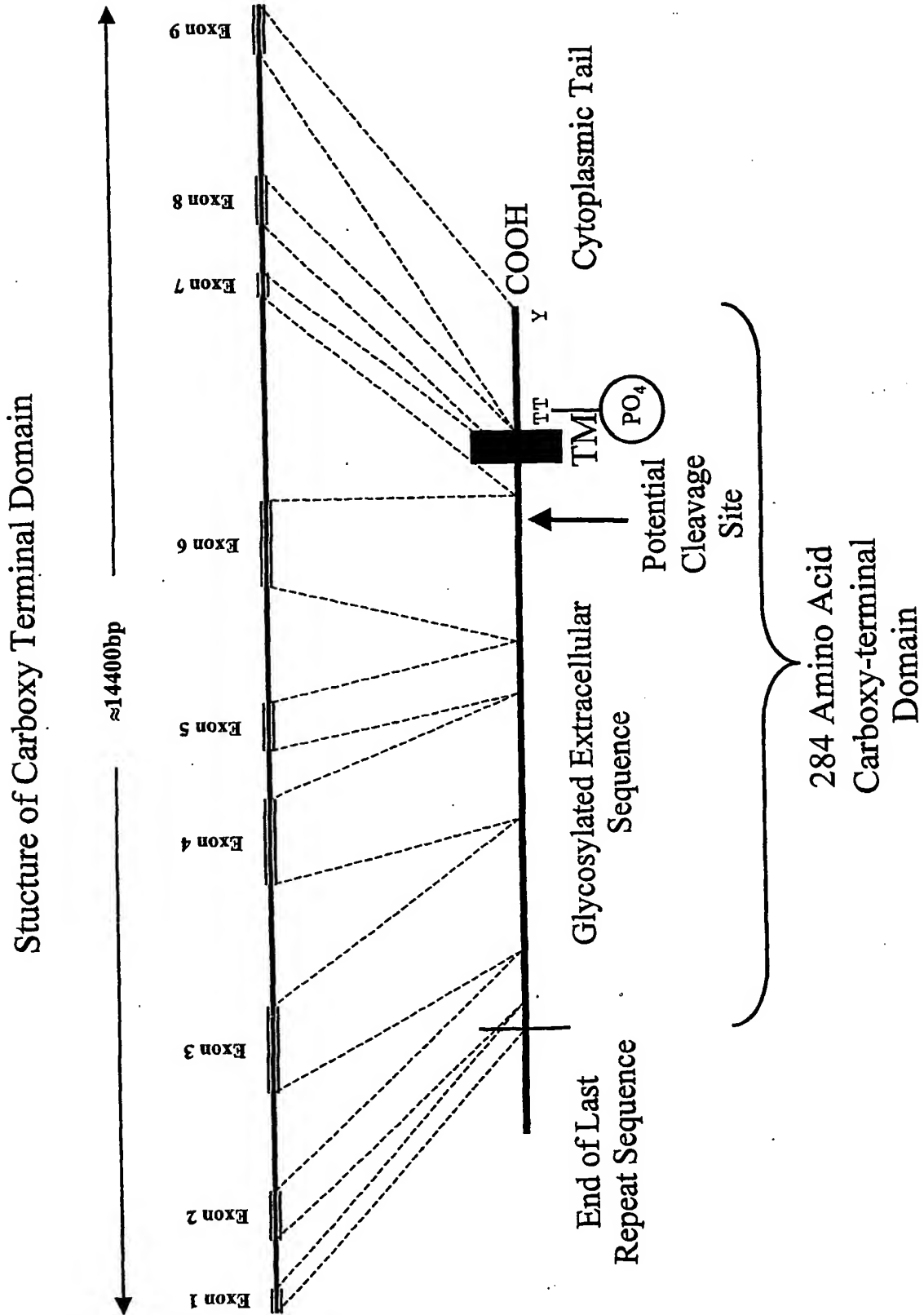


Figure 9A

16/20

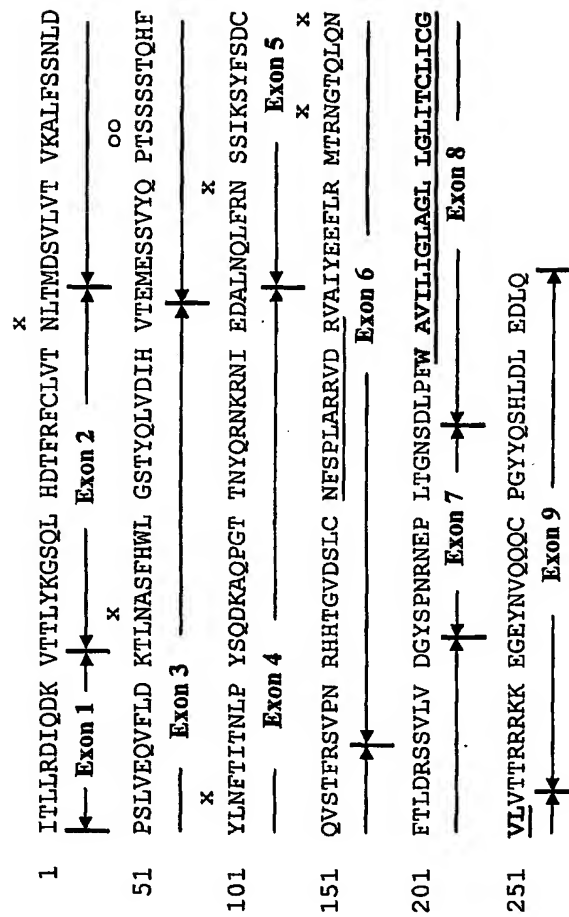


Figure 9B (SEQ ID NO: 300)

17/20

Proposed Structure of CA125

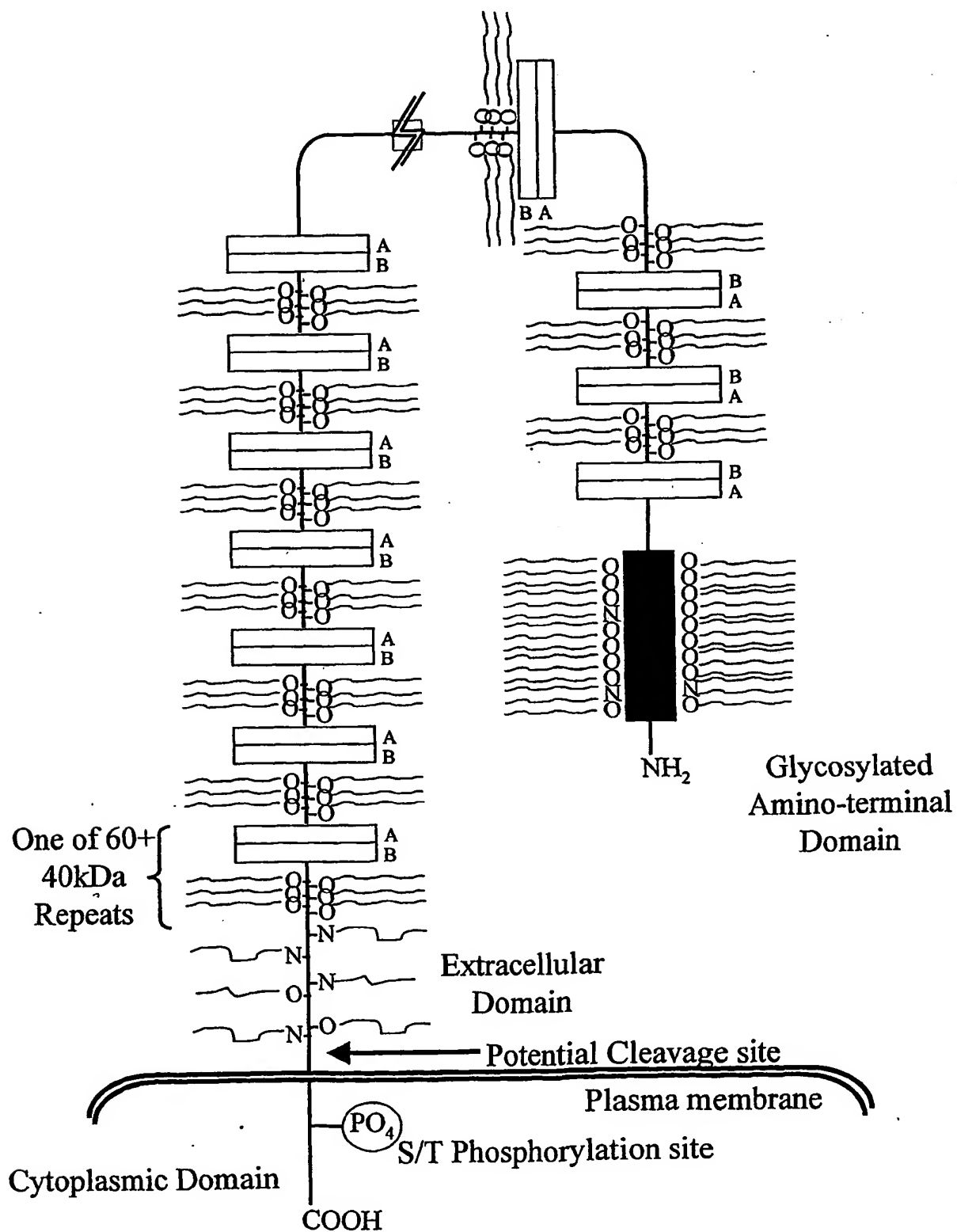


Figure 10

CA125 Gene

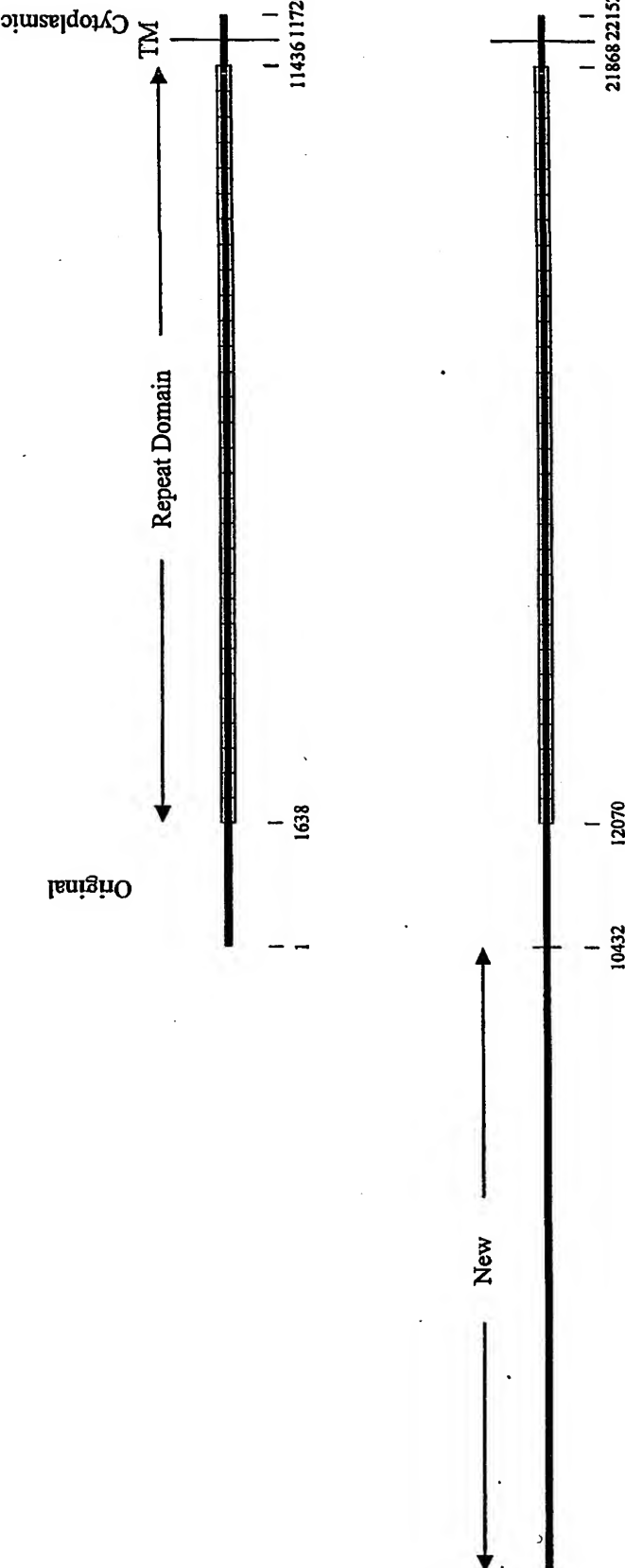


Figure 11

19/20

CA125 Gene: Contig Alignment from Overlapping Chromosome 19 Cosmids

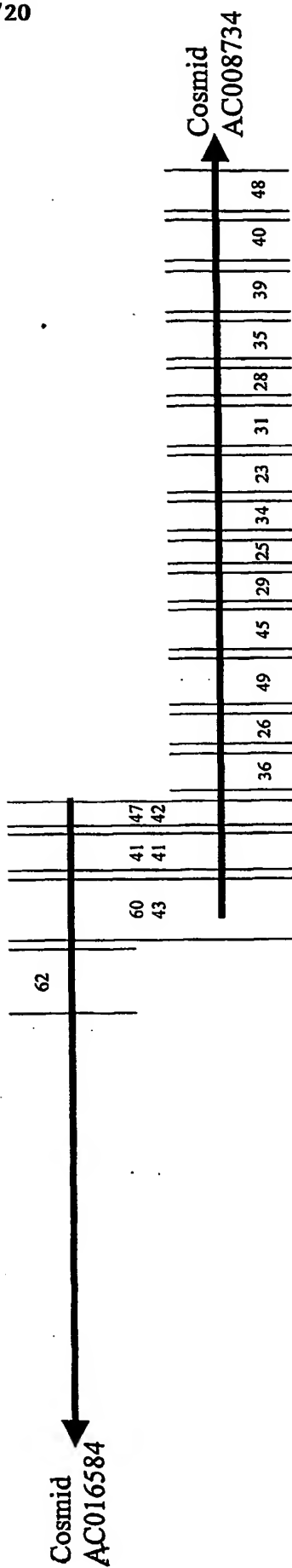


Figure 12

Exon Structure of CA125 Amino Terminal Extension

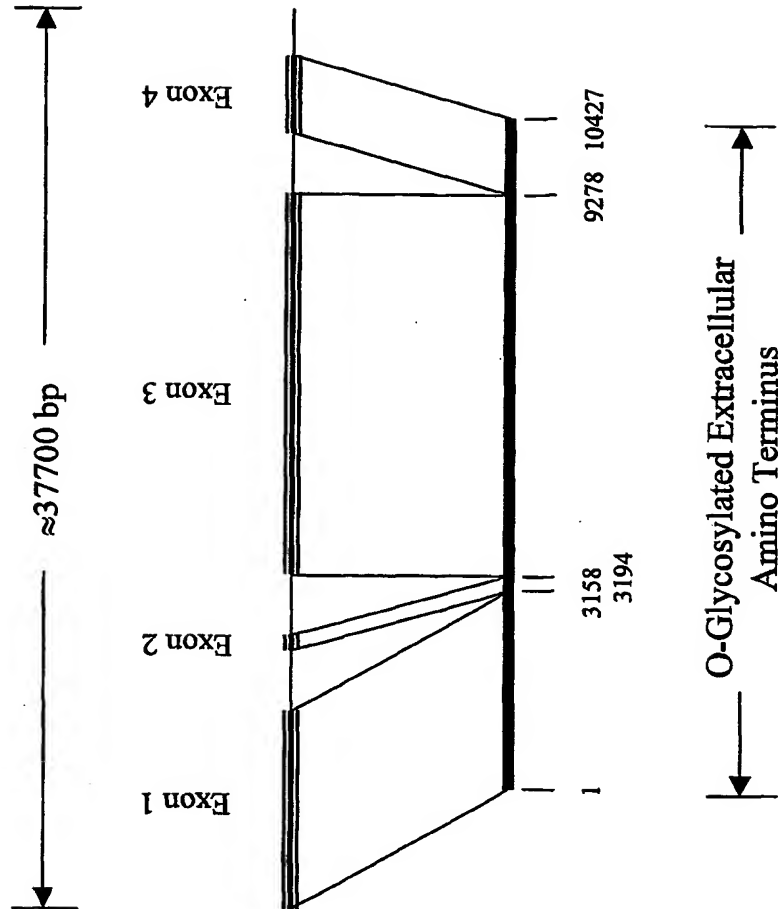


Figure 13

SEQUENCE LISTING

<110> The Board of Trustees of the University of Arkansas

<120> Repeat Sequences of the CA125 Gene and Their Use for Diagnostic and
Therapeutic Interventions

<130> 40715-268163

<150> US 60/284,175

<151> 2001-04-17

<150> US 60/299,380

<151> 2001-06-19

<150> US 09/965,738

<151> 2001-09-27

<150> US 60/345,180

<151> 2001-12-21

<160> 310

<170> PatentIn version 3.1

<210> 1

<211> 13

2

<212> PRT

<213> Homo sapiens

<400> 1

Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Lys	Thr	Thr	Glu	Gly
1				5					10			

<210> 2

<211> 11

<212> PRT

<213> Homo sapiens

<400> 2

Phe	Leu	Thr	Val	Glu	Arg	Val	Leu	Gln	Gly	Leu
1				5					10	

<210> 3

<211> 8

<212> PRT

<213> Homo sapiens

<400> 3

Asp	Thr	Tyr	Val	Gly	Pro	Leu	Tyr
1				5			

<210> 4

<211> 8

<212> PRT

<213> Homo sapiens

<400> 4

Asp Gly Ala Ala Asn Gly Val Asp
 1 5

<210> 5

<211> 240

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(240)

<223>

<400> 5
 cgt cga cct ggc tct aga aag ttt aac acc acg gag aga gtc ctt cag 48
 Arg Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
 1 5 10 15
 ggt ctg ctc agg cct gtg ttc aag aac acc agt gtt ggc cct ctg tac 96
 Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
 20 25 30
 tct ggc tgc aga ctg acc ttg ctc agg ccc aag aag gat ggg gca gcc 144
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala
 35 40 45
 acc aaa gtg gat gcc atc tgc acc tac cgc cct gat ccc aaa agc cct 192
 Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro
 50 55 60
 gga ctg gac aga gag cag cta tac tgg gag ctg agc cag ggt gat gca 240
 Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Gly Asp Ala
 65 70 75 80

<210> 6

<211> 80

<212> PRT

4

<213> Homo sapiens

<400> 6

Arg Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
1 5 10 15

Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
20 25 30

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala
35 40 45

Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro
50 55 60

Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Gly Asp Ala
65 70 75 80

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 7

ggagagggtt ctgcagggtc

20

<210> 8

<211> 6

<212> PRT

<213> Artificial Sequence

5

<220>

<223> Synthetic Primer

<400> 8

Glu Arg Val Leu Gln Gly
1 5

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 9
gtgaatggta tcaggagagg

20

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 10

Pro Leu Leu Ile Pro Phe
1 5

<210> 11

<211> 131

<212> PRT

6

<213> Homo sapiens

<400> 11

Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
 35 40 45

Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ala Leu Asp
 65 70 75 80

Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys
 100 105 110

Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser Pro Leu Leu Ile
 115 120 125

Pro Phe Thr
 130

<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

7

Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser
 1 5 10 15

Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Arg Ala Asp Ala Val Cys Thr His Arg Pro
 35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu
 50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
 85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
 100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile
 115 120 125

Pro Phe
 130

<210> 13

<211> 132

<212> PRT

<213> Homo sapiens

<400> 13

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His Arg Leu
 35 40 45

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu
 115 120 125

Leu Ile Pro Phe
 130

<210> 14

<211> 130

<212> PRT

<213> Homo sapiens

<400> 14

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu
 35 40 45

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
85 90 95

Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile
115 120 125

Pro Phe
130

<210> 15

<211> 130

<212> PRT

<213> Homo sapiens

<400> 15

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu
20 25 30

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu
35 40 45

Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu
50 55 60

Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

24

3

4

1

11

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
 100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe
 130

<210> 17

<211> 130

<212> PRT

<213> Homo sapiens

<400> 17

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
 100 105 110

Thr Pro Ala Ser Leu Pro Gly His Ile Val Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe
130

<210> 18

<211> 131

<212> PRT

<213> Homo sapiens

<400> 18

Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asp Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Pro Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr
130

13

<210> 19

<211> 131

<212> PRT

<213> Homo sapiens

<400> 19

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
 85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
 100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val
 115 120 125

Pro Phe Thr
 130

<210> 20

<211> 130

<212> PRT

14

<213> Homo sapiens

<400> 20

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe
130

<210> 21

<211> 131

<212> PRT

<213> Homo sapiens

<400> 21

15

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
 1 5 10 15

Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro
 35 40 45

Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro Ile Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly
 100 105 110

Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr
 130

<210> 22

<211> 282

<212> PRT

<213> Homo sapiens

<400> 22

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
 1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 225 230 235 240

17

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
 260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu
 275 280

<210> 23

<211> 286

<212> PRT

<213> Homo sapiens

<400> 23

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
 1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
 85 90 95

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile
 115 120 125

18

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Arg Val Asp Ala Val Cys Thr Gln Arg Pro Asp Pro Lys Ser
 195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr
 210 215 220

His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu
 225 230 235 240

Tyr Val Asn Gly Leu Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
 245 250 255

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
 260 265 270

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 24

<211> 250

<212> PRT

<213> Homo sapiens

<400> 24

19

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
 100 105 110

Thr Pro Phe Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val
 115 120 125

Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
 130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
 195 200 205

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

20

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Trp Ile Pro
 245 250

<210> 25

<211> 286

<212> PRT

<213> Homo sapiens

<400> 25

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
 85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
 100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
 115 120 125

21

Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
 130 135 140

Met His His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr
 210 215 220

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr
 245 250 255

Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro
 260 265 270

Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 26

<211> 286

<212> PRT

<213> Homo sapiens

<400> 26

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Ser Arg Gln Ser Ser Met Thr
 85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
 100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Lys Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

23

His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 27

<211> 286

<212> PRT

<213> Homo sapiens

<400> 27

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Phe Gly
 100 105 110

Thr Pro Ala Ser Leu His Gly His Thr Ala Pro Gly Pro Val Leu Val
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
 180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 210 215 220

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
 260 265 270

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 28

<211> 286

<212> PRT

<213> Homo sapiens

25

<400> 28

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
 35 40 45

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
 100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
 180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 210 215 220

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
 260 265 270

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 29

<211> 281

<212> PRT

<213> Homo sapiens

<400> 29

Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
 35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

27

Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
195 200 205

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
260 265 270

Pro Ser Pro Thr Thr Ala Gly Pro Leu
275 280

<210> 30

28

<211> 217

<212> PRT

<213> Homo sapiens

<400> 30

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
 1 5 10 15

Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro
 35 40 45

Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro Ile Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly
 100 105 110

Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Pro Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

29

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 210 215

<210> 31

<211> 286

<212> PRT

<213> Homo sapiens

<400> 31

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
 20 25 30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
 35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
 100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140
 Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu
 145 150 155 160
 Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175
 Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190
 Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205
 Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220
 His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 225 230 235 240
 Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
 245 250 255
 Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
 260 265 270
 Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 32

<211> 288

<212> PRT

<213> Homo sapiens

<400> 32

31

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
20 25 30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Ile
115 120 125

Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

32

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 33

<211> 284

<212> PRT

<213> Homo sapiens

<400> 33

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
 35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu
 50 55 60

Ser Gln Leu Thr His Asp Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
 85 90 95

33

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
 100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
 130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Glu Ala
 180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly
 195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

Asn Ser Ile His Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
 275 280

<210> 34

<211> 288

<212> PRT

34

<213> Homo sapiens

<400> 34

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Ser Lys Asn Ser Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
 35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
 100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Val Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
 130 135 140

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
 180 185 190

35

Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 210 215 220

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 35

<211> 274

<212> PRT

<213> Homo sapiens

<400> 35

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser
 1 5 10 15

Val Gly Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro
 35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu
 50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val
115 120 125

Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Gln Arg Tyr Glu Glu Asn
130 135 140

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
180 185 190

Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile
245 250 255

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser
260 265 270

Leu Pro

37

<210> 36

<211> 386

<212> PRT

<213> Homo sapiens

<400> 36

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
 85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
 100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Ala
 130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Arg Val Asp Ala Ala Cys Thr Tyr Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Val Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro
290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu
305 310 315 320

Arg Pro Leu Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys
325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val
340 345 350

Asp Ala Ile Cys Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn
355 360 365

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr
370 375 380

Glu Leu
385

<210> 37

<211> 438

<212> PRT

<213> Homo sapiens

<400> 37

Glu Arg Val Leu His Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Arg
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Phe Lys Pro Glu Lys His Glu Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly
 195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile
 245 250 255

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser
 260 265 270

Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
 275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
 290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu
 305 310 315 320

Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val
 340 345 350

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp
 355 360 365

41

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile
 370 375 380

Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly
 385 390 395 400

Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser
 405 410 415

Thr Val His Leu Gly Thr Ser Glu Ile His Pro Ser Leu Pro Arg Pro
 420 425 430

Ile Val Pro Gly Pro Leu
 435

<210> 38

<211> 420

<212> PRT

<213> Homo sapiens

<400> 38

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
 1 5 10 15

Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn
 20 25 30

Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
 35 40 45

Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
 50 55 60

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr
 65 70 75 80

Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr
 85 90 95

Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
 100 105 110

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met
 115 120 125

Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Ser Val Leu Gln
 130 135 140

Gly Leu Leu Thr Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
 145 150 155 160

Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala
 165 170 175

Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro
 180 185 190

Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn
 195 200 205

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
 210 215 220

Val Asn Gly Phe Thr His Arg Ser Leu Gly Leu Thr Thr Ser Thr Pro
 225 230 235 240

Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
 245 250 255

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn
 260 265 270

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly
 275 280 285

Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Arg
 290 295 300

43

Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 305 310 315 320

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp
 325 330 335

Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
 340 345 350

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu
 355 360 365

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
 370 375 380

Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr
 385 390 395 400

Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser
 405 410 415

Ala Ala Ser Pro
 420

<210> 39

<211> 439

<212> PRT

<213> Homo sapiens

<400> 39

Glu Arg Val Leu Gln Gly Pro Leu Ser Pro Ile Phe Lys Asn Ser Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
 35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
 100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr
 210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
 245 250 255

45

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
 260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
 275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
 290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu
 305 310 315 320

Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val
 340 345 350

Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp
 355 360 365

Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr
 370 375 380

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 385 390 395 400

Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser
 405 410 415

Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His
 420 425 430

Thr Ala Pro Gly Pro Leu Leu
 435

<210> 40

<211> 424

<212> PRT

46

<213> Homo sapiens

<400> 40

Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
 1 5 10 15

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Tyr Thr His
 20 25 30

Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
 35 40 45

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
 50 55 60

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser
 65 70 75 80

Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
 85 90 95

Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu
 100 105 110

Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu
 115 120 125

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg
 130 135 140

Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
 145 150 155 160

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
 165 170 175

Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro
 180 185 190

Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu Ser Gln
 195 200 205

Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp
 210 215 220

Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr
 225 230 235 240

Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro
 245 250 255

Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe
 260 265 270

Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His
 275 280 285

Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 290 295 300

Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser
 305 310 315 320

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr
 325 330 335

Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly
 340 345 350

Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser
 355 360 365

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val
 370 375 380

Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
 385 390 395 400

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro
 405 410 415

48

Gly His Thr Ala Pro Val Pro Leu
420

<210> 41

<211> 418

<212> PRT

<213> Homo sapiens

<400> 41

Thr Leu Leu Arg Pro Lys Lys Asp Gly Val Ala Thr Gly Val Asp Ala
1 5 10 15

Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu
20 25 30

Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu
35 40 45

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
50 55 60

His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val
65 70 75 80

Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile
85 90 95

Met Ala Ala Gly Pro Leu Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile
100 105 110

Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
115 120 125

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe
130 135 140

Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 145 150 155 160

Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys
 165 170 175

Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu
 180 185 190

Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro
 195 200 205

Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg
 210 215 220

Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val
 225 230 235 240

Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly
 245 250 255

Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
 260 265 270

Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met
 275 280 285

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 290 295 300

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 305 310 315 320

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
 325 330 335

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 340 345 350

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 355 360 365

50

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 370 375 380

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
 385 390 395 400

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile
 405 410 415

Pro Phe

<210> 42

<211> 443

<212> PRT

<213> Homo sapiens

<400> 42

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
 85 90 95

51

Thr Thr Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu
 100 105 110

Thr Pro Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala
 180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Ser Glu
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Ser Gly Val Leu Cys Pro Pro Pro Ser
 245 250 255

Ile Leu Gly Ile Phe Thr Val Gln Pro Glu Thr Phe Glu Thr Pro Ser
 260 265 270

Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr
 275 280 285

Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg
 290 295 300

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
 305 310 315 320

53

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
 195 200 205

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 210 215 220

Asn Asp Ile Glu Glu Val Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Phe Val Ala Pro Thr Ser Thr
 245 250 255

54

Leu Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Pro Ser Pro Thr Thr Gly Val Pro Leu Leu Ile Pro Phe Thr Leu
 275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro
 290 295 300

Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu
 305 310 315 320

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 340 345 350

Val Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 355 360 365

Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
 370 375 380

Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 385 390 395 400

Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 405 410 415

Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 420 425 430

Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
 435 440

<210> 44

<211> 442

55

<212> PRT

<213> Homo sapiens

<400> 44

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
 85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
 100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Ser Ser
 180 185 190

Thr Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp
 195 200 205

Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr
 210 215 220

Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Phe Met Pro Thr Thr Ser Thr
 245 250 255

Leu Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu
 275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
 290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
 305 310 315 320

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 325 330 335

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val
 340 345 350

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
 355 360 365

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu
 370 375 380

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 385 390 395 400

57

Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser
 405 410 415

Thr Val Asp Pro Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro
 420 425 430

Thr Ile Met Ala Ala Gly Pro Leu Leu Ile
 435 440

<210> 45

<211> 379

<212> PRT

<213> Homo sapiens

<400> 45

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
 1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu
 35 40 45

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
 85 90 95

Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
 130 135 140

Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Ser Leu Phe Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Phe Arg Ser Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
 195 200 205

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu
 275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
 290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
 305 310 315 320

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 325 330 335

59

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val
 340 345 350

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
 355 360 365

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu
 370 375

<210> 46

<211> 439

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(439)

<223> Any "X" = any amino acid

<400> 46

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
 35 40 45

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

60

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
 100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
 130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Cys Leu Val Pro Cys Ser Arg Asn Thr Asn Val Gly Leu Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Pro Ser Pro Thr Thr Val Pro Leu Leu Val Pro Phe Thr Leu Asn
 275 280 285

Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly
 290 295 300 *

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
 305 310 315 320

Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 325 330 335

Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 340 345 350

Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg
 355 360 365

Glu Gln Leu Tyr Trp Gln Leu Ser Gln Val Thr Asn Gly Ile Lys Glu
 370 375 380

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe
 385 390 395 400

Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr
 405 410 415

Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr
 420 425 430

Thr Ala Gly Pro Leu Leu Ile
 435

<210> 47

<211> 1366

<212> PRT

<213> Homo sapiens

<400> 47

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
 1 5 10 15

62

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Pro Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro
290 295 300

Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu Gln Gly Leu Leu
305 310 315 320

Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
325 330 335

Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met
340 345 350

Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp
355 360 365

Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr
370 375 380

Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
385 390 395 400

Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser
405 410 415

Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
420 425 430

Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
435 440 445

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys
 450 455 460

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
 465 470 475 480

Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 485 490 495

Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
 500 505 510

Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu
 515 520 525

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro
 530 535 540

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg
 545 550 555 560

Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
 565 570 575

Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly
 580 585 590

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
 595 600 605

Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 610 615 620

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 625 630 635 640

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 645 650 655

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 660 665 670

65

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 675 680 685

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 690 695 700

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
 705 710 715 720

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
 725 730 735

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
 740 745 750

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 755 760 765

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
 770 775 780

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu
 785 790 795 800

Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser
 805 810 815

Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp
 820 825 830

Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr
 835 840 845

Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 850 855 860

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
 865 870 875 880

66

Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
885 890 895

Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu
900 905 910

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
915 920 925

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
930 935 940

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
945 950 955 960

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val
965 970 975

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
980 985 990

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu
995 1000 1005

Glu Val Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
1010 1015 1020

Gly Phe Thr His Arg Ser Phe Val Ala Pro Thr Ser Thr Leu Gly
1025 1030 1035

Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu
1040 1045 1050

Pro Ser Pro Thr Thr Gly Val Pro Leu Leu Ile Pro Phe Thr Leu
1055 1060 1065

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His
1070 1075 1080

Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly
1085 1090 1095

Leu	Leu	Ser	Pro	Ile	Phe	Lys	Asn	Ser	Ser	Val	Gly	Ser	Leu	Tyr
1100						1105					1110			
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Ala
1115						1120					1125			
Ala	Thr	Arg	Val	Asp	Ala	Val	Cys	Thr	His	Arg	Pro	Asp	Pro	Lys
1130						1135					1140			
Ser	Pro	Gly	Leu	Asp	Arg	Glu	Arg	Leu	Tyr	Trp	Lys	Leu	Ser	Gln
1145						1150					1155			
Leu	Thr	His	Gly	Ile	Ile	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg
1160						1165					1170			
His	Ser	Phe	Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Ser	Ser	Met	Thr
1175						1180					1185			
Thr	Thr	Arg	Thr	Pro	Asp	Thr	Ser	Thr	Met	His	Leu	Ala	Thr	Ser
1190						1195					1200			
Arg	Thr	Pro	Ala	Ser	Leu	Ser	Gly	Pro	Thr	Thr	Ala	Ser	Pro	Leu
1205						1210					1215			
Leu	Val	Leu	Phe	Thr	Ile	Asn	Phe	Thr	Ile	Thr	Asn	Gln	Arg	Tyr
1220						1225					1230			
Glu	Glu	Asn	Met	His	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
1235						1240					1245			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Val	Phe	Lys	Asn	Thr
1250						1255					1260			
Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
1265						1270					1275			
Pro	Lys	Lys	Asp	Gly	Ala	Ala	Thr	Lys	Val	Asp	Ala	Ile	Cys	Thr
1280						1285					1290			

68

Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
 1295 1300 1305

Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
 1310 1315 1320

Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
 1325 1330 1335

His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala
 1340 1345 1350

Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro
 1355 1360 1365

<210> 48

<211> 1148

<212> PRT

<213> Homo sapiens

<400> 48

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 1 5 10 15

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 20 25 30

Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 35 40 45

Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Ile
 50 55 60

Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Phe Tyr Val Asn Gly
 65 70 75 80

Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 85 90 95

Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 100 105 110

Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
 115 120 125

Thr Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
 130 135 140

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
 145 150 155 160

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 165 170 175

Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
 180 185 190

Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
 195 200 205

Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 210 215 220

Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg
 225 230 235 240

Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
 245 250 255

Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly Pro Ser Ala Ala Ser
 260 265 270

Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
 275 280 285

Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 290 295 300

70

Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser
305 310 315 320

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
325 330 335

Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
340 345 350

Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
355 360 365

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp
370 375 380

Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser
385 390 395 400

Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys
405 410 415

Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile
420 425 430

Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
435 440 445

Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
450 455 460

Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
465 470 475 480

Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala
485 490 495

Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro
500 505 510

Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His
515 520 525

Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
 530 535 540

Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly
 545 550 555 560

Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu
 565 570 575

Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile
 580 585 590

Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser
 595 600 605

Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser
 610 615 620

Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu
 625 630 635 640

Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu
 645 650 655

Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu
 660 665 670

Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Leu Asp
 675 680 685

Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu
 690 695 700

Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu
 705 710 715 720

Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly
 725 730 735

72

Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
 740 745 750

Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln
 755 760 765

Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 770 775 780

Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
 785 790 795 800

Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
 805 810 815

Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr
 820 825 830

Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
 835 840 845

Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr
 850 855 860

Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
 865 870 875 880

Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
 885 890 895

Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
 900 905 910

Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
 915 920 925

Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
 930 935 940

Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
 945 950 955 960

Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
 965 970 975

Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
 980 985 990

Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
 995 1000 1005

Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro
 1010 1015 1020

Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro
 1025 1030 1035

Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu
 1040 1045 1050

Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp
 1055 1060 1065

Arg Ser Ser Val Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu
 1070 1075 1080

Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu
 1085 1090 1095

Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys
 1100 1105 1110

Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr
 1115 1120 1125

Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp
 1130 1135 1140

Leu Glu Asp Leu Gln
 1145

<210> 49

<211> 6833

<212> DNA

<213> Homo sapiens

<400> 49

```
gagaggggttc tgcaggggtct gctcaaacc tttgttcagga atagcagtct ggaatacctc      60
tattcaggct gcagactagc ctactcagg ccagagaagg atagctcagc catggcagtg      120
gatgccatct gcacacatcg ccctgaccct gaagacctcg gactggacag agagcgactg      180
tactgggagc tgagcaatct gacaaatggc atccaggagc tgggccccta caccctggac      240
cggaacagtc tctatgtcaa tggtttcacc catcgaagct ctatgccac caccagcact      300
cctgggacct ccacagtgga tgtgggaacc tcagggactc catcctccag cccagcccc      360
acgactgctg gccctctcct gatgccgttc accctcaact tcaccatcac caacctgcag      420
tacgaggagg acatgcgtcg cactggctcc aggaagttca acaccatgga gagggttctg      480
caggggtccgc ttagtcccat attcaagaac tccagtgttg gccctctgta ctctggctgc      540
agactgacct ctctcaggcc cgagaaggat ggggcagcaa ctggaatgga tgctgtctgc      600
ctctaccacc ctaatcccaa aagacctggg ctggacagag agcagctgta ctgggagcta      660
agccagctga cccacaacat cactgagctg ggcccctaca gcctggacag ggacagtctc      720
tatgtcaatg gtttcaccca tcagaactct gtgccacca ccagtactcc tgggacctcc      780
acagtgtact gggcaaccac tgggactcca tctccttcc ccggccacac agagcctggc      840
cctctcctga taccattcac gctcaacttc accatcacta acctacagta tgaggagaac      900
atgggtcacc ctggctccag gaagtcaac atcacggaga gggttctgca gggctctgctt      960
aatcccattt tcaagaactc cagtgttggc cctctgtact ctggctgcag actgacctct     1020
ctcaggcccc agaaggatgg ggcagcaact ggaatggatg ctgtctgcct ctaccacctt     1080
aatcccaaaa gacctgggct ggacagagag cagctgtact gcgagctaag ccagctgacc     1140
cacaacatca ctgagctggg cccctacagc ttggacaggg acagtcttta tgtcaatggc     1200
ttcacccatc agaactctgt gccaccacc agtactcctg ggacctccac agtgtactgg     1260
gcaaccactg ggactccatc ctcttcccc ggccacacag agcctggccc tctcctgata     1320
```

ccattcacc tcaacttcac catcaccaac ctgcagtagc aggaggacat gcgtcgact 1380
 ggctccagga agttcaacac catggagagg gttctgcagg gtctgctcaa gcccttgctc 1440
 aagagcacca gcgttgcccc tctgtactct ggctgcagac tgaccttgct cagacctgag 1500
 aaacatgggg cagccactgg agtggacgcc atctgcaccc tccgccttga tcccactggc 1560
 cctggactgg acagagagcg gctatactgg gagctgagcc agctgaccaa cagcggtaca 1620
 gagctggggc cctacaccct ggacagggac agtctctatg tcaatggctt caccatcgg 1680
 agctctgtgc caaccaccag tattcctggg acctctgcag tgcacctgga aacctctggg 1740
 actccagcct ccctccctgg ccacacagcc cctggccctc tcctgggtgcc attcaccctc 1800
 aacttacta tcaccaacct gcagtatgag gaggacatgc gtcaccctgg ttccaggaag 1860
 ttcaacacca cggagagagt cctgcagggt ctgctcaagc ccttggtcaa gagcaccagt 1920
 gttggccctc tgtactctgg ctgcagactg accttgctca ggctgaaaa acgtggggca 1980
 gccaccggcg tggacaccat ctgcactcac cgccttgacc ctctaaacct tggactggac 2040
 agagagcagc tatactggga gctgagcaaa ctgaccctg gcacatcga gctgggcccc 2100
 tacctcctgg acagaggcag tctctatgtc aatgggttca cccatcgga ctttggtgcc 2160
 atcaccagca ctccctgggac ctccacagta caccataggaa cctctgaaac tccatcctcc 2220
 ctacctagac ccatagtgcc tggccctctc ctgataccat tcacactcaa cttcaccatc 2280
 actaacctac agtatgagga gaacatgggt caccctggct ccaggaagtt caacatcacg 2340
 gagagggttc tgcagggtct gctcaaacct ttgttcagga atagcagtct ggaatacctc 2400
 tattcaggct gcagactaac ctactcagg ccagagaagg atagctcaac catggcagtg 2460
 gatgccatct gcacacatcg ccctgaccct gaagacctcg gactggacag agagcgactg 2520
 tactgggagc tgagcaatct gacaaatggc atccaggagc tgggccccta caccctggac 2580
 cggaacagtc tctatgtcaa tggtttcacc catcgaagct ctatgcccac caccagcact 2640
 cctgggacct ccacagtgga tgtgggaacc tcagggactc catcctccag cccagcccc 2700
 acgactgctg gccctctcct gatgccgttc accctcaact tcaccatcac caacctgcag 2760
 tacgaggagg acatgcgtcg cactggctcc aggaagttca acaccatgga gagtgtcctg 2820
 cagggtctgc tcaagccctt gttcaagaac accagtgttg gccctctgta ctctggctgc 2880
 agattgacct tgctcaggcc caagaaagat ggggcagcca ctggagtgga tgccatctgc 2940

accacccgcc ttgaccccaa aagccctgga ctcaacaggg agcagctgta ctgggagtta 3000
agcaaactga ccaatgacat tgaagaggtg ggcccctaca ccttgacag gaacagtctc 3060
tatgtcaatg gtttcaccca tcggagcttt gtggccccc cagcactct tgggacctcc 3120
acagtggacc ttgggacctc agggactcca tcctccctcc ccagccccac aacaggtggt 3180
cctctcctga taccattcac actcaacttc accatcacta acctacagta tgaggagaac 3240
atgggtcacc ctggctccag gaagttcaac atcatggaga gggttctgca gggctctgctt 3300
atgcccttgt tcaagaacac cagtgtcagc tctctgtact ctgggtgcag actgaccttg 3360
ctcaggcctg agaaggatgg ggcagccacc agagtgggtg ctgtctgcac ccacgtcct 3420
gaccocaaaa gccctggact ggacagagag cggctgtact ggaagctgag ccagctgacc 3480
cacggcatca ctgagctggg cccctacacc ctggacaggc acagtctcta tgtcaatggg 3540
ttcaccatc agagctctat gacgaccacc agaactcctg atacctccac aatgcacctg 3600
gcaacctcga gaactccagc ctccctgtct ggacctacga ccgccagccc tctcctgata 3660
ccattcacia ttaacttcac catcactaac ctgcggtatg aggagaacat gcatcacct 3720
ggctctagaa agtttaaac cagggagaga gtccttcagg gtctgctcag gcctgtgttc 3780
aagaacacca gtgttgccc tctgtactct ggctgcagac tgaccttgct caggcccaag 3840
aaggatgggg cagccaccaa agtggatgcc atctgcacct accgccctga tccaaaagc 3900
cctggactgg acagagagca gctatactgg gagctgagcc agctaacca cagcatcact 3960
gagctggggc cctacacct ggacaggagc agtctctatg tcaatgggtt cacacagcgg 4020
agctctgtgc ccaccactag cattcctggg acccccacag tggacctggg aacatctggg 4080
actccagttt ctaaacctgg tccctcggct gccagccctc tcctggtgct attcactctc 4140
aacttcacca tcaccaacct gcggtatgag gagaacatgc agcaccctgg ctccaggaag 4200
ttcaacacca cggagagggt ccttcagggc ctgctcaggt ccctgttcaa gagcaccagt 4260
gttgccctc tgtactctgg ctgcagactg actttgctca ggcctgaaa ggatgggaca 4320
gccactggag tggatgcat ctgcaccac caccctgacc caaaagccc taggctggac 4380
agagagcagc tgtattggga gctgagccag ctgaccaca atatcactga gctgggccac 4440
tatgccctgg acaacgacag cctctttgtc aatggtttca ctcatcgag ctctgtgtcc 4500
accaccagca ctctggggac cccacagtg tatctgggag catctaagac tccagcctcg 4560

atatttggcc cttcagctgc cagccatctc ctgatactat tcaccctcaa cttcaccatc 4620
actaacctgc ggtatgagga gaacatgtgg cctggctcca ggaagttcaa cactacagag 4680
agggtccttc agggcctgct aaggcccttg ttcaagaaca ccagtgttgg ccctctgtac 4740
tctggctcca ggtgacctt gctcaggcca gagaaagatg gggaagccac cggagtggat 4800
gccatctgca cccaccgccc tgaccccaaca ggccctgggc tggacagaga gcagctgtat 4860
ttggagctga gccagctgac ccacagcatc actgagctgg gccctacac actggacagg 4920
gacagtctct atgtcaatgg tttcacccat cggagctctg taccaccac cagcaccggg 4980
gtggtcagcg aggagccatt cacactgaac ttcacatca acaacctgcg ctacatggcg 5040
gacatgggccc aaccgggctc cctcaagttc aacatcacag acaacgtcat gaagcacctg 5100
ctcagtcctt tgttccagag gagcagcctg ggtgcacggt acacaggctg cagggtcatc 5160
gcactaaggt ctgtgaagaa cgggtgctgag acacgggtgg acctcctctg cacctacctg 5220
cagcccctca gcggcccagg tctgcctatc aagcagggtg tccatgagct gagccagcag 5280
acccatggca tcaccgggct gggcccctac tctctggaca aagacagcct ctaccttaac 5340
ggttacaatg aacctggtct agatgagcct cctacaactc ccaagccagc caccacattc 5400
ctgcctcctc tgtcagaagc cacaacagcc atgggggtacc acctgaagac cctcacactc 5460
aacttcacca tctccaatct ccagtattca ccagatatgg gcaagggtc agctacattc 5520
aactccaccg aggggggtcct tcagcacctg ctcagaccct tgttccagaa gagcagcatg 5580
ggccccttct acttgggttg ccaactgatc tccctcaggc ctgagaagga tggggcagcc 5640
actggtgtgg acaccacctg cacctaccac cctgaccctg tggggcccg gctggacata 5700
cagcagcttt actgggagct gagtcagctg acccatgggtg tcacccaact gggcttctat 5760
gtcctggaca gggatagcct cttcatcaat ggctatgcac cccagaattt atcaatccgg 5820
ggcgagtacc agataaattt ccacattgtc aactggaacc tcagtaatcc agaccacaca 5880
tcctcagagt acatcaccct gctgaggggac atccaggaca aggtcaccac actctacaaa 5940
ggcagtcaac tacatgacac attccgcttc tgccctggtca ccaacttgac gatggactcc 6000
gtgttgggtca ctgtcaaggc attgttctcc tccaatttgg accccagcct ggtggagcaa 6060
gtctttctag ataagaccct gaatgcctca ttccattggc tgggctccac ctaccagttg 6120
gtggacatcc atgtgacaga aatggagtca tcagtttctc aaccaacaag cagctccagc 6180

acccagcact tctaccgaa tttcaccatc accaacctac cataattcca ggacaaagcc 6240
 cagccaggca ccaccaatta ccagaggaac aaaaggaata ttgaggatgc gctcaaccaa 6300
 ctcttccgaa acagcagcat caagagttat ttttctgact gtcaagtttc aacattcagg 6360
 tctgtcccca acaggcacca caccggggtg gactccctgt gtaacttctc gccactggct 6420
 cggagagtag acagagttgc catctatgag gaatttctgc ggatgacccg gaatggtacc 6480
 cagctgcaga acttcaccct ggacaggagc agtgtccttg tggatgggta ttctcccaac 6540
 agaaatgagc ccttaactgg gaattctgac cttcccttct gggctgtcat cttcatcggc 6600
 ttggcaggac tcctgggact catcacatgc ctgatctgcg gtgtcctggt gaccacccgc 6660
 cggcggaaga aggaaggaga atacaacgtc cagcaacagt gccaggcta ctaccagtca 6720
 cacctagacc tggaggatct gcaatgactg gaacttgccg gtgcctgggg tgcctttccc 6780
 ccagccaggg tccaaagaag cttggctggg gcagaaataa accatattgg tcg 6833

<210> 50

<211> 2248

<212> PRT

<213> Homo sapiens

<400> 50

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
 1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

79

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Pro Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
 260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
 275 280 285

80

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro
 290 295 300

Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu Gln Gly Leu Leu
 305 310 315 320

Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
 325 330 335

Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met
 340 345 350

Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp
 355 360 365

Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr
 370 375 380

Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 385 390 395 400

Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser
 405 410 415

Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
 420 425 430

Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
 435 440 445

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys
 450 455 460

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
 465 470 475 480

Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 485 490 495

Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
 500 505 510

Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu
 515 520 525

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro
 530 535 540

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg
 545 550 555 560

Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
 565 570 575

Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly
 580 585 590

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
 595 600 605

Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 610 615 620

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 625 630 635 640

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 645 650 655

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 660 665 670

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 675 680 685

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 690 695 700

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
 705 710 715 720

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 945 950 955 960

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val
 965 970 975

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
 980 985 990

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu
 995 1000 1005

Glu Val Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 1010 1015 1020

Gly Phe Thr His Arg Ser Phe Val Ala Pro Thr Ser Thr Leu Gly
 1025 1030 1035

Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu
 1040 1045 1050

Pro Ser Pro Thr Thr Gly Val Pro Leu Leu Ile Pro Phe Thr Leu
 1055 1060 1065

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His
 1070 1075 1080

Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly
 1085 1090 1095

Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Ser Leu Tyr
 1100 1105 1110

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
 1115 1120 1125

Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys
 1130 1135 1140

Ser	Pro	Gly	Leu	Asp	Arg	Glu	Arg	Leu	Tyr	Trp	Lys	Leu	Ser	Gln
1145						1150					1155			
Leu	Thr	His	Gly	Ile	Ile	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg
1160						1165					1170			
His	Ser	Phe	Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Ser	Ser	Met	Thr
1175						1180					1185			
Thr	Thr	Arg	Thr	Pro	Asp	Thr	Ser	Thr	Met	His	Leu	Ala	Thr	Ser
1190						1195					1200			
Arg	Thr	Pro	Ala	Ser	Leu	Ser	Gly	Pro	Thr	Thr	Ala	Ser	Pro	Leu
1205						1210					1215			
Leu	Val	Leu	Phe	Thr	Ile	Asn	Phe	Thr	Ile	Thr	Asn	Gln	Arg	Tyr
1220						1225					1230			
Glu	Glu	Asn	Met	His	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
1235						1240					1245			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Val	Phe	Lys	Asn	Thr
1250						1255					1260			
Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
1265						1270					1275			
Pro	Lys	Lys	Asp	Gly	Ala	Ala	Thr	Lys	Val	Asp	Ala	Ile	Cys	Thr
1280						1285					1290			
Tyr	Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu
1295						1300					1305			
Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly
1310						1315					1320			
Pro	Tyr	Thr	Gln	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
1325						1330					1335			
His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Ser	Ala
1340						1345					1350			

Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly Pro
1355 1360 1365

Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
1370 1375 1380

Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser
1385 1390 1395

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
1400 1405 1410

Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
1415 1420 1425

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly
1430 1435 1440

Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg
1445 1450 1455

Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
1460 1465 1470

Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu
1475 1480 1485

Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser
1490 1495 1500

Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro
1505 1510 1515

Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu
1520 1525 1530

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
1535 1540 1545

Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu
1550						1555					1560			
Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro
1565						1570					1575			
Leu	Tyr	Ser	Gly	Ser	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp
1580						1585					1590			
Gly	Glu	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp
1595						1600					1605			
Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu
1610						1615					1620			
Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu
1625						1630					1635			
Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser
1640						1645					1650			
Val	Pro	Thr	Thr	Ser	Thr	Gly	Val	Val	Ser	Glu	Glu	Pro	Phe	Thr
1655						1660					1665			
Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu	Arg	Tyr	Met	Ala	Asp	Met	Gly
1670						1675					1680			
Gln	Pro	Gly	Ser	Leu	Lys	Phe	Asn	Ile	Thr	Asp	Asn	Val	Met	Lys
1685						1690					1695			
His	Leu	Leu	Ser	Pro	Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly	Ala	Arg
1700						1705					1710			
Tyr	Thr	Gly	Cys	Arg	Val	Ile	Ala	Leu	Arg	Ser	Val	Lys	Asn	Gly
1715						1720					1725			
Ala	Glu	Thr	Arg	Val	Asp	Leu	Leu	Cys	Thr	Tyr	Leu	Gln	Pro	Leu
1730						1735					1740			
Ser	Gly	Pro	Gly	Leu	Pro	Ile	Lys	Gln	Val	Phe	His	Glu	Leu	Ser
1745						1750					1755			

Gln Gln	Thr His	Gly Ile	Thr	Arg Leu	Gly Pro	Tyr	Ser Leu	Asp
1760			1765			1770		
Lys Asp	Ser Leu	Tyr Leu	Asn	Gly Tyr	Asn Glu	Pro	Gly Leu	Asp
1775			1780			1785		
Glu Pro	Pro Thr	Thr Pro	Lys	Pro Ala	Thr Thr	Phe	Leu Pro	Pro
1790			1795			1800		
Leu Ser	Glu Ala	Thr Thr	Ala	Met Gly	Tyr His	Leu	Lys Thr	Leu
1805			1810			1815		
Thr Leu	Asn Phe	Thr Ile	Ser	Asn Leu	Gln Tyr	Ser	Pro Asp	Met
1820			1825			1830		
Gly Lys	Gly Ser	Ala Thr	Phe	Asn Ser	Thr Glu	Gly	Val Leu	Gln
1835			1840			1845		
His Leu	Leu Arg	Pro Leu	Phe	Gln Lys	Ser Ser	Met	Gly Pro	Phe
1850			1855			1860		
Tyr Leu	Gly Cys	Gln Leu	Ile	Ser Leu	Arg Pro	Glu	Lys Asp	Gly
1865			1870			1875		
Ala Ala	Thr Gly	Val Asp	Thr	Thr Cys	Thr Tyr	His	Pro Asp	Pro
1880			1885			1890		
Val Gly	Pro Gly	Leu Asp	Ile	Gln Gln	Leu Tyr	Trp	Glu Leu	Ser
1895			1900			1905		
Gln Leu	Thr His	Gly Val	Thr	Gln Leu	Gly Phe	Tyr	Val Leu	Asp
1910			1915			1920		
Arg Asp	Ser Leu	Phe Ile	Asn	Gly Tyr	Ala Pro	Gln	Asn Leu	Ser
1925			1930			1935		
Ile Arg	Gly Glu	Tyr Gln	Ile	Asn Phe	His Ile	Val	Asn Trp	Asn
1940			1945			1950		

Leu Ser	Asn Pro	Asp Pro	Thr	Ser Ser	Glu Tyr	Ile	Thr Leu Leu
1955			1960			1965	
Arg Asp	Ile Gln	Asp Lys	Val	Thr Thr	Leu Tyr	Lys	Gly Ser Gln
1970			1975			1980	
Leu His	Asp Thr	Phe Arg	Phe	Cys Leu	Val Thr	Asn	Leu Thr Met
1985			1990			1995	
Asp Ser	Val Leu	Val Thr	Val	Lys Ala	Leu Phe	Ser	Ser Asn Leu
2000			2005			- 2010	
Asp Pro	Ser Leu	Val Glu	Gln	Val Phe	Leu Asp	Lys	Thr Leu Asn
2015			2020			2025	
Ala Ser	Phe His	Trp Leu	Gly	Ser Thr	Tyr Gln	Leu	Val Asp Ile
2030			2035			2040	
His Val	Thr Glu	Met Glu	Ser	Ser Val	Tyr Gln	Pro	Thr Ser Ser
2045			2050			2055	
Ser Ser	Thr Gln	His Phe	Tyr	Leu Asn	Phe Thr	Ile	Thr Asn Leu
2060			2065			2070	
Pro Tyr	Ser Gln	Asp Lys	Ala	Gln Pro	Gly Thr	Thr	Asn Tyr Gln
2075			2080			2085	
Arg Asn	Lys Arg	Asn Ile	Glu	Asp Ala	Leu Asn	Gln	Leu Phe Arg
2090			2095			2100	
Asn Ser	Ser Ile	Lys Ser	Tyr	Phe Ser	Asp Cys	Gln	Val Ser Thr
2105			2110			2115	
Phe Arg	Ser Val	Pro Asn	Arg	His His	Thr Gly	Val	Asp Ser Leu
2120			2125			2130	
Cys Asn	Phe Ser	Pro Leu	Ala	Arg Arg	Val Asp	Arg	Val Ala Ile
2135			2140			2145	
Tyr Glu	Glu Phe	Leu Arg	Met	Thr Arg	Asn Gly	Thr	Gln Leu Gln
2150			2155			2160	

89

Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser
 2165 2170 2175

Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe
 2180 2185 2190

Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile
 2195 2200 2205

Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys
 2210 2215 2220

Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr
 2225 2230 2235

Gln Ser His Leu Asp Leu Glu Asp Leu Gln
 2240 2245

<210> 51

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 51
 cagcagagac cagcacgagt actc

24

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 52

tccactgccca tggctgagct

20

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 53

ccagcacagc tcttcccagg ac

22

<210> 54

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 54

ggaatggctg agctgacgtc tg

22

<210> 55

<211> 21

<212> DNA

<213> Artificial Sequence

91

<220>

<223> Synthetic Primer

<400> 55

cttcccagga caacctcaag g

21

<210> 56

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 56

gcaggatgag tgagccacgt g

21

<210> 57

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 57

gtcagatctg gtgacctcac tg

22

<210> 58

<211> 21

<212> DNA

<213> Artificial Sequence

92

<220>

<223> Synthetic Primer

<400> 58

gaggcactgg aaagcccaga g

21

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 59

ctgatggcat tatggaacac atcac

25

<210> 60

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 60

cccagaacga gagaccagtg ag

22

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

93

<220>

<223> Synthetic Primer

<400> 61

gctgatggcg atgaatgaac actg

24

<210> 62

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 62

cccagaacga gagaccagtg ag

22

<210> 63

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 63

cgcgatccg aacactgcgt ttgctggctt tgatg

35

<210> 64

<211> 23

<212> DNA

<213> Artificial Sequence

94

<220>

<223> Synthetic Primer

<400> 64

cctctgtgtg ctgcttcatt ggg

23

<210> 65

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 65

accggatcca tgggccacac agagcctggc cc

32

<210> 66

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 66

tgtaagctta ggcagggagg atggagtcc

29

<210> 67

<211> 507

<212> DNA

<213> Homo sapien

95

<400> 67
 atgagaggat cgcatacca tcacatcac ggatccatgg gccacacaga gcctggccct 60
 ctctgatac cattcacttt caactttacc atcaccaacc tgcattatga ggaaaacatg 120
 caacaccctg gttccaggaa gttcaacacc acggagaggg ttctgcaggg tctgctcaag 180
 cccttggtta agaacaccag tgttggccct ctgtactctg gctgcagact gaccttgctc 240
 agacctgaga agcatgaggc agccactgga gtggacacca tctgtaccca ccgcgttgat 300
 cccatcggac ctggactgga cagagagcgg ctatactggg agctgagcca gctgaccaac 360
 agcatcacag agctgggacc ctacaccctg gacagggaca gtctctatgt caatggcttc 420
 aaccctcgga gctctgtgcc aaccaccagc actcctggga cctccacagt gcacctggca 480
 acctctggga ctccatcctc cctgcct 507

<210> 68

<211> 169

<212> PRT

<213> Homo sapiens

<400> 68

Met Arg Gly Ser His His His His His His Gly Ser Met Gly His Thr
 1 5 10 15

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
 20 25 30

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
 35 40 45

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
 50 55 60

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 65 70 75 80

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
 85 90 95

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
35 40 45

97

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
 100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
 195 200 205

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 210 215 220

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
 275 280 285

Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met His
 290 295 300

His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly
 305 310 315 320

Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser
 325 330 335

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr
 340 345 350

Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly
 355 360 365

Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly
 370 375 380

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
 385 390 395 400

Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly
 405 410 415

Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro
 420 425 430

Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe
 435 440 445

Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser
 450 455 460

Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys Pro
 465 470 475 480

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
 485 490 495

Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala
 500 505 510

Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu
 515 520 525

Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu
 530 535 540

Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
 545 550 555 560

His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val
 565 570 575

His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala
 580 585 590

Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
 595 600 605

Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn
 610 615 620

Thr Met Glu Arg Val Leu Gln Gly Cys Leu Val Pro Cys Ser Arg Asn
 625 630 635 640

Thr Asn Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
 645 650 655

Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa
 660 665 670

Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp
 675 680 685

100

Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Thr
 690 695 700

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser
 705 710 715 720

Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
 725 730 735

Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Val Pro Leu Leu
 740 745 750

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu
 755 760 765

Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
 770 775 780

Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro
 785 790 795 800

Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly
 805 810 815

Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln
 820 825 830

Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Val
 835 840 845

Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser
 850 855 860

Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser
 865 870 875 880

Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser
 885 890 895

Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile
 900 905

101

<210> 70

<211> 525

<212> PRT

<213> Homo sapiens

<400> 70

Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
 1 5 10 15

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
 20 25 30

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
 35 40 45

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 50 55 60

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
 65 70 75 80

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
 85 90 95

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
 100 105 110

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu
 115 120 125

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro
 130 135 140

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu
 145 150 155 160

102

Arg Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 165 170 175

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 180 185 190

Asp Ala Ala Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 195 200 205

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr
 210 215 220

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Val Ser Leu Tyr Val Asn Gly
 225 230 235 240

Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser
 245 250 255

Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His
 260 265 270

Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
 275 280 285

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys
 290 295 300

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe
 305 310 315 320

Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu
 325 330 335

Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys
 340 345 350

Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu
 355 360 365

Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro
 370 375 380

103

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp
 385 390 395 400

Ser Pro Ile Pro Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu
 405 410 415

Gly Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly
 420 425 430

Pro Leu Leu Ile Pro Phe Thr Pro Asn Phe Thr Ile Thr Asn Leu Gln
 435 440 445

Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met
 450 455 460

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser
 465 470 475 480

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
 485 490 495

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
 500 505 510

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 515 520 525

<210> 71

<211> 594

<212> PRT

<213> Homo sapiens

<400> 71

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

104

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu
 100 105 110

Thr Pro Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala
 180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Ser Glu
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 210 215 220

Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 225 230 235 240

106

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
 450 455 460

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
 465 470 475 480

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 485 490 495

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
 500 505 510

Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln
 515 520 525

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
 530 535 540

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His
 545 550 555 560

Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp
 565 570 575

Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly
 580 585 590

Pro Leu

<210> 72

<211> 424

<212> PRT

<213> Homo sapiens

<400> 72

Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
 1 5 10 15

107

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Tyr Thr His
20 25 30

Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
35 40 45

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
50 55 60

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser
65 70 75 80

Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
85 90 95

Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu
100 105 110

Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu
115 120 125

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg
130 135 140

Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
145 150 155 160

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
165 170 175

Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro
180 185 190

Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu Ser Gln
195 200 205

Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp
210 215 220

108

Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr
 225 230 235 240

Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro
 245 250 255

Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe
 260 265 270

Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His
 275 280 285

Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 290 295 300

Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser
 305 310 315 320

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr
 325 330 335

Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly
 340 345 350

Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser
 355 360 365

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val
 370 375 380

Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
 385 390 395 400

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro
 405 410 415

Gly His Thr Ala Pro Val Pro Leu
 420

<210> 73

109

<211> 286

<212> PRT

<213> Homo sapiens

<400> 73

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
 100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
225 230 235 - 240

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
260 265 270

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile Pro Phe
275 280 285

<213> Homo sapiens

<400> 74

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
 20 25 30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

111

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
245 250 255

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
260 265 270

112

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 75

<211> 286

<212> PRT

<213> Homo sapiens

<400> 75

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
 35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
 65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Ser Arg Gln Ser Ser Met Thr
 85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
 100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
 145 150 155 160

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
20 25 30

114

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
 35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
 85 90 95

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
 100 105 110

Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
 130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
 180 185 190

Ala Thr Arg Val Asp Ala Val Cys Thr Gln Arg Pro Asp Pro Lys Ser
 195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr
 210 215 220

His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu
 225 230 235 240

Tyr Val Asn Gly Leu Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
 245 250 255

115

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
 260 265 270

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 77

<211> 288

<212> PRT

<213> Homo sapiens

<400> 77

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Ser Lys Asn Ser Ser
 1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
 20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
 35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
 100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
 115 120 125

116

Pro Phe Thr Val Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
 130 135 140

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
 180 185 190

Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
 195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
 210 215 220

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
 245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
 260 265 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
 275 280 285

<210> 78

<211> 597

<212> PRT

<213> Homo sapiens

<400> 78

Glu Arg Val Leu His Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Arg
 1 5 10 15

117

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
 35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
 85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
 100 105 110

Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
 115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
 130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Phe Lys Pro Glu Lys His Glu Ala
 180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly
 195 200 205

Pro Gly Leu Asp Arg Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
 210 215 220

118

Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
 225 230 235 240

Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro
 245 250 255

Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu
 260 265 270

Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn
 275 280 285

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly
 290 295 300

Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys
 305 310 315 320

Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 325 330 335

Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp
 340 345 350

Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg
 355 360 365

Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile Glu
 370 375 380

Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe
 385 390 395 400

Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr
 405 410 415

Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile
 420 425 430

Val Pro Gly Pro Leu Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile Thr
 435 440 445

119

Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe
 450 455 460

Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys
 465 470 475 480

Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu
 485 490 495

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
 500 505 510

His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 515 520 525

Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
 530 535 540

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
 545 550 555 560

Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly
 565 570 575

Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro
 580 585 590

Leu Leu Ile Pro Phe
 595

<210> 79

<211> 420

<212> PRT

<213> Homo sapiens

<400> 79

120

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
 1 5 10 15
 Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn
 20 25 30
 Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
 35 40 45
 Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
 50 55 60
 Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr
 65 70 75 80
 Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr
 85 90 95
 Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
 100 105 110
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met
 115 120 125
 Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Ser Val Leu Gln
 130 135 140
 Gly Leu Leu Thr Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
 145 150 155 160
 Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala
 165 170 175
 Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro
 180 185 190
 Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn
 195 200 205
 Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
 210 215 220

121

Val Asn Gly Phe Thr His Arg Ser Leu Gly Leu Thr Thr Ser Thr Pro
 225 230 235 240

Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
 245 250 255

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn
 260 265 270

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly
 275 280 285

Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Arg
 290 295 300

Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 305 310 315 320

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp
 325 330 335

Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
 340 345 350

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu
 355 360 365

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
 370 375 380

Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr
 385 390 395 400

Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser
 405 410 415

Ala Ala Ser Pro
 420

122

<210> 80

<211> 479

<212> PRT

<213> Homo sapiens

<400> 80

Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu
 1 5 10 15

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
 20 25 30

His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val
 35 40 45

Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile
 50 55 60

Met Ala Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
 65 70 75 80

Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly Ser Arg Lys
 85 90 95

Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
 100 105 110

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 115 120 125

Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys
 130 135 140

Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu
 145 150 155 160

Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro
 165 170 175

123

Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg
 180 185 190

Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
 195 200 205

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val
 210 215 220

Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys
 225 230 235 240

Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr
 245 250 255

Glu Arg Val Leu Gln Ser Leu Phe Gly Pro Met Phe Lys Asn Thr Ser
 260 265 270

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu
 275 280 285

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
 290 295 300

Asp Pro Lys Ser Leu Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 305 310 315 320

Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
 325 330 335

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro
 340 345 350

Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
 355 360 365

Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val
 370 375 380

124

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
385 390 395 400

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu
405 410 415

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
420 425 430

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
435 440 - 445

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
450 455 460

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu
465 470 475

<210> 81

<211> 5465

<212> DNA

<213> Homo sapiens

<400> 81

```

cagagagcgt tgagctggga acagtgacaa gtgcttatca agttccttca ctctcaacac      60
ggttgacaag aactgatggc attatggaac acatcacaaa aatacccaat gaagcagcac      120
acagaggtac cataagacca gtcaaaggcc ctcagacatc cacttcgcct gccagtccta      180
aaggactaca cacaggaggg acaaaaagaa tggagaccac caccacagct ttgaagacca      240
ccaccacagc tttgaagacc acttccagag ccaccttgac caccagtgtc tatactccca      300
ctttgggaac actgactccc ctcaatgcat caaggcaa at gccagcaca atcctcacag      360
aatgatgat cacaaccca tatgttttcc ctgatgttcc agaaacgaca tcctcattgg      420
ctaccagcct gggagcagaa accagcacag ctcttcccag gacaaccca tctgttctca      480
atagagaatc agagaccaca gcctcactgg tctctcgttc tggggcagag agaagtccgg      540
ttattcaaac tctagatgtt tcttctagtg agccagatac aacagcttca tgggttatcc      600

```

atcctgcaga gaccatccca actgtttcca agacaacccc caattttttc cacagtgaat	660
tagacactgt atcttcaca gccaccagtc atggggcaga cgtcagctca gccattccaa	720
caaatatctc acctagtga ctagatgcac tgacccact ggtcactatt tcggggacag	780
atactagtag aacattccca aactgacta agtccccaca tgaaacagag acaagaacca	840
catggctcac tcatcctgca gagaccagct caactattcc cagaacaatc cccaattttt	900
ctcatcatga atcagatgcc acaccttcaa tagccaccag tcctggggca gaaaccagtt	960
cagctattcc aattatgact gtctcacctg gtgcagaaga tctggtgacc tcacaggtca	1020
ctagttctgg gacagacaga aatatgacta ttccaacttt gactctttct cctggtgaac	1080
caaagacgat agcctcatta gtcacccatc ctgaagcaca gacaagttcg gccattccaa	1140
cttcaactat ctgcctgct gtatcacggg tggtagctc aatggtcacc agtttggcgg	1200
caaagacaag tacaactaat cgagctctga caaactccc tggtagacca gctacaacag	1260
tttcattggg cagcatcct gcacagacca gcccaacagt tccctggaca acttccattt	1320
ttttccatag taaatcagac accacacctt caatgaccac cagtcatggg gcagaatcca	1380
gttcagctgt tccaactcca actgtttcaa ctgaggtacc aggagtagtg acccctttgg	1440
tcaccagttc tagggcagtg atcagtacaa ctattccaat tctgactctt tctcctggtg	1500
aaccagagac cacaccttca atggccacca gtcatgggga agaagccagt tctgctattc	1560
caactccaac tgtttcacct ggggtaccag gagtggtagc ctctctggtc actagttcta	1620
gggcagtgac tagtacaact attccaatc tgactttttc tcttggtgaa ccagagacca	1680
caccttcaat ggccaccagt catgggacag aagctggctc agctgttcca actgttttac	1740
ctgaggtacc aggaatggg accctctctg ttgctagttc tagggcagta accagtacaa	1800
ctcttccaac tctgactctt tctcctggtg aaccagagac cacaccttca atggccacca	1860
gtcatggggc agaagccagc tcaactgttc caactgtttc acctgaggta ccaggagtgg	1920
tgacctctct ggtcactagt tctagtggag taaacagtag aagtattcca actctgattc	1980
tttctcctgg tgaactagaa accacacctt caatggccac cagtcatggg gcagaagcca	2040
gctcagctgt tccaactcca actgtttcac ctggggatc aggagtggg acccctctgg	2100
tcactagttc cagggcagtg accagtacaa ctattccaat tctaactctt tcttctagtg	2160
agccagagac cacaccttca atggccacca gtcatggggg agaagccagc tcagctgttc	2220

taactgtttc acctgaggta ccaggaatgg tgacctctct ggtcac	tact tagagcag	2280
taaccagtac aactattcca actctgacta tttcttctga tgaaccagag accacaactt		2340
cattggtcac ccattctgag gcaaagatga tttcagccat tccaacttta gctgtctccc		2400
ctactgtaca agggctggtg acttcactgg tcactagttc tgggtcagag accagtgcg		2460
tttcaaactc aactgttgcc tcaagtcaac cagagaccat agactcatgg gtcgctcatc		2520
ctgggacaga agcaagttct gttgttccaa ctttgactgt ctccactggg gagccgttta		2580
caaatatctc attggtcacc catcctgcag agagtagctc aactcttccc aggacaacct		2640
caagggtttc ccacagtga ttagacacta tgccttctac agtcaccagt cctgaggcag		2700
aatccagctc agccatttca actactattt cacctggtat accaggtgtg ctgacatcac		2760
tggctactag ctctgggaga gacatcagtg caacttttcc aacagtgcct gagtccccac		2820
atgaatcaga ggcaacagcc tcatgggtta ctcatcctgc agtcaccagc acaacagttc		2880
ccaggacaac ccctaattat tctcatagtg aaccagacac cacaccatca atagccacca		2940
gtcctggggc agaagccact tcagattttc caacaataac tgtctcacct gatgtaccag		3000
atatggtaac ctacaggtc actagttctg ggacagacac cagtataact attccaactc		3060
tgactctttc ttctggtgag ccagagacca caacctcatt tatcacctat tctgagacac		3120
acacaagttc agccattcca actctccctg tctcccctgg tgcacaaag atgctgacct		3180
cactggctcat cagttctggg acagacagca ctacaacttt cccaactg acggagaccc		3240
catatgaacc agagacaaca gccatacagc tcattcatcc tgcagagacc aacacaatgg		3300
ttcccaagac aactcccaag ttttccata gtaagtcaga caccacactc ccagtagcca		3360
tcaccagtcc tgggccagaa gccagttcag ctgtttcaac gacaactatc tcacctgata		3420
tgtcagatct ggtgacctca ctggtcccta gttctgggac agacaccagt acaaccttcc		3480
caacattgag tgagaccca tatgaaccag agactacagt cacgtggctc actcatcctg		3540
cagaaaccag cacaacggtt tctgggacaa ttcccaactt tcccatagg ggatcagaca		3600
ctgcaccctc aatgggtcacc agtctggag tagacacgag gtcaggtgtt ccaactacaa		3660
ccatcccacc cagtatacca ggggtagtga cctcacaggt cactagttct gcaacagaca		3720
ctagtacagc tattccaact ttgactcctt ctctggtga accagagacc acagcctcat		3780
cagctaccca tctgggaca cagactggct tcactgttcc aattcggact gttccctcta		3840

gtgagccaga tacaatggct tcctgggtca ctcacctcc acagaccagc acacctgttt 3900
ccagaacaac ctccagtttt tcccatagta gtccagatgc cacacctgta atggccacca 3960
gtcctaggac agaagccagt tcagctgtac tgacaacaat ctcacctggt gcaccagaga 4020
tggtgacttc acagatcact agttctgggg cagcaaccag tacaactgtt ccaactttga 4080
ctcattctcc tggatgcca gagaccacag ccttattgag caccatccc agaacaggga 4140
caagtaaaac atttcctgct tcaactgtgt ttctcaagt atcagagacc acagcctcac 4200
tcaccattag acctggtgca gagactagca cagctctccc aactcagaca acatcctctc 4260
tcttcacct acttgtaact ggaaccagca gagttgatct aagtccaact gttcacctg 4320
gtgtttctgc aaaaacagcc ccactttcca cccatccagg gacagagacc agcacaatga 4380
ttccaacttc aactctttcc cttggtttac tagagactac aggttactg gccaccagct 4440
cttcagcaga gaccagcacg agtactctaa ctctgactgt tccccctgct gtctctgggc 4500
ttccagtgct ctctataaca actgataagc cccaaactgt gacctcctgg aacacagaaa 4560
cctcaccatc tgtaacttca gttggacccc cagaattttc caggactgtc acaggcacca 4620
ctatgacctt gataccatca gagatgcca caccaccta aaccagtcac ggagaaggag 4680
tgagtccaac cactatcttg agaactacaa tgggtgaagc cactaattta gctaccacag 4740
gttccagtc cactgtggcc aagacaacaa ccaccttcaa tacactggct ggaagcctct 4800
ttactcctct gaccacacct gggatgtcca ccttggcctc tgagagtgtg acctcaagaa 4860
caagttataa ccatcgggtc tggatctcca ccaccagcag ttataaccgt cggtagtgga 4920
cccctgccac cagcactcca gtgacttcta cattctcccc agggatttcc acatcctcca 4980
tccccagctc cacagcagcc acagtcccat tcatggtgcc attcaccctc aacttcacca 5040
tcaccaacct gcagtacgag gaggacatgc ggcaccctgg ttccaggaag ttcaacgcca 5100
cagagagaga actgcagggt ctgctcaaac ccttgttcag gaatagcagt ctggaatacc 5160
tctattcagg ctgcagacta gcctcactca ggccagagaa ggatagctca gccatggcag 5220
tggtatgcat ctgcacacat cgccctgacc ctgaagacct cggactggac agagagcgac 5280
tgtactggga gctgagcaat ctgacaaatg gcatccagga gctgggcccc tacaccctgg 5340
accggaacag tctctatgtc aatgggttca cccatcgaag ctctatgccc accaccagca 5400
ctcctgggac ctccacagtg gatgtgggaa cctcagggac tccatcctcc agccccagcc 5460

128

ccacg

5465

<210> 82

<211> 1821

<212> PRT

<213> Homo sapiens

<400> 82

Glu Ser Val Leu Glu Gly Thr Val Thr Ser Ala Tyr Gln Val Pro Ser
 1 5 10 15

Leu Ser Thr Arg Leu Thr Arg Thr Asp Gly Ile Met Glu His Ile Thr
 20 25 30

Lys Ile Pro Asn Glu Ala Ala His Arg Gly Thr Ile Arg Pro Val Lys
 35 40 45

Gly Pro Gln Thr Ser Thr Ser Pro Ala Ser Pro Lys Gly Leu His Thr
 50 55 60

Gly Gly Thr Lys Arg Met Glu Thr Thr Thr Thr Ala Leu Lys Thr Thr
 65 70 75 80

Thr Thr Ala Leu Lys Thr Thr Ser Arg Ala Thr Leu Thr Thr Ser Val
 85 90 95

Tyr Thr Pro Thr Leu Gly Thr Leu Thr Pro Leu Asn Ala Ser Arg Gln
 100 105 110

Met Ala Ser Thr Ile Leu Thr Glu Met Met Ile Thr Thr Pro Tyr Val
 115 120 125

Phe Pro Asp Val Pro Glu Thr Thr Ser Ser Leu Ala Thr Ser Leu Gly
 130 135 140

Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr Pro Ser Val Leu Asn
 145 150 155 160

Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser Arg Ser Gly Ala Glu
 165 170 175

Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser Ser Ser Glu Pro Asp
 180 185 190

Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu Thr Ile Pro Thr Val
 195 200 205

Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu Leu Asp Thr Val Ser
 210 215 220

Ser Thr Ala Thr Ser His Gly Ala Asp Val Ser Ser Ala Ile Pro Thr
 225 230 235 240

Asn Ile Ser Pro Ser Glu Leu Asp Ala Leu Thr Pro Leu Val Thr Ile
 245 250 255

Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr Leu Thr Lys Ser Pro
 260 265 270

His Glu Thr Glu Thr Arg Thr Thr Trp Leu Thr His Pro Ala Glu Thr
 275 280 285

Ser Ser Thr Ile Pro Arg Thr Ile Pro Asn Phe Ser His His Glu Ser
 290 295 300

Asp Ala Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu Thr Ser Ser
 305 310 315 320

Ala Ile Pro Ile Met Thr Val Ser Pro Gly Ala Glu Asp Leu Val Thr
 325 330 335

Ser Gln Val Thr Ser Ser Gly Thr Asp Arg Asn Met Thr Ile Pro Thr
 340 345 350

Leu Thr Leu Ser Pro Gly Glu Pro Lys Thr Ile Ala Ser Leu Val Thr
 355 360 365

130

His Pro Glu Ala Gln Thr Ser Ser Ala Ile Pro Thr Ser Thr Ile Ser
 370 375 380

Pro Ala Val Ser Arg Leu Val Thr Ser Met Val Thr Ser Leu Ala Ala
 385 390 395 400

Lys Thr Ser Thr Thr Asn Arg Ala Leu Thr Asn Ser Pro Gly Glu Pro
 405 410 415

Ala Thr Thr Val Ser Leu Val Thr His Pro Ala Gln Thr Ser Pro Thr
 420 425 430

Val Pro Trp Thr Thr Ser Ile Phe Phe His Ser Lys Ser Asp Thr Thr
 435 440 445

Pro Ser Met Thr Thr Ser His Gly Ala Glu Ser Ser Ser Ala Val Pro
 450 455 460

Thr Pro Thr Val Ser Thr Glu Val Pro Gly Val Val Thr Pro Leu Val
 465 470 475 480

Thr Ser Ser Arg Ala Val Ile Ser Thr Thr Ile Pro Ile Leu Thr Leu
 485 490 495

Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly
 500 505 510

Glu Glu Ala Ser Ser Ala Ile Pro Thr Pro Thr Val Ser Pro Gly Val
 515 520 525

Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser Arg Ala Val Thr Ser
 530 535 540

Thr Thr Ile Pro Ile Leu Thr Phe Ser Leu Gly Glu Pro Glu Thr Thr
 545 550 555 560

Pro Ser Met Ala Thr Ser His Gly Thr Glu Ala Gly Ser Ala Val Pro
 565 570 575

Thr Val Leu Pro Glu Val Pro Gly Met Val Thr Ser Leu Val Ala Ser
 580 585 590

Ser Arg Ala Val Thr Ser Thr Thr Leu Pro Thr Leu Thr Leu Ser Pro
595 600 605

Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu
610 615 620

Ala Ser Ser Thr Val Pro Thr Val Ser Pro Glu Val Pro Gly Val Val
625 630 635 640

Thr Ser Leu Val Thr Ser Ser Ser Gly Val Asn Ser Thr Ser Ile Pro
645 650 655

Thr Leu Ile Leu Ser Pro Gly Glu Leu Glu Thr Thr Pro Ser Met Ala
660 665 670

Thr Ser His Gly Ala Glu Ala Ser Ser Ala Val Pro Thr Pro Thr Val
675 680 685

Ser Pro Gly Val Ser Gly Val Val Thr Pro Leu Val Thr Ser Ser Arg
690 695 700

Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr Leu Ser Ser Ser Glu
705 710 715 720

Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Val Glu Ala Ser
725 730 735

Ser Ala Val Leu Thr Val Ser Pro Glu Val Pro Gly Met Val Thr Ser
740 745 750

Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Thr Leu
755 760 765

Thr Ile Ser Ser Asp Glu Pro Glu Thr Thr Thr Ser Leu Val Thr His
770 775 780

Ser Glu Ala Lys Met Ile Ser Ala Ile Pro Thr Leu Ala Val Ser Pro
785 790 795 800

132

Thr Val Gln Gly Leu Val Thr Ser Leu Val Thr Ser Ser Gly Ser Glu
 805 810 815

Thr Ser Ala Phe Ser Asn Leu Thr Val Ala Ser Ser Gln Pro Glu Thr
 820 825 830

Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu Ala Ser Ser Val Val
 835 840 845

Pro Thr Leu Thr Val Ser Thr Gly Glu Pro Phe Thr Asn Ile Ser Leu
 850 855 860

Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu Pro Arg Thr Thr Ser
 865 870 875 880

Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro Ser Thr Val Thr Ser
 885 890 895

Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr Thr Ile Ser Pro Gly
 900 905 910

Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser Ser Gly Arg Asp Ile
 915 920 925

Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro His Glu Ser Glu Ala
 930 935 940

Thr Ala Ser Trp Val Thr His Pro Ala Val Thr Ser Thr Thr Val Pro
 945 950 955 960

Arg Thr Thr Pro Asn Tyr Ser His Ser Glu Pro Asp Thr Thr Pro Ser
 965 970 975

Ile Ala Thr Ser Pro Gly Ala Glu Ala Thr Ser Asp Phe Pro Thr Ile
 980 985 990

Thr Val Ser Pro Asp Val Pro Asp Met Val Thr Ser Gln Val Thr Ser
 995 1000 1005

Ser Gly Thr Asp Thr Ser Ile Thr Ile Pro Thr Leu Thr Leu Ser
 1010 1015 1020

Ser Gly	Glu Pro Glu Thr Thr	Thr Ser Phe Ile Thr	Tyr Ser Glu
1025		1030	1035
Thr His	Thr Ser Ser Ala Ile	Pro Thr Leu Pro Val	Ser Pro Gly
1040		1045	1050
Ala Ser	Lys Met Leu Thr Ser	Leu Val Ile Ser Ser	Gly Thr Asp
1055		1060	1065
Ser Thr	Thr Thr Phe Pro Thr	Leu Thr Glu Thr Pro	Tyr Glu Pro
1070		1075	1080
Glu Thr	Thr Ala Ile Gln Leu	Ile His Pro Ala Glu	Thr Asn Thr
1085		1090	1095
Met Val	Pro Arg Thr Thr Pro	Lys Phe Ser His Ser	Lys Ser Asp
1100		1105	1110
Thr Thr	Leu Pro Val Ala Ile	Thr Ser Pro Gly Pro	Glu Ala Ser
1115		1120	1125
Ser Ala	Val Ser Thr Thr Thr	Ile Ser Pro Asp Met	Ser Asp Leu
1130		1135	1140
Val Thr	Ser Leu Val Pro Ser	Ser Gly Thr Asp Thr	Ser Thr Thr
1145		1150	1155
Phe Pro	Thr Leu Ser Glu Thr	Pro Tyr Glu Pro Glu	Thr Thr Ala
1160		1165	1170
Thr Trp	Leu Thr His Pro Ala	Glu Thr Ser Thr Thr	Val Ser Gly
1175		1180	1185
Thr Ile	Pro Asn Phe Ser His	Arg Gly Ser Asp Thr	Ala Pro Ser
1190		1195	1200
Met Val	Thr Ser Pro Gly Val	Asp Thr Arg Ser Gly	Val Pro Thr
1205		1210	1215

134

Thr Thr	Ile Pro Pro Ser Ile	Pro Gly Val Val Thr	Ser Gln Val
1220	1225	1230	
Thr Ser	Ser Ala Thr Asp Thr	Ser Thr Ala Ile Pro	Thr Leu Thr
1235	1240	1245	
Pro Ser	Pro Gly Glu Pro Glu	Thr Thr Ala Ser Ser	Ala Thr His
1250	1255	1260	
Pro Gly	Thr Gln Thr Gly Phe	Thr Val Pro Ile Arg	Thr Val Pro
1265	1270	1275	
Ser Ser	Glu Pro Asp Thr Met	Ala Ser Trp Val Thr	His Pro Pro
1280	1285	1290	
Gln Thr	Ser Thr Pro Val Ser	Arg Thr Thr Ser Ser	Phe Ser His
1295	1300	1305	
Ser Ser	Pro Asp Ala Thr Pro	Val Met Ala Thr Ser	Pro Arg Thr
1310	1315	1320	
Glu Ala	Ser Ser Ala Val Leu	Thr Thr Ile Ser Pro	Gly Ala Pro
1325	1330	1335	
Glu Met	Val Thr Ser Gln Ile	Thr Ser Ser Gly Ala	Ala Thr Ser
1340	1345	1350	
Thr Thr	Val Pro Thr Leu Thr	His Ser Pro Gly Met	Pro Glu Thr
1355	1360	1365	
Thr Ala	Leu Leu Ser Thr His	Pro Arg Thr Glu Thr	Ser Lys Thr
1370	1375	1380	
Phe Pro	Ala Ser Thr Val Phe	Pro Gln Val Ser Glu	Thr Thr Ala
1385	1390	1395	
Ser Leu	Thr Ile Arg Pro Gly	Ala Glu Thr Ser Thr	Ala Leu Pro
1400	1405	1410	
Thr Gln	Thr Thr Ser Ser Leu	Phe Thr Leu Leu Val	Thr Gly Thr
1415	1420	1425	

135

Ser Arg	Val Asp	Leu Ser	Pro Thr	Ala Ser	Pro Gly	Val Ser	Ala
1430			1435		1440		
Lys Thr	Ala Pro	Leu Ser	Thr His	Pro Gly	Thr Glu	Thr Ser	Thr
1445			1450		1455		
Met Ile	Pro Thr	Ser Thr	Leu Ser	Leu Gly	Leu Leu	Glu Thr	Thr
1460			1465		1470		
Gly Leu	Leu Ala	Thr Ser	Ser Ser	Ala Glu	Thr Ser	Thr Ser	Thr
1475			1480		1485		
Leu Thr	Leu Thr	Val Ser	Pro Ala	Val Ser	Gly Leu	Ser Ser	Ala
1490			1495		1500		
Ser Ile	Thr Thr	Asp Lys	Pro Gln	Thr Val	Thr Ser	Trp Asn	Thr
1505			1510		1515		
Glu Thr	Ser Pro	Ser Val	Thr Ser	Val Gly	Pro Pro	Glu Phe	Ser
1520			1525		1530		
Arg Thr	Val Thr	Gly Thr	Thr Met	Thr Leu	Ile Pro	Ser Glu	Met
1535			1540		1545		
Pro Thr	Pro Pro	Lys Thr	Ser His	Gly Glu	Gly Val	Ser Pro	Thr
1550			1555		1560		
Thr Ile	Leu Arg	Thr Thr	Met Val	Glu Ala	Thr Asn	Leu Ala	Thr
1565			1570		1575		
Thr Gly	Ser Ser	Pro Thr	Val Ala	Lys Thr	Thr Thr	Thr Phe	Asn
1580			1585		1590		
Thr Leu	Ala Gly	Ser Leu	Phe Thr	Pro Leu	Thr Thr	Pro Gly	Met
1595			1600		1605		
Ser Thr	Leu Ala	Ser Glu	Ser Val	Thr Ser	Arg Thr	Ser Tyr	Asn
1610			1615		1620		

136

His Arg Ser Trp Ile Ser Thr Thr Ser Ser Tyr Asn Arg Arg Tyr
 1625 1630 1635

Trp Thr Pro Ala Thr Ser Thr Pro Val Thr Ser Thr Phe Ser Pro
 1640 1645 1650

Gly Ile Ser Thr Ser Ser Ile Pro Ser Ser Thr Ala Ala Thr Val
 1655 1660 1665

Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 1670 1675 - 1680

Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn
 1685 1690 1695

Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg
 1700 1705 1710

Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser
 1715 1720 1725

Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile
 1730 1735 1740

Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu
 1745 1750 1755

Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu
 1760 1765 1770

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 1775 1780 1785

Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr
 1790 1795 1800

Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro
 1805 1810 1815

Ser Pro Thr
 1820

137

<210> 83

<211> 468

<212> DNA

<213> Homo sapiens

<400> 83

```
gccacagtcc cattcatggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac      60
gaggaggaca tgcggcacc tggttccagg aagttcaacg ccacagagag agaactgcag      120
ggtctgctca aacccttggt caggaatagc agtctggaat acctctattc aggctgcaga      180
ctagcctcac tcaggccaga gaaggatagc tcagccatgg cagtggatgc catctgcata      240
catcgccctg accctgaaga cctcggactg gacagagagc gactgtactg ggagctgagc      300
aatctgacaa atggcatcca ggagctgggc ccctacaccc tggaccggaa cagtctctat      360
gtcaatggtt tcacccatcg aagctctatg cccaccacca gcactcctgg gacctccaca      420
gtggatgtgg gaacctcagg gactccatcc tccagcccca gcccacg                    468
```

<210> 84

<211> 474

<212> DNA

<213> Homo sapiens

<400> 84

```
gctgctggcc ctctcctgat gccgttcacc ctcaacttca ccatcaccaa cctgcagtac      60
gaggaggaca tgcgtgcac tggctccagg aagttcaaca ccatggagag tgtcctgcag      120
ggtctgctca agcccttggt caagaacacc agtggtggcc ctctgtactc tggctgcaga      180
ttgaccttgc tcaggcccaa gaaagatggg gcagccactg gagtggatgc catctgcacc      240
caccgccttg accccaaaag ccctggactc aacagggagc agctgtactg ggagctaagc      300
aaactgacca atgacattga agagctgggc ccctacaccc tggacaggaa cagtctctat      360
gtcaatggtt tcacccatca gagctctgtg tccaccacca gcactcctgg gacctccaca      420
```

138

gtggatctca gaacctcagg gactccatcc tccctctcca gccccaciat tatg 474

<210> 85

<211> 468

<212> DNA

<213> Homo sapiens

<400> 85
 gctgctggcc ctctcctggg accattcacc ctcaacttca ccatcaccaa cctgcagtat 60
 ggggaggaca tgggtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120
 ggtctgcttg gtcccatatt caagaacacc agtggtggcc ctctgtactc tggctgcaga 180
 ctgacctctc tcaggtctga gaaggatgga gcagccactg gagtggatgc catctgcac 240
 catcatcttg accccaaaag ccctggactc aacagagagc ggctgtactg ggagctgagc 300
 caactgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360
 gtcaatgggt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca 420
 gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca 468

<210> 86

<211> 465

<212> DNA

<213> Homo sapiens

<400> 86
 actgctggcc ctctcctggg gctgttcacc ctcaacttca ccatcaccaa cctgaagtat 60
 gaggaggaca tgcctcgccc tggctccagg aagttcaaca ccactgagag ggtcctgcag 120
 actctgcttg gtcctatgtt caagaacacc agtggtggcc ttctgtactc tggctgcaga 180
 ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240
 caccgtcttg accccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300
 cagctgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

139

gtcaatggtt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca 420
 gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca 465

<210> 87

<211> 468

<212> DNA

<213> Homo sapiens

<400> 87
 gctgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac 60
 gaggaggaca tgcattcacc aggctccagg aagttcaaca ccacggagcg ggtcctgcag 120
 ggtctgcttg gtcccatggt caagaacacc agtgtcggcc ttctgtactc tggctgcaga 180
 ctgaccttgc tcagggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240
 caccgtcttg accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300
 cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360
 gtcaatggtt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420
 gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca 468

<210> 88

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

140

<400> 88
 ncnncctgncc ctctcctgnt ncnnttcacc ntcaacttna ccatcaccaa cctgcantan 60
 gnggannaca tgcnnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120
 ggtctgctnn nccccntntt caagaacacc agtggtggcc ctctgtactc tggctgcaga 180
 ctgaccttgc tcaggctcca gaaggatgga gcagccactg gaggatgc catctgcacc 240
 caccgtcttg accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300
 cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360
 gtcaatggtt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420
 gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca 468

<210> 89

<211> 468

<212> DNA

<213> Homo sapiens

<400> 89
 tctgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac 60
 gaggaggaca tgcattaccc aggtccagg aagttcaaca ccacggagcg ggtcctgcag 120
 ggtctgcttg gtcccatgtt caagaacacc agtgctggcc ttctgtactc tggctgcaga 180
 ctgaccttgc tcaggcctga gaagaatggg gcagccactg gaatggatgc catctgcagc 240
 caccgtcttg accccaaaag ccctggactc aacagagagc agctgtactg ggagctgagc 300
 cagctgaccc atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360
 gtcaatggtt tcacccatcg gagctctgtg gccccacca gcactcctgg gacctccaca 420
 gtggaccttg ggacctcagg gactccatcc tccctcccca gcccaca 468

<210> 90

<211> 468

<212> DNA

<213> Homo sapiens

141

<400> 90
acagctgttc ctctcctggt gccgttcacc ctcaacttta ccatcaccaa tctgcagtat 60
ggggaggaca tgcgtcaccc tggtccagg aagttcaaca ccacagagag ggtcctgcag 120
ggtctgcttg gtcccttggt caagaactcc agtgtcggcc ctctgtactc tggtgcaga 180
ctgatctctc tcaggctctga gaaggatggg gcagccactg gagtggatgc catctgcacc 240
caccacctta accctcaaag ccctggactg gacagggagc agctgtactg gcagctgagc 300
cagatgacca atggcatcaa agagctgggc ccctacaccc tggaccggaa cagtctctac 360
gtcaatggtt tcacccatcg gagctctggg ctccaccacca gactccttg gacttccaca 420
gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 91

<211> 468

<212> DNA

<213> Homo sapiens

<400> 91
actgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtat 60
gaggaggaca tgcctcgccc tggatctagg aagttcaaca ccacagagag ggtcctgcag 120
ggtctgctta gtccattttt caagaactcc agtgttggcc ctctgtactc tggtgcaga 180
ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc 240
taccacccta atcccaaaag acctggactg gacagagagc agctgtactg ggagctaagc 300
cagctgaccc acaacatcac tgagctgggc ccctacagcc tggacaggga cagtctctat 360
gtcaatggtt tcacccatca gaactctgtg cccaccacca gtactcctgg gacctccaca 420
gtgtactggg caaccactgg gactccatcc tccttccccg gccacaca 468

<210> 92

<211> 468

<212> DNA

142

<213> Homo sapiens

<400> 92

```
gagcctggcc ctctcctgat accattcact ttcaacttta ccatcaccaa cctgcattat      60
gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag      120
ggtctgctca agcccttggt caagaacacc agtggtggcc ctctgtactc tggctgcaga      180
ctgacctctc tcaggccoga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc      240
taccacccta atcccaaaag acctgggctg gacagagagc agctgtactg ggagctaagc      300
cagctgaccc acaacatcac tgagctgggc ccctacagcc tggacagga cagtctctat      360
gtcaatgggt tcacccatca gaactctgtg cccaccacca gtactcctgg gacctccaca      420
gtgtactggg caacctctgg gactccatcc tccttccccg gccacaca      468
```

<210> 93

<211> 468

<212> DNA

<213> Homo sapiens

<400> 93

```
gagcctggcc ctctcctgat accattcact ttcaacttta ccatcaccaa cctgcattat      60
gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag      120
ggtctgctca agcccttggt caagaacacc agtggtggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcagacctga gaagcatgag gcagccactg gagtggacac catctgtacc      240
caccgcgttg atcccatcgg acctggactg gacagggagc ggctatactg ggagctgagc      300
cagctgacca acagcattac cgaactggga ccctacaccc tggacagga cagtctctat      360
gtcaatgggt tcaacctctg gagctctgtg ccaaccacca gcaactcctg gacctccaca      420
gtgcacctgg caacctctgg gactccatcc tcctgcctg gccacaca      468
```

<210> 94

<211> 468

143

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

```

<400> 94
gccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcattat      60
gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag      120
ggtctgctca agcccttggt caagaacacc agtgttggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcagacctga gaagcatgag gcagccactg gagtggacac catctgtacc      240
caccgcgttg atcccatcgg acctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca      420
gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca                      468

```

<210> 95

<211> 468

<212> DNA

<213> Homo sapiens

```

<400> 95
tctgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac      60
gaggaggaca tgcattaccc aggctccagg aagttcaaca ccacggagcg ggtcctgcag      120
ggtctgcttg gtcccatggt caagaacacc agtgtcggcc ttctgtactc tggctgcaga      180
ctgaccttgc tcaggcctga gaagaatggg gcagccactg gaatggatgc catctgcagc      240
caccgtcttg accccaaaag ccctggactc gacagagagc agctgtactg ggagctgagc      300

```

144

cagctgaccc atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360
 gtcaatggtt tcacccatcg gagctctgtg gccccacca gcactcctgg gacctccaca 420
 gtggaccttg ggacctcagg gactccatcc tccctcccca gccccaca 468

<210> 96

<211> 468

<212> DNA

<213> Homo sapiens

<400> 96
 acagctgttc ctctcctggt gccgttcacc ctcaacttta ccatcaccaa tctgcagtat 60
 ggggaggaca tgcgtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120
 ggtctgcttg gtcccttggt caagaactcc agtgtcggcc ctctgtactc tggctgcaga 180
 ctgatctctc tcaggtctga gaaggatggg gcagccactg gagtggatgc catctgcacc 240
 caccacctta accctcaaag ccctggactg gacagggagc agctgtactg gcagctgagc 300
 cagatgacca atggcatcaa agagctgggc ccctacaccc tggaccggaa cagtctctac 360
 gtcaatggtt tcacccatcg gagctctggg ctcaccacca gcactccttg gacttccaca 420
 gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 97

<211> 468

<212> DNA

<213> Homo sapiens

<400> 97
 actgctggcc ctctcctggt gccattcacc ctaaacttca ccatcaccaa cctgcagtat 60
 gaggaggaca tgcctcgccc tggatctagg aagttcaacg ccacagagag ggtcctgcag 120
 ggtctgctta gtcccatatt caagaactcc agtgttggcc ctctgtactc tggctgcaga 180
 ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc 240

145

taccacccta atcccaaaag acctggactg gacagagagc agctgtactg ggagctaagc 300
cagctgaccc acaacatcac tgagctgggc ccctacagcc tggacaggga cagtctctat 360
gtcaatgggt tcacccatca gagctctatg acgaccacca gaactcctga tacctccaca 420
atgcacctgg caacctcgag aactccagcc tccctgtctg gacctacg 468

<210> 98

<211> 474

<212> DNA

<213> Homo sapiens

<400> 98
accgccagcc ctctcctggt gctattcaca atcaactgca ccatcaccaa cctgcagtac 60
gaggaggaca tgcgtcgac tggctccagg aagttcaaca ccatggagag tgtcctgcag 120
ggtctgctca agcccttggt caagaacacc agtgttgcc ctctgtactc tggctgcaga 180
ttgaccttgc tcaggcccaa gaaagatggg gcagccactg gagtggatgc catctgcacc 240
caccgccttg acccaaaaag ccctggactc aacagggagc agctgtactg ggagctaagc 300
aaactgacca atgacattga agagctgggc ccctacaccc tggacaggaa cagtctctat 360
gtcaatgggt tcacccatca gagctctgtg tccaccacca gcactcctgg gacctccaca 420
gtggatctca gaacctcagg gactccatcc tccctctcca gcccacaat tatg 474

<210> 99

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

146

<223> All N's = any nucleotide

<400> 99

```

ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan      60
gnggannaca tgcnnncnccc nggntccagg aagttcaaca ccacngagag ggtcctacag      120
ggtctgctca ggcccttggt caagaacacc agtgtcagct ctctgtactc tggttgcaga      180
ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgcctgcacc      240
taccgccttg atcccaaaag ccctggactg gacagagagc aactatactg ggagctgagc      300
cagctaaccc acagcatcac tgagctggga ccctacaccc tggacagggg cagtctctat      360
gtcaatggct tcaaccctcg gagctctgtg ccaaccacca gcactcctgg gacctccaca      420
gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca      468

```

<210> 100

<211> 468

<212> DNA

<213> Homo sapiens

<400> 100

```

gccccgtgcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcattat      60
gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag      120
ggtctgctca agcccttggt caagagcacc agcgttggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcagacctga gaaacatggg gcagccactg gagtggacgc catctgcacc      240
ctccgccttg atcccactgg tcctggactg gacagagagc ggctatactg ggagctgagc      300
cagctgacca acagcgttac agagctgggc ccctacaccc tggacagggg cagtctctat      360
gtcaatggct tcacccagcg gagctctgtg ccaaccacca gtattcctgg gacctctgca      420
gtgcacctgg aaacctctgg gactccagcc tccctccctg gccacaca      468

```

<210> 101

<211> 468

147

<212> DNA

<213> Homo sapiens

<400> 101

```
gcccctggcc ctctcctggg gccattcacc ctcaacttca ctatcaccaa cctgcagtat      60
gaggtggaca tgcgtcacc tggttccagg aagttcaaca ccacggagag agtcctgcag      120
ggtctgctca agcccttggt caagagcacc agtggtggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcaggcctga aaaacgtggg gcagccaccg gcgtggacac catctgcact      240
caccgccttg accctctaaa ccctggactg gacagagagc agctatactg ggagctgagc      300
aaactgaccc gtggcatcat cgagctgggc ccctacctcc tggacagagg cagtctctat      360
gtcaatgggt tcacccatcg gaactttgtg cccatcacca gcactcctgg gacctccaca      420
gtacacctag gaacctctga aactccatcc tccctacctg gaccata      468
```

<210> 102

<211> 468

<212> DNA

<213> Homo sapiens

<400> 102

```
gtgcctggcc ctctcctggg gccattcacc ctcaacttca ccatcaccaa cttgcagtat      60
gaggaggcca tgcgacacc tggctccagg aagttcaata ccacggagag ggtcctacag      120
ggtctgctca ggccttggt caagaatacc agtatcggcc ctctgtactc cagctgcaga      180
ctgaccttgc tcaggccaga gaaggacaag gcagccacca gagtggatgc catctgtacc      240
caccaccctg accctcaaag ccctggactg aacagagagc agctgtactg ggagctgagc      300
cagctgaccc acggcatcac tgagctgggc ccctacaccc tggacaggga cagtctctat      360
gtcgatgggt tcactcattg gagccccata cggaccacca gcactcctgg gacctccata      420
gtgaacctgg gaacctctgg gatccacact tccctccctg aaactaca      468
```

<210> 103

148

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 103

```

ncnnctgncc ctctcctgnt ncnnttcacc ntcaacttna ccatcaccaa cctgcantan      60
gnggannaca tgcnnncnccc nggntccagg aagttcaaca ccacngagag ggttctgcag      120
ggtctgctca aacccttggt caggaatagc agtctggaat acctctattc aggctgcaga      180
ctagcctcac tcaggccaga gaaggatagc tcagccatgg cagtggatgc catctgcaca      240
catcgccctg accctgaaga cctcggactg gacagagagc gactgtactg ggagctgagc      300
aatctgacaa atggcatcca ggagctgggc ccctacaccc tggaccggaa cagtctctac      360
gtcaatgggt tcacccatcg gagctctggg ctacccacca gcactccttg gacttccaca      420
gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca      468

```

<210> 104

<211> 468

<212> DNA

<213> Homo sapiens

<400> 104

```

actgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtat      60
gaggaggaca tgcattgccc tggttccagg aggttcaaca ccacggagag ggttctgcag      120
ggtctgctca cgcccttggt caagaacacc agtggtggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcagacctga gaagcaagag gcagccactg gagtggacac catctgtacc      240

```

149

caccgcgttg atcccatcgg acctggactg gacagagagc ggctatactg ggagctgagc 300
 cagctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat 360
 gtcaatggct tcaacccttg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420
 gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 105

<211> 468

<212> DNA

<213> Homo sapiens

<400> 105
 gccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccga cctgcattat 60
 gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120
 ggtctgctca agcccttggt caagagcacc agcgttggcc ctctgtactc tggctgcaga 180
 ctgacctgac tcagacctga gaaacatggg gcagccactg gaggggacgc catctgcacc 240
 ctccgccttg atcccactgg tcctggactg gacagagagc ggctatactg ggagctgagc 300
 cagctgacca acagcgttac agagctgggc ccctacaccc tggacaggga cagtctctat 360
 gtcaatggct tcacccatcg gagctctgtg ccaaccacca gtattcctgg gacctctgca 420
 gtgcacctgg aaacctctgg gactccagcc tccctccctg gccacaca 468

<210> 106

<211> 468

<212> DNA

<213> Homo sapiens

<400> 106
 gccctgggcc ctctcctggt gccattcacc ctcaacttca ctatcaccaa cctgcagtat 60
 gaggaggaca tgcgtcacc tggttccagg aagttcagca ccacggagag agtccctgcag 120
 ggtctgctca agcccttggt caagaacacc agtgcagct ctctgtactc tggttgcaga 180

150

ctgacottgc tcaggcctga gaaggatggg gcagccacca gagggatgc tgtctgcacc 240
catogtcctg accccaaaag ccctggactg gacagagagc ggctgtactg gaagctgagc 300
cagctgaccc acggcatcac tgagctgggc ccctacaccc tggacaggca cagtctctat 360
gtcaatgggt tcacccatca gagctctatg acgaccacca gaactcctga tacctccaca 420
atgcacctgg caacctcgag aactccagcc tcctgtctg gacctacg 468

<210> 107

<211> 468

<212> DNA

<213> Homo sapiens

<400> 107
accgccagcc ctctcctggg gctattcaca attaacttca ccatcactaa cctgcgggtat 60
gaggagaaca tgcattaccc tggctctaga aagtttaaca ccacggagag agtccttcag 120
ggctctgctca ggctgtgtt caagaacacc agtggtggcc ctctgtactc tggctgcaga 180
ctgaccacgc tcaggcccaa gaaggatggg gcagccacca aagggatgc catctgcacc 240
taccgccctg atcccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300
cagctaacc acagcatcac tgagctgggc ccctacaccc aggacaggga cagtctctat 360
gtcaatgggt tcacccatcg gagctctgtg ccaaccacca gtattcctgg gacctctgca 420
gtgcacctgg aaacctctgg gactccagcc tcctccctg gccacaca 468

<210> 108

<211> 468

<212> DNA

<213> Homo sapiens

<400> 108
gcccctggcc ctctcctggg gccattcacc ctcaacttca ctatcaccaa cctgcagtat 60
gaggaggaca tgcgtcacc tggttccagg aagttcaaca ccacggagag agtcctgcag 120

151

```

ggctctgtca agcccttggt caagagcacc agtggtggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcaggcctga aaaacgtggg gcagccaccg gcgtggacac catctgcact      240
caccgccttg accctctaaa cccaggactg gacagagagc agctatactg ggagctgagc      300
aaactgaccc gtggcatcat cgagctgggc ccctacctcc tggacagagg cagtctctat      360
gtcaatgggt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca      420
gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca                    468

```

<210> 109

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(465)

<223> All N's = any nucleotide

```

<400> 109
nennctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan      60
gnggannaca tgcnnncncc nggntccagg aagttcaaca ccacngagag ggtcctgcag      120
actctgcttg gtcctatggt caagaacacc agtggtggcc ttctgtactc tggctgcaga      180
ctgaccttgc tcagggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc      240
caccgtcttg accccaaaag ccctggagtg gacagggagc aactatactg ggagctgagc      300
cagctgacca atggcattaa agaactgggc ccctacaccc tggacaggaa cagtctctat      360
gtcaatgggt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca      420
gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca                    465

```

<210> 110

152

<211> 468

<212> DNA

<213> Homo sapiens

<400> 110

```

actgctggcc ctctcctggt gccgttcacc ctcaacttca ccatcaccaa cctgaagtac      60
gaggaggaca tgcattgccc tggctccagg aagttcaaca ccacagagag agtctgcag      120
agtctgcttg gtcccatggt caagaacacc agtgttggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcaggtccga gaaggatgga gcagccactg gaggatgac catctgcacc      240
cacctgtctt accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc      300
cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat      360
gtcaatggtt tcacccatca gacctctgcg cccaacacca gactcctgg gacctccaca      420
gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca      468

```

<210> 111

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(465)

<223> All N's = any nucleotide

<400> 111

```

ncnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan      60
ngggannaca tgcnnncncc nggntccagg aagttcaaca ccacngagng ngtnctgcag      120
ggtctgctnn nccccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga      180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc      240

```

153

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300
 canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360
 gtcaatgggt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca 420
 gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca 465

<210> 112

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 112
 actgctggcc ctctcctggt gccgttcacc ctcaacttca ccatcaccaa cctgaagtac 60
 gaggaggaca tgcattgccc tggctccagg aagttcaaca ccacagagag agtcctgcag 120
 agtctgcttg gtcccatggt caagaacacc agtggtggcc ctctgtactc tggctgcaga 180
 ctgacctcgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240
 caccgtgttg acccaaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300
 cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360
 gtcaatgggt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420
 gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca 468

<210> 113

<211> 468

<212> DNA

154

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 113

tctgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac	60
gaggaggaca tgcatacccc aggtccagg aagttcaaca ccacggagcg ggtcctgcag	120
ggtctgcttg gtcccatgtt caagaacacc agtgtcggcc ttctgtactc tggctgcaga	180
ctgaccttgc tcaggcctga gaagaatggg gcaaccactg gaatggatgc catctgcacc	240
caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc	300
cantgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat	360
gtcaatgggt tcacccatcn gantctgng ccaccacca gactcctgg gacctccaca	420
gtgnacntng gnacctcngg gactccatcc tcctccccn gccncaca	468

<210> 114

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 114

ncnctgncc ctctcctgnt nccttcacc ntcaacttna ccatcaccaa cctgcantan	60
---	----

155

gnggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagag ggttctgcag 120
 ggtctgctca aacccttggt caggaatagc agtctggaat acctctattc aggctgcaga 180
 ctagcctcac tcaggccaga gaaggatagc tcagccatgg cagtggatgc catctgcaca 240
 catcgccctg accctgaaga cctcggactg gacagagagc gactgtactg ggagctgagc 300
 aatctgacaa atggcatcca ggagctgggc ccctacaccc tggaccggaa cagtctctat 360
 gtcaatgggt tcacccatcg aagctctatg cccaccacca gactcctgg gacctccaca 420
 gtggatgtgg gaacctcagg gactccatcc tccagcccca gccccacg 468

<210> 115

<211> 468

<212> DNA

<213> Homo sapiens

<400> 115
 actgctggcc ctctcctgat accattcacc ctcaacttca ccatcaccaa cctgcagtat 60
 ggggaggaca tgggtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120
 ggtctgcttg gtcccatatt caagaacacc agtggtggcc ctctgtactc tggctgcaga 180
 ctgäcctctc tcaggcttga gaaggatgga gcagccactg gagtggatgc catctgcatc 240
 catcatcttg accccaaaag ccctggactc aacagagagc ggctgtactg ggagctgagc 300
 caactgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360
 gtcaatgggt tcacccatcg gacctctgtg cccaccacca gactcctgg gacctccaca 420
 gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca 468

<210> 116

<211> 468

<212> DNA

<213> Homo sapiens

156

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 116

```
actgctggcc ctctcctggt gctgttcacc ctcaacttca ccatcaccaa cctgaagtat      60
gaggaggaca tgcatcgccc tggctccagg aagttcaaca ccactgagag ggtcctgcag      120
actctgcttg gtcctatggt caagaacacc agtgttggcc ttctgtactc tggctgcaga      180
ctgaccttgc tcaggtcgga gaaggatgga gcagccactg gagtggatgc catctgcacc      240
cacggtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagetgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca      420
gtgnacntng gnacctcngg gactccatcc tccttcccn gccncaca      468
```

<210> 117

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 117

```
ncnctgncc ctctcctgnt ncncttcacc ntcaacttna ccatcaccaa cctgcantan      60
ngggannaca tgcnncccc nggntccagg aagttcaaca ccacngagag agtccttcag      120
ggtctgtca ggctgtgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga      180
```

157

ctgaccttgc tcaggcccaa gaaggatggg gcagccacca aagtggatgc catctgcacc 240
taccgccctg atcccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300
cagctaacc acagcatcac tgagctgggc ccctacaccc aggacagga cagtctctat 360
gtcaatggct tcacccatcg gagctctgtg ccaaccacca gtattcctgg gacctctgca 420
gtgcacctgg aaaccactgg gactccatcc tccttccccg gccacaca 468

<210> 118

<211> 468

<212> DNA

<213> Homo sapiens

<400> 118
gagcctggcc ctctcctgat accattcact ttcaacttta ccatcaccaa cctgcgttat 60
gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120
ggtctgtctca cgcccttggt caagaacacc agtgttggtc ctctgtactc tggctgcaga 180
ctgaccttgc tcagacctga gaagcaggag gcagccactg gagtggacac catctgtacc 240
caccgcgttg atcccatcgg acctggactg gacagagagc ggctatactg ggagctgagc 300
cagctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat 360
gtcgatggct tcaacccttg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420
gtgcacctgg caacctctgg gactccatcc ccctgcctg gccacaca 468

<210> 119

<211> 468

<212> DNA

<213> Homo sapiens

<400> 119
gccccgtgcc ctctcttgat accattcacc ctcaacttta ccatcaccga cctgcattat 60
gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120

158

```

ggctctgctca agcccttggt caagagcacc agcgttggcc ctctgtactc tggctgcaga      180
ctgaccttgcc tcagacctga gaaacatggg gcagccactg gagtggacgc catctgcacc      240
ctccgccttg atcccactgg tcctggactg gacagagagc ggctatactg ggagctgagc      300
cagctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat      360
gtcaatggct tcaacccttg gagctctgtg ccaaccacca gcactcctgg gacctccaca      420
gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca      468

```

<210> 120

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 120

```

actgctggcc ctctcctggt gccgttcacc ctcaacttca ccatacacia cctgaagtac      60
gaggaggaca tgcattgcc tggctccagg aagttcaaca ccacagagag agtcctgcag      120
agtctgcatg gtcccatggt caagaacacc agtggttggcc ctctgtactc tggctgcaga      180
ctgaccttgcc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc      240
caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca      420
gtgnacntng gnacctngg gactccatcc tccntcccn gccncaca      468

```

<210> 121

159

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 121

```

ncnctgncc ctctcctgnt ncncttcacc ntcaacttna ccatcaccaa cctgcantan      60
ngggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag      120
gggtctgctnn nccccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga      180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc      240
caccnncntn ancccaaaaag ncctggactg nacagnagagc ngctntactg ggagctnagc      300
canctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat      360
gtcaatggtt tcacccatcg aagctctatg cccaccacca gtattcctgg gacctctgca      420
gtgcacctgg aaacctctgg gactccagcc tcctccctg gccacaca                      468

```

<210> 122

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

160

```

<400> 122
gccctggcc ctctcctggt gccattcacc ctcaacttca ctatcaccaa cctgcagtat      60
gaggaggaca tgcgtcaccc tggttccagg aagttcaaca ccacggagag agtcctgcag      120
ggtctgctca agcccttggt caagagcacc agtggtggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcaggcctga aaaacgtggg gcagccaccg gcgtaggacac catctgcact      240
caccgccttg accctctaaa ccctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggt tcacccatcn ganctctgng cccaccacca gactcctgg gacctccaca      420
gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca      468

```

<210> 123

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

```

<400> 123
ncnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan      60
gnggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag      120
ggtctgctnn nccccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga      180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc      240
caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggt ttcaccctcg gagctctgtg ccaaccacca gactcctgg gacctccaca      420

```

161

gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca

468

<210> 124

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 124

```

gccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcattat      60
gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagcg ggtcctgcag      120
ggtctgcttg gtcccatgtt caagaacaca agtgtcggcc ttctgtactc tggctgcaga      180
ctgaccttgc tcaggcctga gaagaatggg gcagccactg gaatggatgc catctgcagc      240
caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggtt tcacccatcn ganctctgng ccaccacca gcactcctgg gacctccaca      420
gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca      468

```

<210> 125

<211> 468

<212> DNA

<213> Homo sapiens

<220>

162

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 125

```

ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan      60
gnggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag      120
ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga      180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc      240
caccnnentn ancccaaaag nccctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggtt tcacccatca gaactctgtg cccaccacca gtactcctgg gacctccaca      420
gtgtactggg caaccactgg gactccatcc tccttccccg gccacaca      468

```

<210> 126

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 126

```

gagcctggcc ctctcctgat accattcact ttcaacttta ccatcaccaa cctgcattat      60
gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag      120
ggtctgctca cgcccttggt caagaacacc agtgttggcc ctctgtactc tggctgcaga      180
ctgaccttgc tcagacctga gaagcaggag gcagccactg gagtggacac catctgtacc      240

```

163

caccgcgttg atcccatcgg acctggactg nacagngagc ngctntactg ggagctnagc 300
 canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360
 gtcaatgggtt tcacccatcn gantctgng cccaccacca gcactcctgg gacctccaca 420
 gtgnaentng gnacctcngg gactccatcc tccntcccn gccncaca 468

<210> 127

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 127
 ncnctgncc ctctcctgnt ncncttcacc ntcaacttna ccatcaccaa cctgcantan 60
 gnggannaca tgcnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120
 ggtctgctnn nccccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180
 ctgacctnnc tcaggnnga gaagnatggn gcagccactg gantggatgc catctgcanc 240
 caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300
 canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360
 gtcaatgggtt tcacccatcg gagctctgtg ccaaccacca gcagtcctgg gacctccaca 420
 gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 128

<211> 468

<212> DNA

164

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 128
gccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcattat 60
gaagaaaaca tgcaacaccc tggttccagg aagttaaca ccacggagag ggttctgcag 120
ggtctgctca agcccttggt caagagcacc agtggtggcc ctctgtactc tggctgcaga 180
ctgaccttgc tcagacctga gaaacatggg gcagccactg gagtggacgc catctgcacc 240
ctccgccttg atcccactgg tcctggactg nacagngagc ngctntactg ggagctnagc 300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360
gtcaatgggt tcacccatcn ganctctgng ccacacacca gcactcctgg gacctccaca 420
gtgnacntng gnacctcngg gactccatcc tcntcccn gccncaca 468

<210> 129

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 129
ncnctgncc ctctcctgnt ncncttcacc ntcaacttna ccatcaccaa cctgcantan 60

165

```

gnggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag      120
ggctctgctnn nccccntntt caagaacncc agtgtnnggcc ntctgtactc tggctgcaga      180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc      240
caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca      420
gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca                      468

```

<210> 130

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

```

<400> 130
gcccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcagtat      60
gaggaggaca tgcacgccc tggatctagg aagttcaaca ccacagagag ggtcctgcag      120
ggctctgctta gtcccatttt caagaactcc agtgtnnggcc ctctgtactc tggctgcaga      180
ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc      240
taccacccta atcccaaaag acctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggtt tcacccatcn gantctgng cccaccacca gcactcctgg gacctccaca      420
gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca                      468

```

166

<210> 131

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 131

ncnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan	60
gnggannaca tgcnnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag	120
ggtctgctnn nccccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga	180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc	240
caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc	300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat	360
gtcaatggtt tcacccattg gagctctggg ctcaccacca gcactccttg gacttccaca	420
gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca	468

<210> 132

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

167

<223> All N's = any nucleotide

```

<400> 132
actgctggcc ctctcctggt gccattcacc ctaaacttca ccatcaccaa cctgcagtat    60
gaggaggaca tgcacgccc tggatctagg aagttcaacg ccacagagag ggtcctgcag    120
ggtctgctta gtcccatatt caagaacacc agtggttgcc ctctgtactc tggctgcaga    180
ctgaccttgc tcagacctga gaagcaggag gcagccactg gagtggacac catctgtacc    240
caccgcgttg atcccatcgg acctggactg nacagngagc ngctntactg ggagctnagc    300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat    360
gtcaatggtt tcacccatch ganctctgng cccaccacca gcaactcctgg gacctccaca    420
gtgnacntng gnacctcngg gactccatcc tcctccccc gccncaca                    468

```

<210> 133

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

```

<400> 133
nennctgncc ctctcctgnt ncnnttcacc ntcaacttna ccatcaccaa cctgcantan    60
gnggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag    120
ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga    180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc    240
caccnnctn ancccaaaag nctggactg nacagngagc ngctntactg ggagctnagc    300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat    360

```

168

gtcaatggtt tcacccatcg gagctttggg ctcaccacca gcactccttg gacttccaca 420

gttgaccttg gaacctcagg gactccatcc ccggtcccca gccccaca 468

<210> 134

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 134

actgctggcc ctctcctggt gccattcacc ctaaacttca ccatcaccaa cctgcagtat 60

gaggaggaca tgcacgccc tggctccagg aagttcaaca ccacggagag ggtccttcag 120

ggtctgctta cgcccttggt caggaacacc agtgtcagct ctctgtactc tggttgcaga 180

ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgtctgcacc 240

catcgtcctg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca 468

<210> 135

<211> 465

<212> DNA

<213> Homo sapiens

169

<220>

<221> misc_feature

<222> (1)..(465)

<223> All N's = any nucleotide

<400> 135

```

ncnctgncc ctctcctgnt ncncttcacc ntcaacttna ccatcaccaa cctgcantan      60
gnggannaca tgcnnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag      120
ggctctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga      180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc      240
caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca      420
gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca                        465

```

<210> 136

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 136

```

actgctggcc ctctcctggt accattcacc ctcaacttca ccatcaccaa cctgcagtat      60
ggggaggaca tgggtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag      120
ggctctgcttg gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga      180

```

170

```

ctgacctctc tcaggtccga gaaggatgga gcagccactg gaggatgc catctgcatc 240
catcatcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360
gtcaatgggt tcacccatcn ganctctgng cccaccacca gactcctgg gacctccaca 420
gtgnacntng gnacctcngg gactccatcc tccntcccn gccncaca 468

```

<210> 137

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

```

<400> 137
nennctgncc ctctctgnt ncncttcacc ntcaacttna ccatcaccaa cctgcantan 60
gnggannaca tgcnncccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120
ggtctgctnn nccccnttt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180
ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240
caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360
gtcaatgggt tcacccatca gacctttgcy cccaacacca gactcctgg gacctccaca 420
gtggaccttg ggacctcagg gactccatcc tccctccca gccctaca 468

```

<210> 138

<211> 468

171

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 138

```
tctgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac      60
gaggaggaca tgcattacccc aggtccagg aagttcaaca ccacggagcg ggtcctgcag      120
ggtctgcttg gtcccatggt caagaacacc agtgctggcc ttctgtactc tggctgcaga      180
ctgaccttgc tcaggcctga gaagaatggg gcagccacca gagtggatgc tgtctgcacc      240
catcgtcctg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc      300
canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat      360
gtcaatgggt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctocaca      420
gtgnacntng gnacctcngg gactccatcc tcntccccc gccncaca      468
```

<210> 139

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

172

<400> 139
 ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60
 gnggannaca tgcnnncccc nggntccagg aagttcaaca ccacngagag ggttctgcag 120
 ggtctgctca agcccttggt caagagcacc agtggtggcc ctctgtattc tggctgcaga 180
 ctgaccttgc tcaggcctga gaaggacgga gtagccacca gagtggacgc catctgcacc 240
 caccgccctg accccaaaat ccctgggcta gacagacagc agctatactg ggagctgagc 300
 cagctgaccc acagcatcac tgagctggga ccctacacc tggataggga cagtctctat 360
 gtcaatgggt tcaccagcg gagctctgtg cccaccacca gactcctgg gactttcaca 420
 gtacagccgg aaacctctga gactccatca tccctccctg gccccaca 468

<210> 140

<211> 468

<212> DNA

<213> Homo sapiens

<400> 140
 gccactggcc ctgtcctgct gccattcacc ctcaatttta ccatcactaa cctgcagtat 60
 gaggaggaca tgcacgccc tggctccagg aagttcaaca ccacggagag ggtccttcag 120
 ggtctgctta tgcccttggt caagaacacc agtgtcagct ctctgtactc tggttgcaga 180
 ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgtctgcacc 240
 catcgtcctg accccaaaag ccctggactg gacagagagc ggctgtactg gaagctgagc 300
 cagctgaccc acggcatcac tgagctgggc ccctacacc tggacaggca cagtctctat 360
 gtcaatgggt tcacccatca gagctctatg acgaccacca gaactcctga tacctccaca 420
 atgcacctgg caacctcgag aactccagcc tccctgtctg gacctacg 468

<210> 141

<211> 468

<212> DNA

<213> Homo sapiens

173

<400> 141
accgccagcc ctctcctggt gctattcaca attaacttca ccatcactaa cctgcggtat 60
gaggagaaca tgcataccccc tggctctaga aagtttaaca ccacggagag agtccttcag 120
ggtctgctca ggcctgtgtt caagaacacc agtggtggcc ctctgtactc tggctgcaga 180
ctgaccttgc tcaggcccaa gaaggatggg gcagccacca aagtggatgc catctgcacc 240
taccgccctg atccccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300
cagctaacc cagcatcac tgagctgggc ccctacaccc tggacaggga cagtctctat 360
gtcaatggtt tcacacagcg gagctctgtg cccaccacta gcattcctgg gacccccaca 420
gtggacctgg gaacatctgg gactccagtt tctaaacctg gtcctcgc 468

<210> 142

<211> 468

<212> DNA

<213> Homo sapiens

<400> 142
gctgccagcc ctctcctggt gctattcact ctcaacttca ccatcaccaa cctgcggtat 60
gaggagaaca tgcagcacc tggctccagg aagttcaaca ccacggagag ggtccttcag 120
ggcctgctca ggtccctgtt caagagcacc agtggtggcc ctctgtactc tggctgcaga 180
ctgactttgc tcaggcctga aaaggatggg acagccactg gagtggatgc catctgcacc 240
caccaccctg accccaaaag ccctaggctg gacagagagc agctgtattg ggagctgagc 300
cagctgaccc acaatatcac tgagctgggc cactatgccc tggacaacga cagcctcttt 360
gtcaatggtt tcaactcatcg gagctctgtg tccaccacca gcactcctgg gacccccaca 420
gtgtatctgg gagcatctaa gactccagcc tcgatatttg gcccttca 468

<210> 143

<211> 399

<212> DNA

174

<213> Homo sapiens

<400> 143

```

gctgccagcc atctcctgat actattcacc ctcaacttca ccatcactaa cctgcggtat      60
gaggagaaca tgtggcctgg ctccaggaag ttcaacta cagagaggggt ccttcagggc      120
ctgctaaggc ccttgttcaa gaacaccagt gttggccctc tgtactctgg ctccaggctg      180
accttgtcga ggccagagaa agatggggaa gccaccggag tggatgccat ctgcaccac      240
cgccctgacc ccacaggccc tgggctggac agagagcagc tgtatttgga gctgagccag      300
ctgaccaca gcatcactga gctgggcccc tacacactgg acagggacag tctctatgtc      360
aatggtttca cccatcggag ctctgtaccc accaccagc                               399

```

<210> 144

<211> 453

<212> DNA

<213> Homo sapiens

<400> 144

```

accggggtgg tcagcgagga gccattcaca ctgaacttca ccatcaacaa cctgcgctac      60
atggcggaca tgggccaacc cggtccctc aagttcaaca tcacagacaa cgatcatgaag      120
cacctgctca gtcctttgtt ccagaggagc agcctgggtg cacggtacac aggctgcagg      180
gtcatcgcac taaggtctgt gaagaacggt gctgagacac ggggtggacct cctctgcacc      240
tacctgcagc ccctcagcgg ccaggtctg cctatcaagc aggtgttcca tgagctgagc      300
cagcagaccc atggcatcac ccggtgggc ccctactctc tggacaaaga cagcctctac      360
cttaacgggtt acaatgaacc tgggtctagat gagcctccta caactccaa gccagccacc      420
acattcctgc ctctctgtc agaagccaca aca                               453

```

<210> 145

<211> 465

<212> DNA

175

<213> Homo sapiens

<400> 145
 gccatggggg accacctgaa gaccctcaca ctcaacttca ccatctccaa tctccagtat 60
 tcaccagata tgggcaaggg ctcagctaca ttcaactcca ccgagggggg ccttcagcac 120
 ctgctcagac ccttggtcca gaagagcagc atggggccct tctacttggg ttgccaactg 180
 atctccctca ggcctgagaa ggatggggca gccactgggtg tggacaccac ctgcacctac 240
 caccctgacc ctgtggggcc cgggctggac atacagcagc tttactggga gctgagtcag 300
 ctgacccatg gtgtcaccca actgggcttc tatgtcctgg acagggatag cctcttcac 360
 aatggctatg caccacagaa tttatcaatc cggggcgagt accagataaa tttccacatt 420
 gtcaactgga acctcagtaa tccagacccc acatcctcag agtac 465

<210> 146

<211> 9799

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(9799)

<223> Any "X" = any amino acid

<400> 146

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg
 35 40 45

176

Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu
 50 55 60

Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr
 65 70 75 80

His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr
 85 90 95

Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr
 100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
 115 120 125

Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly
 130 135 140

Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Ala Ala Gly Pro
 145 150 155 160

Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 165 170 175

Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu
 180 185 190

Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val
 195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
 210 215 220

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
 225 230 235 240

Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser
 245 250 255

177

Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 260 265 270

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr
 275 280 285

Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr
 290 295 300

Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu
 305 310 315 320

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu
 325 330 335

Asp Met Gly His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
 340 345 350

Leu Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro
 355 360 365

Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly
 370 375 380

Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys
 385 390 395 400

Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu
 405 410 415

Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser
 420 425 430

Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Ser Ser
 435 440 445

Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe
 450 455 460

Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr
 465 470 475 480

178

Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg
485 490 495

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu
500 505 510

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly
515 520 525

Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
530 535 540

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu
545 550 555 560

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile
565 570 575

Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
580 585 590

Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
595 600 605

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
610 615 620

Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
625 630 635 640

Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys
645 650 655

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
660 665 670

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
675 680 685

179

Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
 690 695 700

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu
 705 710 715 720

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro
 725 730 735

Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln
 740 745 750

Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
 755 760 765

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly
 770 775 780

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
 785 790 795 800

Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 805 810 815

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
 820 825 830

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu
 835 840 845

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
 850 855 860

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 865 870 875 880

Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
 885 890 895

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro
 900 905 910

180

Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
 915 920 925

Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val
 930 935 940

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
 945 950 955 960

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 965 970 975

Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
 980 985 990

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala
 995 1000 1005

Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu Asp Pro Lys
 1010 1015 1020

Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln
 1025 1030 1035

Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 1040 1045 1050

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
 1055 1060 1065

Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser
 1070 1075 1080

Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu
 1085 1090 1095

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 1100 1105 1110

181

Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr	
1115	1120 1125
Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser	
1130	1135 1140
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg	
1145	1150 1155
Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr	
1160	1165 1170
His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu	
1175	1180 1185
Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly	
1190	1195 1200
Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr	
1205	1210 1215
His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr	
1220	1225 1230
Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro	
1235	1240 1245
Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr	
1250	1255 1260
Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser	
1265	1270 1275
Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser	
1280	1285 1290
Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys	
1295	1300 1305
Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly	
1310	1315 1320

Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
1325 1330 1335

Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
1340 1345 1350

Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
1355 1360 1365

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser
1370 1375 1380

Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro
1385 1390 1395

Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
1400 1405 1410

Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
1415 1420 1425

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
1430 1435 1440

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
1445 1450 1455

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
1460 1465 1470

Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
1475 1480 1485

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys Glu
1490 1495 1500

Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
1505 1510 1515

183

Leu Asp	Arg Asp	Ser Leu	Tyr	Val Asn	Gly Phe	Thr	His Gln	Asn
1520			1525			1530		
Ser Val	Pro Thr	Thr Ser	Thr	Pro Gly	Thr Ser	Thr	Val Tyr	Trp
1535			1540			1545		
Ala Thr	Thr Gly	Thr Pro	Ser	Ser Phe	Pro Gly	His	Thr Glu	Pro
1550			1555			1560		
Gly Pro	Leu Leu	Ile Pro	Phe	Thr Phe	Asn Phe	Thr	Ile Thr	Asn
1565			1570			1575		
Leu His	Tyr Glu	Glu Asn	Met	Gln His	Pro Gly	Ser	Arg Lys	Phe
1580			1585			1590		
Asn Thr	Thr Glu	Arg Val	Leu	Gln Gly	Leu Leu	Lys	Pro Leu	Phe
1595			1600			1605		
Lys Asn	Thr Ser	Val Gly	Pro	Leu Tyr	Ser Gly	Cys	Arg Leu	Thr
1610			1615			1620		
Leu Leu	Arg Pro	Glu Lys	His	Glu Ala	Ala Thr	Gly	Val Asp	Thr
1625			1630			1635		
Ile Cys	Thr His	Arg Val	Asp	Pro Ile	Gly Pro	Gly	Leu Asp	Arg
1640			1645			1650		
Glu Arg	Leu Tyr	Trp Glu	Leu	Ser Gln	Leu Thr	Asn	Ser Ile	Thr
1655			1660			1665		
Glu Leu	Gly Pro	Tyr Thr	Leu	Asp Arg	Asp Ser	Leu	Tyr Val	Asn
1670			1675			1680		
Gly Phe	Asn Pro	Arg Ser	Ser	Val Pro	Thr Thr	Ser	Thr Pro	Gly
1685			1690			1695		
Thr Ser	Thr Val	His Leu	Ala	Thr Ser	Gly Thr	Pro	Ser Ser	Leu
1700			1705			1710		
Pro Gly	His Thr	Ala Pro	Val	Pro Leu	Leu Ile	Pro	Phe Thr	Leu
1715			1720			1725		

184

Asn	Phe	Thr	Ile	Thr	Asn	Leu	His	Tyr	Glu	Glu	Asn	Met	Gln	His
1730						1735					1740			
Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly
1745						1750					1755			
Leu	Leu	Lys	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr
1760						1765					1770			
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	His	Glu	Ala
1775						1780					1785			
Ala	Thr	Gly	Val	Asp	Thr	Ile	Cys	Thr	His	Arg	Val	Asp	Pro	Ile
1790						1795					1800			
Gly	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
1805						1810					1815			
Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
1820						1825					1830			
Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1835						1840					1845			
Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa	Val	Xaa	Leu	Xaa	Thr	Ser
1850						1855					1860			
Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Ser	Ala	Gly	Pro	Leu
1865						1870					1875			
Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr
1880						1885					1890			
Glu	Glu	Asp	Met	His	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
1895						1900					1905			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr
1910						1915					1920			

185

Ser Val 1925	Gly Leu Leu Tyr	Ser 1930	Gly Cys Arg Leu Thr	Leu Leu Arg 1935
Pro Glu 1940	Lys Asn Gly Ala	Ala 1945	Thr Gly Met Asp Ala	Ile Cys Ser 1950
His Arg 1955	Leu Asp Pro Lys	Ser 1960	Pro Gly Leu Asp Arg	Glu Gln Leu 1965
Tyr Trp 1970	Glu Leu Ser Gln	Leu 1975	Thr His Gly Ile Lys	Glu Leu Gly 1980
Pro Tyr 1985	Thr Leu Asp Arg	Asn 1990	Ser Leu Tyr Val Asn	Gly Phe Thr 1995
His Arg 2000	Ser Ser Val Ala	Pro 2005	Thr Ser Thr Pro Gly	Thr Ser Thr 2010
Val Asp 2015	Leu Gly Thr Ser	Gly 2020	Thr Pro Ser Ser Leu	Pro Ser Pro 2025
Thr Thr 2030	Ala Val Pro Leu	Leu 2035	Val Pro Phe Thr Leu	Asn Phe Thr 2040
Ile Thr 2045	Asn Leu Gln Tyr	Gly 2050	Glu Asp Met Arg His	Pro Gly Ser 2055
Arg Lys 2060	Phe Asn Thr Thr	Glu 2065	Arg Val Leu Gln Gly	Leu Leu Gly 2070
Pro Leu 2075	Phe Lys Asn Ser	Ser 2080	Val Gly Pro Leu Tyr	Ser Gly Cys 2085
Arg Leu 2090	Ile Ser Leu Arg	Ser 2095	Glu Lys Asp Gly Ala	Ala Thr Gly 2100
Val Asp 2105	Ala Ile Cys Thr	His 2110	His Leu Asn Pro Gln	Ser Pro Gly 2115
Leu Asp 2120	Arg Glu Gln Leu	Tyr 2125	Trp Gln Leu Ser Gln	Met Thr Asn 2130

Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu
2135						2140					2145			
Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Gly	Leu	Thr	Thr	Ser
2150						2155					2160			
Thr	Pro	Trp	Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro
2165						2170					2175			
Ser	Pro	Val	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro
2180						2185					2190			
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp
2195						2200					2205			
Met	His	Arg	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Ala	Thr	Glu	Arg	Val
2210						2215					2220			
Leu	Gln	Gly	Leu	Leu	Ser	Pro	Ile	Phe	Lys	Asn	Ser	Ser	Val	Gly
2225						2230					2235			
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Ser	Leu	Arg	Pro	Glu	Lys
2240						2245					2250			
Asp	Gly	Ala	Ala	Thr	Gly	Met	Asp	Ala	Val	Cys	Leu	Tyr	His	Pro
2255						2260					2265			
Asn	Pro	Lys	Arg	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu
2270						2275					2280			
Leu	Ser	Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Ser
2285						2290					2295			
Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Ser
2300						2305					2310			
Ser	Met	Thr	Thr	Thr	Arg	Thr	Pro	Asp	Thr	Ser	Thr	Met	His	Leu
2315						2320					2325			

187

Ala Thr	Ser Arg Thr Pro	Ala	Ser Leu Ser Gly	Pro	Thr Thr Ala
2330		2335		2340	
Ser Pro	Leu Leu Val Leu Phe	Thr Ile Asn Cys	Thr	Ile Thr Asn	
2345		2350		2355	
Leu Gln	Tyr Glu Glu Asp Met	Arg Arg Thr Gly	Ser	Arg Lys Phe	
2360		2365		2370	
Asn Thr	Met Glu Ser Val Leu	Gln Gly Leu Leu Lys	Pro	Leu Phe	
2375		2380		2385	
Lys Asn	Thr Ser Val Gly Pro	Leu Tyr Ser Gly Cys	Arg	Leu Thr	
2390		2395		2400	
Leu Leu	Arg Pro Lys Lys Asp	Gly Ala Ala Thr Gly	Val	Asp Ala	
2405		2410		2415	
Ile Cys	Thr His Arg Leu Asp	Pro Lys Ser Pro Gly	Leu	Asn Arg	
2420		2425		2430	
Glu Gln	Leu Tyr Trp Glu Leu	Ser Lys Leu Thr Asn	Asp	Ile Glu	
2435		2440		2445	
Glu Leu	Gly Pro Tyr Thr Leu	Asp Arg Asn Ser Leu	Tyr	Val Asn	
2450		2455		2460	
Gly Phe	Thr His Gln Ser Ser	Val Ser Thr Thr Ser	Thr	Pro Gly	
2465		2470		2475	
Thr Ser	Thr Val Asp Leu Arg	Thr Ser Gly Thr Pro	Ser	Ser Leu	
2480		2485		2490	
Ser Ser	Pro Thr Ile Met Xaa	Xaa Xaa Pro Leu Leu	Xaa	Pro Phe	
2495		2500		2505	
Thr Leu	Asn Phe Thr Ile Thr	Asn Leu Xaa Tyr Glu	Glu	Xaa Met	
2510		2515		2520	
Xaa Xaa	Pro Gly Ser Arg Lys	Phe Asn Thr Thr Glu	Arg	Val Leu	
2525		2530		2535	

188

Gln Gly	Leu Leu Arg Pro Leu	Phe Lys Asn Thr Ser	Val Ser Ser
2540	2545	2550	
Leu Tyr	Ser Gly Cys Arg Leu	Thr Leu Leu Arg Pro	Glu Lys Asp
2555	2560	2565	
Gly Ala	Ala Thr Arg Val Asp	Ala Ala Cys Thr Tyr	Arg Pro Asp
2570	2575	2580	
Pro Lys	Ser Pro Gly Leu Asp	Arg Glu Gln Leu Tyr	Trp Glu Leu
2585	2590	2595	
Ser Gln	Leu Thr His Ser Ile	Thr Glu Leu Gly Pro	Tyr Thr Leu
2600	2605	2610	
Asp Arg	Val Ser Leu Tyr Val	Asn Gly Phe Asn Pro	Arg Ser Ser
2615	2620	2625	
Val Pro	Thr Thr Ser Thr Pro	Gly Thr Ser Thr Val	His Leu Ala
2630	2635	2640	
Thr Ser	Gly Thr Pro Ser Ser	Leu Pro Gly His Thr	Ala Pro Val
2645	2650	2655	
Pro Leu	Leu Ile Pro Phe Thr	Leu Asn Phe Thr Ile	Thr Asn Leu
2660	2665	2670	
His Tyr	Glu Glu Asn Met Gln	His Pro Gly Ser Arg	Lys Phe Asn
2675	2680	2685	
Thr Thr	Glu Arg Val Leu Gln	Gly Leu Leu Arg Pro	Leu Phe Lys
2690	2695	2700	
Ser Thr	Ser Val Gly Pro Leu	Tyr Ser Gly Cys Arg	Leu Thr Leu
2705	2710	2715	
Leu Arg	Pro Glu Lys His Gly	Ala Ala Thr Gly Val	Asp Ala Ile
2720	2725	2730	

189

Cys Thr	Leu Arg Leu Asp	Pro	Thr Gly Pro Gly	Leu	Asp Arg Glu
2735		2740		2745	
Arg Leu	Tyr Trp Glu Leu	Ser	Gln Leu Thr Asn	Ser	Val Thr Glu
2750		2755		2760	
Leu Gly	Pro Tyr Thr Leu	Asp	Arg Asp Ser Leu	Tyr	Val Asn Gly
2765		2770		2775	
Phe Thr	Gln Arg Ser Ser	Val	Pro Thr Thr Ser	Ile	Pro Gly Thr
2780		2785		2790	
Ser Ala	Val His Leu Glu	Thr	Ser Gly Thr Pro	Ala	Ser Leu Pro
2795		2800		2805	
Gly His	Thr Ala Pro Gly	Pro	Leu Leu Val Pro	Phe	Thr Leu Asn
2810		2815		2820	
Phe Thr	Ile Thr Asn Leu	Gln	Tyr Glu Val Asp	Met	Arg His Pro
2825		2830		2835	
Gly Ser	Arg Lys Phe Asn	Thr	Thr Glu Arg Val	Leu	Gln Gly Leu
2840		2845		2850	
Leu Lys	Pro Leu Phe Lys	Ser	Thr Ser Val Gly	Pro	Leu Tyr Ser
2855		2860		2865	
Gly Cys	Arg Leu Thr Leu	Leu	Arg Pro Glu Lys	Arg	Gly Ala Ala
2870		2875		2880	
Thr Gly	Val Asp Thr Ile	Cys	Thr His Arg Leu	Asp	Pro Leu Asn
2885		2890		2895	
Pro Gly	Leu Asp Arg Glu	Gln	Leu Tyr Trp Glu	Leu	Ser Lys Leu
2900		2905		2910	
Thr Arg	Gly Ile Ile Glu	Leu	Gly Pro Tyr Leu	Leu	Asp Arg Gly
2915		2920		2925	
Ser Leu	Tyr Val Asn Gly	Phe	Thr His Arg Asn	Phe	Val Pro Ile
2930		2935		2940	

Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	His	Leu	Gly	Thr	Ser	Glu
2945						2950					2955			
Thr	Pro	Ser	Ser	Leu	Pro	Arg	Pro	Ile	Val	Pro	Gly	Pro	Leu	Leu
2960						2965					2970			
Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu
2975						2980					2985			
Glu	Ala	Met	Arg	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu
2990						2995					3000			
Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser
3005						3010					3015			
Ile	Gly	Pro	Leu	Tyr	Ser	Ser	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro
3020						3025					3030			
Glu	Lys	Asp	Lys	Ala	Ala	Thr	Arg	Val	Asp	Ala	Ile	Cys	Thr	His
3035						3040					3045			
His	Pro	Asp	Pro	Gln	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Gln	Leu	Tyr
3050						3055					3060			
Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Gly	Ile	Thr	Glu	Leu	Gly	Pro
3065						3070					3075			
Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asp	Gly	Phe	Thr	His
3080						3085					3090			
Trp	Ser	Pro	Ile	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Ile	Val
3095						3100					3105			
Asn	Leu	Gly	Thr	Ser	Gly	Ile	Pro	Pro	Ser	Leu	Pro	Glu	Thr	Thr
3110						3115					3120			
Xaa	Xaa	Xaa	Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile
3125						3130					3135			

191

Thr Asn	Leu Xaa	Tyr Glu	Glu Xaa	Met Xaa	Xaa Pro	Gly Ser	Arg
3140			3145		3150		
Lys Phe	Asn Thr	Thr Glu	Arg Val	Leu Gln	Gly Leu	Leu Lys	Pro
3155			3160		3165		
Leu Phe	Arg Asn	Ser Ser	Leu Glu	Tyr Leu	Tyr Ser	Gly Cys	Arg
3170			3175		3180		
Leu Ala	Ser Leu	Arg Pro	Glu Lys	Asp Ser	Ser Ala	Met Ala	Val
3185			3190		3195		
Asp Ala	Ile Cys	Thr His	Arg Pro	Asp Pro	Glu Asp	Leu Gly	Leu
3200			3205		3210		
Asp Arg	Glu Arg	Leu Tyr	Trp Glu	Leu Ser	Asn Leu	Thr Asn	Gly
3215			3220		3225		
Ile Gln	Glu Leu	Gly Pro	Tyr Thr	Leu Asp	Arg Asn	Ser Leu	Tyr
3230			3235		3240		
Val Asn	Gly Phe	Thr His	Arg Ser	Ser Phe	Leu Thr	Thr Ser	Thr
3245			3250		3255		
Pro Trp	Thr Ser	Thr Val	Asp Leu	Gly Thr	Ser Gly	Thr Pro	Ser
3260			3265		3270		
Pro Val	Pro Ser	Pro Thr	Thr Ala	Gly Pro	Leu Leu	Val Pro	Phe
3275			3280		3285		
Thr Leu	Asn Phe	Thr Ile	Thr Asn	Leu Gln	Tyr Glu	Glu Asp	Met
3290			3295		3300		
His Arg	Pro Gly	Ser Arg	Arg Phe	Asn Thr	Thr Glu	Arg Val	Leu
3305			3310		3315		
Gln Gly	Leu Leu	Thr Pro	Leu Phe	Lys Asn	Thr Ser	Val Gly	Pro
3320			3325		3330		
Leu Tyr	Ser Gly	Cys Arg	Leu Thr	Leu Leu	Arg Pro	Glu Lys	Gln
3335			3340		3345		

Glu Ala	Ala Thr	Gly Val	Asp Thr	Ile Cys	Thr His	Arg Val	Asp
3350			3355			3360	
Pro Ile	Gly Pro	Gly Leu	Asp Arg	Glu Arg	Leu Tyr	Trp Glu	Leu
3365			3370			3375	
Ser Gln	Leu Thr	Asn Ser	Ile Thr	Glu Leu	Gly Pro	Tyr Thr	Leu
3380			3385			3390	
Asp Arg	Asp Ser	Leu Tyr	Val Asn	Gly Phe	Asn Pro	Trp Ser	Ser
3395			3400			3405	
Val Pro	Thr Thr	Ser Thr	Pro Gly	Thr Ser	Thr Val	His Leu	Ala
3410			3415			3420	
Thr Ser	Gly Thr	Pro Ser	Ser Leu	Pro Gly	His Thr	Ala Pro	Val
3425			3430			3435	
Pro Leu	Leu Ile	Pro Phe	Thr Leu	Asn Phe	Thr Ile	Thr Asp	Leu
3440			3445			3450	
His Tyr	Glu Glu	Asn Met	Gln His	Pro Gly	Ser Arg	Lys Phe	Asn
3455			3460			3465	
Thr Thr	Glu Arg	Val Leu	Gln Gly	Leu Leu	Lys Pro	Leu Phe	Lys
3470			3475			3480	
Ser Thr	Ser Val	Gly Pro	Leu Tyr	Ser Gly	Cys Arg	Leu Thr	Leu
3485			3490			3495	
Leu Arg	Pro Glu	Lys His	Gly Ala	Ala Thr	Gly Val	Asp Ala	Ile
3500			3505			3510	
Cys Thr	Leu Arg	Leu Asp	Pro Thr	Gly Pro	Gly Leu	Asp Arg	Glu
3515			3520			3525	
Arg Leu	Tyr Trp	Glu Leu	Ser Gln	Leu Thr	Asn Ser	Val Thr	Glu
3530			3535			3540	

193

Leu Gly 3545	Pro Tyr Thr	Leu Asp 3550	Arg Asp Ser	Leu Tyr 3555	Val Asn Gly
Phe Thr 3560	His Arg Ser Ser	Val 3565	Pro Thr Thr Ser	Ile 3570	Pro Gly Thr
Ser Ala 3575	Val His Leu Glu	Thr 3580	Ser Gly Thr Pro	Ala 3585	Ser Leu Pro
Gly His 3590	Thr Ala Pro Gly	Pro 3595	Leu Leu Val Pro	Phe 3600	Thr Leu Asn
Phe Thr 3605	Ile Thr Asn Leu	Gln 3610	Tyr Glu Glu Asp	Met 3615	Arg His Pro
Gly Ser 3620	Arg Lys Phe Ser	Thr 3625	Thr Glu Arg Val	Leu 3630	Gln Gly Leu
Leu Lys 3635	Pro Leu Phe Lys	Asn 3640	Thr Ser Val Ser	Ser 3645	Leu Tyr Ser
Gly Cys 3650	Arg Leu Thr Leu	Leu 3655	Arg Pro Glu Lys	Asp 3660	Gly Ala Ala
Thr Arg 3665	Val Asp Ala Val	Cys 3670	Thr His Arg Pro	Asp 3675	Pro Lys Ser
Pro Gly 3680	Leu Asp Arg Glu	Arg 3685	Leu Tyr Trp Lys	Leu 3690	Ser Gln Leu
Thr His 3695	Gly Ile Thr Glu	Leu 3700	Gly Pro Tyr Thr	Leu 3705	Asp Arg His
Ser Leu 3710	Tyr Val Asn Gly	Phe 3715	Thr His Gln Ser	Ser 3720	Met Thr Thr
Thr Arg 3725	Thr Pro Asp Thr	Ser 3730	Thr Met His Leu	Ala 3735	Thr Ser Arg
Thr Pro 3740	Ala Ser Leu Ser	Gly 3745	Pro Thr Thr Ala	Ser 3750	Pro Leu Leu

Val	Leu	Phe	Thr	Ile	Asn	Phe	Thr	Ile	Thr	Asn	Gln	Arg	Tyr	Glu
3755						3760					3765			
Glu	Asn	Met	His	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu
3770						3775					3780			
Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Val	Phe	Lys	Asn	Thr	Ser
3785						3790					3795			
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro
3800						3805					3810			
Lys	Lys	Asp	Gly	Ala	Ala	Thr	Lys	Val	Asp	Ala	Ile	Cys	Thr	Tyr
3815						3820					3825			
Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr
3830						3835					3840			
Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro
3845						3850					3855			
Tyr	Thr	Gln	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His
3860						3865					3870			
Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Ser	Ala	Val
3875						3880					3885			
His	Leu	Glu	Thr	Ser	Gly	Thr	Pro	Ala	Ser	Leu	Pro	Gly	His	Thr
3890						3895					3900			
Ala	Pro	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile
3905						3910					3915			
Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	Arg	His	Pro	Gly	Ser	Arg
3920						3925					3930			
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys	Pro
3935						3940					3945			

195

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 3950 3955 3960

Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val
 3965 3970 3975

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu
 3980 3985 3990

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly
 3995 4000 4005

Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr
 4010 4015 4020

Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr
 4025 4030 4035

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe
 4040 4045 4050

Ser Leu Pro Ser Pro Ala Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
 4055 4060 4065

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
 4070 4075 4080

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 4085 4090 4095

Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu
 4100 4105 4110

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp
 4115 4120 4125

Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
 4130 4135 4140

Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 4145 4150 4155

Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu
4160						4165					4170			
Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Trp	Ile	Pro
4175						4180					4185			
Val	Pro	Thr	Ser	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Gly
4190						4195					4200			
Ser	Gly	Thr	Pro	Ser	Leu	Pro	Ser	Ser	Pro	Thr	Thr	Ala	Gly	Pro
4205						4210					4215			
Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Lys
4220						4225					4230			
Tyr	Glu	Glu	Asp	Met	His	Cys	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr
4235						4240					4245			
Thr	Glu	Arg	Val	Leu	Gln	Ser	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn
4250						4255					4260			
Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu
4265						4270					4275			
Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys
4280						4285					4290			
Thr	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Val	Asp	Arg	Glu	Gln
4295						4300					4305			
Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu
4310						4315					4320			
Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe
4325						4330					4335			
Thr	His	Gln	Thr	Ser	Ala	Pro	Asn	Thr	Ser	Thr	Pro	Gly	Thr	Ser
4340						4345					4350			

Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser
4355 4360 4365

Pro Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe
4370 4375 4380

Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly
4385 4390 4395

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu
4400 4405 4410

Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly
4415 4420 4425

Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr
4430 4435 4440

Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro
4445 4450 4455

Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr
4460 4465 4470

Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser
4475 4480 4485

Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser
4490 4495 4500

Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro
4505 4510 4515

Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
4520 4525 4530

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
4535 4540 4545

Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
4550 4555 4560

Leu Gln Ser Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly
4565 4570 4575

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys
4580 4585 4590

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Val
4595 4600 4605

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu
4610 4615 4620

Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
4625 4630 4635

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr
4640 4645 4650

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
4655 4660 4665

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala
4670 4675 4680

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
4685 4690 4695

Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
4700 4705 4710

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
4715 4720 4725

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
4730 4735 4740

Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala
4745 4750 4755

199

Ile Cys Thr His Arg Leu Asp	Pro Lys Ser Pro Gly	Leu Asp Arg
4760	4765	4770
Glu Xaa Leu Tyr Trp Glu Leu	Ser Xaa Leu Thr Xaa	Xaa Ile Xaa
4775	4780	4785
Glu Leu Gly Pro Tyr Xaa Leu	Asp Arg Xaa Ser Leu	Tyr Val Asn
4790	4795	4800
Gly Phe Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa Thr Ser	Thr Pro Gly
4805	4810	4815
Thr Ser Xaa Val Xaa Leu Xaa	Thr Ser Gly Thr Pro	Xaa Xaa Xaa
4820	4825	4830
Pro Xaa Xaa Thr Xaa Xaa Xaa	Pro Leu Leu Xaa Pro	Phe Thr Leu
4835	4840	4845
Asn Phe Thr Ile Thr Asn Leu	Xaa Tyr Glu Glu Xaa	Met Xaa Xaa
4850	4855	4860
Pro Gly Ser Arg Lys Phe Asn	Thr Thr Glu Arg Val	Leu Gln Gly
4865	4870	4875
Leu Leu Lys Pro Leu Phe Arg	Asn Ser Ser Leu Glu	Tyr Leu Tyr
4880	4885	4890
Ser Gly Cys Arg Leu Ala Ser	Leu Arg Pro Glu Lys	Asp Ser Ser
4895	4900	4905
Ala Met Ala Val Asp Ala Ile	Cys Thr His Arg Pro	Asp Pro Glu
4910	4915	4920
Asp Leu Gly Leu Asp Arg Glu	Arg Leu Tyr Trp Glu	Leu Ser Asn
4925	4930	4935
Leu Thr Asn Gly Ile Gln Glu	Leu Gly Pro Tyr Thr	Leu Asp Arg
4940	4945	4950
Asn Ser Leu Tyr Val Asn Gly	Phe Thr His Arg Ser	Ser Met Pro
4955	4960	4965

Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Val	Gly	Thr	Ser
4970						4975						4980		
Gly	Thr	Pro	Ser	Ser	Ser	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu
4985						4990						4995		
Leu	Ile	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr
5000						5005						5010		
Gly	Glu	Asp	Met	Gly	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
5015						5020						5025		
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Ile	Phe	Lys	Asn	Thr
5030						5035						5040		
Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Ser	Leu	Arg
5045						5050						5055		
Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Ile
5060						5065						5070		
His	His	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Arg	Leu
5075						5080						5085		
Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly
5090						5095						5100		
Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
5105						5110						5115		
His	Arg	Thr	Ser	Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr
5120						5125						5130		
Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Phe	Ser	Leu	Pro	Ser	Pro
5135						5140						5145		
Ala	Thr	Ala	Gly	Pro	Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr
5150						5155						5160		

Ile Thr	Asn Leu Lys Tyr	Glu	Glu Asp Met His Arg	Pro Gly Ser
5165		5170		5175
Arg Lys	Phe Asn Thr Thr	Glu	Arg Val Leu Gln Thr	Leu Leu Gly
5180		5185		5190
Pro Met	Phe Lys Asn Thr	Ser	Val Gly Leu Leu Tyr	Ser Gly Cys
5195		5200		5205
Arg Leu	Thr Leu Leu Arg	Ser	Glu Lys Asp Gly Ala	Ala Thr Gly
5210		5215		5220
Val Asp	Ala Ile Cys Thr	His	Arg Leu Asp Pro Lys	Ser Pro Gly
5225		5230		5235
Leu Asp	Arg Glu Xaa Leu Tyr	Trp Glu Leu Ser	Xaa	Leu Thr Xaa
5240		5245		5250
Xaa Ile	Xaa Glu Leu Gly	Pro	Tyr Xaa Leu Asp Arg	Xaa Ser Leu
5255		5260		5265
Tyr Val	Asn Gly Phe Xaa Xaa	Xaa Xaa Xaa Xaa Xaa	Xaa	Xaa Thr Ser
5270		5275		5280
Thr Pro	Gly Thr Ser Xaa Val	Xaa Leu Xaa Thr	Ser	Gly Thr Pro
5285		5290		5295
Xaa Xaa	Xaa Pro Xaa Xaa Thr	Xaa Xaa Xaa Pro	Leu	Leu Xaa Pro
5300		5305		5310
Phe Thr	Leu Asn Phe Thr Ile	Thr Asn Leu Xaa Tyr	Glu Glu Xaa	
5315		5320		5325
Met Xaa	Xaa Pro Gly Ser Arg	Lys Phe Asn Thr Thr	Glu Arg Val	
5330		5335		5340
Leu Gln	Gly Leu Leu Arg Pro	Val Phe Lys Asn Thr	Ser Val Gly	
5345		5350		5355
Pro Leu	Tyr Ser Gly Cys Arg	Leu Thr Leu Leu Arg	Pro Lys Lys	
5360		5365		5370

202

Asp Gly	Ala Ala	Thr Lys	Val	Asp Ala	Ile Cys	Thr	Tyr Arg	Pro
5375			5380			5385		
Asp Pro	Lys Ser	Pro Gly	Leu	Asp Arg	Glu Gln	Leu	Tyr Trp	Glu
5390			5395			5400		
Leu Ser	Gln Leu	Thr His	Ser	Ile Thr	Glu Leu	Gly	Pro Tyr	Thr
5405			5410			5415		
Gln Asp	Arg Asp	Ser Leu	Tyr	Val Asn	Gly Phe	Thr	His Arg	Ser
5420			5425			5430		
Ser Val	Pro Thr	Thr Ser	Ile	Pro Gly	Thr Ser	Ala	Val His	Leu
5435			5440			5445		
Glu Thr	Thr Gly	Thr Pro	Ser	Ser Phe	Pro Gly	His	Thr Glu	Pro
5450			5455			5460		
Gly Pro	Leu Leu	Ile Pro	Phe	Thr Phe	Asn Phe	Thr	Ile Thr	Asn
5465			5470			5475		
Leu Arg	Tyr Glu	Glu Asn	Met	Gln His	Pro Gly	Ser	Arg Lys	Phe
5480			5485			5490		
Asn Thr	Thr Glu	Arg Val	Leu	Gln Gly	Leu Leu	Thr	Pro Leu	Phe
5495			5500			5505		
Lys Asn	Thr Ser	Val Gly	Pro	Leu Tyr	Ser Gly	Cys	Arg Leu	Thr
5510			5515			5520		
Leu Leu	Arg Pro	Glu Lys	Gln	Glu Ala	Ala Thr	Gly	Val Asp	Thr
5525			5530			5535		
Ile Cys	Thr His	Arg Val	Asp	Pro Ile	Gly Pro	Gly	Leu Asp	Arg
5540			5545			5550		
Glu Arg	Leu Tyr	Trp Glu	Leu	Ser Gln	Leu Thr	Asn	Ser Ile	Thr
5555			5560			5565		

203

Glu Leu Gly Pro Tyr Thr	Leu Asp Arg Asp Ser Leu Tyr Val Asp
5570	5575 5580
Gly Phe Asn Pro Trp Ser	Ser Val Pro Thr Thr Ser Thr Pro Gly
5585	5590 5595
Thr Ser Thr Val His Leu	Ala Thr Ser Gly Thr Pro Ser Pro Leu
5600	5605 5610
Pro Gly His Thr Ala Pro	Val Pro Leu Leu Ile Pro Phe Thr Leu
5615	5620 5625
Asn Phe Thr Ile Thr Asp	Leu His Tyr Glu Glu Asn Met Gln His
5630	5635 5640
Pro Gly Ser Arg Lys Phe	Asn Thr Thr Glu Arg Val Leu Gln Gly
5645	5650 5655
Leu Leu Lys Pro Leu Phe	Lys Ser Thr Ser Val Gly Pro Leu Tyr
5660	5665 5670
Ser Gly Cys Arg Leu Thr	Leu Leu Arg Pro Glu Lys His Gly Ala
5675	5680 5685
Ala Thr Gly Val Asp Ala	Ile Cys Thr Leu Arg Leu Asp Pro Thr
5690	5695 5700
Gly Pro Gly Leu Asp Arg	Glu Arg Leu Tyr Trp Glu Leu Ser Gln
5705	5710 5715
Leu Thr Asn Ser Ile Thr	Glu Leu Gly Pro Tyr Thr Leu Asp Arg
5720	5725 5730
Asp Ser Leu Tyr Val Asn	Gly Phe Asn Pro Trp Ser Ser Val Pro
5735	5740 5745
Thr Thr Ser Thr Pro Gly	Thr Ser Thr Val His Leu Ala Thr Ser
5750	5755 5760
Gly Thr Pro Ser Ser Leu	Pro Gly His Thr Thr Ala Gly Pro Leu
5765	5770 5775

Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Lys	Tyr
5780						5785					5790			
Glu	Glu	Asp	Met	His	Cys	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
5795						5800					5805			
Glu	Arg	Val	Leu	Gln	Ser	Leu	His	Gly	Pro	Met	Phe	Lys	Asn	Thr
5810						5815					5820			
Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
5825						5830					5835			
Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr
5840						5845					5850			
His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu
5855						5860					5865			
Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly
5870						5875					5880			
Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa
5885						5890					5895			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa
5900						5905					5910			
Val	Xaa	Leu	Xaa	Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa
5915						5920					5925			
Thr	Xaa	Xaa	Xaa	Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu	Asn	Phe	Thr
5930						5935					5940			
Ile	Thr	Asn	Leu	Xaa	Tyr	Glu	Glu	Xaa	Met	Xaa	Xaa	Pro	Gly	Ser
5945						5950					5955			
Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Xaa
5960						5965					5970			

205

Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys
5975 5980 5985

Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa
5990 5995 6000

Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly
6005 6010 6015

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Asn
6020 6025 6030

Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
6035 6040 6045

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser
6050 6055 6060

Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro
6065 6070 6075

Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro
6080 6085 6090

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
6095 6100 6105

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
6110 6115 6120

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
6125 6130 6135

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
6140 6145 6150

Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
6155 6160 6165

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
6170 6175 6180

206

Leu Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa
6185					6190					6195			
Leu Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa
6200					6205					6210			
Xaa Xaa	Xaa	Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa	Val	Xaa	Leu
6215					6220					6225			
Xaa Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Xaa	Xaa
6230					6235					6240			
Xaa Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn
6245					6250					6255			
Leu Xaa	Tyr	Glu	Glu	Xaa	Met	Xaa	Xaa	Pro	Gly	Ser	Arg	Lys	Phe
6260					6265					6270			
Asn Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Xaa	Pro	Xaa	Phe
6275					6280					6285			
Lys Xaa	Thr	Ser	Val	Gly	Xaa	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr
6290					6295					6300			
Leu Leu	Arg	Xaa	Glu	Lys	Xaa	Xaa	Ala	Ala	Thr	Xaa	Val	Asp	Xaa
6305					6310					6315			
Xaa Cys	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa	Xaa	Pro	Gly	Leu	Asp	Arg
6320					6325					6330			
Glu Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa
6335					6340					6345			
Glu Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn
6350					6355					6360			
Gly Phe	His	Pro	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly
6365					6370					6375			

207

Thr Ser	Thr Val	His Leu	Ala	Thr Ser	Gly Thr	Pro	Ser Ser	Leu
6380			6385			6390		
Pro Gly	His Thr	Ala Pro	Val	Pro Leu	Leu Ile	Pro	Phe Thr	Leu
6395			6400			6405		
Asn Phe	Thr Ile	Thr Asn	Leu	His Tyr	Glu Glu	Asn	Met Gln	His
6410			6415			6420		
Pro Gly	Ser Arg	Lys Phe	Asn	Thr Thr	Glu Arg	Val	Leu Gln	Gly
6425			6430			6435		
Leu Leu	Gly Pro	Met Phe	Lys	Asn Thr	Ser Val	Gly	Leu Leu	Tyr
6440			6445			6450		
Ser Gly	Cys Arg	Leu Thr	Leu	Leu Arg	Pro Glu	Lys	Asn Gly	Ala
6455			6460			6465		
Ala Thr	Gly Met	Asp Ala	Ile	Cys Ser	His Arg	Leu	Asp Pro	Lys
6470			6475			6480		
Ser Pro	Gly Leu	Asp Arg	Glu	Xaa Leu	Tyr Trp	Glu	Leu Ser	Xaa
6485			6490			6495		
Leu Thr	Xaa Xaa	Ile Xaa	Glu	Leu Gly	Pro Tyr	Xaa	Leu Asp	Arg
6500			6505			6510		
Xaa Ser	Leu Tyr	Val Asn	Gly	Phe Xaa	Xaa Xaa	Xaa	Xaa Xaa	Xaa
6515			6520			6525		
Xaa Thr	Ser Thr	Pro Gly	Thr	Ser Xaa	Val Xaa	Leu	Xaa Thr	Ser
6530			6535			6540		
Gly Thr	Pro Xaa	Xaa Xaa	Pro	Xaa Xaa	Thr Xaa	Xaa	Xaa Pro	Leu
6545			6550			6555		
Leu Xaa	Pro Phe	Thr Leu	Asn	Phe Thr	Ile Thr	Asn	Leu Xaa	Tyr
6560			6565			6570		
Glu Glu	Xaa Met	Xaa Xaa	Pro	Gly Ser	Arg Lys	Phe	Asn Thr	Thr
6575			6580			6585		

Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Xaa	Pro	Xaa	Phe	Lys	Xaa	Thr
6590						6595					6600			
Ser	Val	Gly	Xaa	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
6605						6610					6615			
Xaa	Glu	Lys	Xaa	Xaa	Ala	Ala	Thr	Xaa	Val	Asp	Xaa	Xaa	Cys	Xaa
6620						6625					6630			
Xaa	Xaa	Xaa	Asp	Pro	Xaa	Xaa	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu
6635						6640					6645			
Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly
6650						6655					6660			
Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
6665						6670					6675			
His	Gln	Asn	Ser	Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr
6680						6685					6690			
Val	Tyr	Trp	Ala	Thr	Thr	Gly	Thr	Pro	Ser	Ser	Phe	Pro	Gly	His
6695						6700					6705			
Thr	Glu	Pro	Gly	Pro	Leu	Leu	Ile	Pro	Phe	Thr	Phe	Asn	Phe	Thr
6710						6715					6720			
Ile	Thr	Asn	Leu	His	Tyr	Glu	Glu	Asn	Met	Gln	His	Pro	Gly	Ser
6725						6730					6735			
Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Thr
6740						6745					6750			
Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys
6755						6760					6765			
Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Gln	Glu	Ala	Ala	Thr	Gly
6770						6775					6780			

Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly
6785 6790 6795

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
6800 6805 6810

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
6815 6820 6825

Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser
6830 6835 6840

Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro
6845 6850 6855

Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro
6860 6865 6870

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa
6875 6880 6885

Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
6890 6895 6900

Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly
6905 6910 6915

Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys
6920 6925 6930

Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa
6935 6940 6945

Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
6950 6955 6960

Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
6965 6970 6975

Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
6980 6985 6990

210

Ser Val	Pro Thr Thr Ser Ser	Pro Gly Thr Ser Thr	Val His Leu
6995		7000	7005
Ala Thr	Ser Gly Thr Pro Ser	Ser Leu Pro Gly His	Thr Ala Pro
7010		7015	7020
Val Pro	Leu Leu Ile Pro Phe	Thr Leu Asn Phe Thr	Ile Thr Asn
7025		7030	7035
Leu His	Tyr Glu Glu Asn Met	Gln His Pro Gly Ser	Arg Lys Phe
7040		7045	7050
Asn Thr	Thr Glu Arg Val Leu	Gln Gly Leu Leu Lys	Pro Leu Phe
7055		7060	7065
Lys Ser	Thr Ser Val Gly Pro	Leu Tyr Ser Gly Cys	Arg Leu Thr
7070		7075	7080
Leu Leu	Arg Pro Glu Lys His	Gly Ala Ala Thr Gly	Val Asp Ala
7085		7090	7095
Ile Cys	Thr Leu Arg Leu Asp	Pro Thr Gly Pro Gly	Leu Asp Arg
7100		7105	7110
Glu Xaa	Leu Tyr Trp Glu Leu	Ser Xaa Leu Thr Xaa	Xaa Ile Xaa
7115		7120	7125
Glu Leu	Gly Pro Tyr Xaa Leu	Asp Arg Xaa Ser Leu	Tyr Val Asn
7130		7135	7140
Gly Phe	Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa Thr Ser	Thr Pro Gly
7145		7150	7155
Thr Ser	Xaa Val Xaa Leu Xaa	Thr Ser Gly Thr Pro	Xaa Xaa Xaa
7160		7165	7170
Pro Xaa	Xaa Thr Xaa Xaa Xaa	Pro Leu Leu Xaa Pro	Phe Thr Leu
7175		7180	7185

211

Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa 7190 7195 7200
Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly 7205 7210 7215
Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr 7220 7225 7230
Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala 7235 7240 7245
Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa 7250 7255 7260
Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa 7265 7270 7275
Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg 7280 7285 7290
Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro 7295 7300 7305
Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser 7310 7315 7320
Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu 7325 7330 7335
Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr 7340 7345 7350
Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr 7355 7360 7365
Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser 7370 7375 7380
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg 7385 7390 7395

Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu
7595						7600					7605			
Tyr	Val	Asn	Gly	Phe	Thr	His	Trp	Ser	Ser	Gly	Leu	Thr	Thr	Ser
7610						7615					7620			
Thr	Pro	Trp	Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro
7625						7630					7635			
Ser	Pro	Val	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro
7640						7645					7650			
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp
7655						7660					7665			
Met	His	Arg	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Ala	Thr	Glu	Arg	Val
7670						7675					7680			
Leu	Gln	Gly	Leu	Leu	Ser	Pro	Ile	Phe	Lys	Asn	Thr	Ser	Val	Gly
7685						7690					7695			
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys
7700						7705					7710			
Gln	Glu	Ala	Ala	Thr	Gly	Val	Asp	Thr	Ile	Cys	Thr	His	Arg	Val
7715						7720					7725			
Asp	Pro	Ile	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu
7730						7735					7740			
Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa
7745						7750					7755			
Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa
7760						7765					7770			
Xaa	Xaa	Xaa	Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa	Val	Xaa	Leu
7775						7780					7785			
Xaa	Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Xaa	Xaa
7790						7795					7800			

Xaa Pro	Leu Leu	Xaa Pro	Phe Thr	Leu Asn	Phe Thr	Ile Thr	Asn	7805	7810	7815
Leu Xaa	Tyr Glu	Glu Xaa	Met Xaa	Xaa Xaa	Pro Gly	Ser Arg	Lys Phe	7820	7825	7830
Asn Thr	Thr Glu	Arg Val	Leu Gln	Gly Leu	Leu Xaa	Pro Xaa	Phe	7835	7840	7845
Lys Xaa	Thr Ser	Val Gly	Xaa Leu	Tyr Ser	Gly Cys	Arg Leu	Thr	7850	7855	7860
Leu Leu	Arg Xaa	Glu Lys	Xaa Xaa	Ala Ala	Thr Xaa	Val Asp	Xaa	7865	7870	7875
Xaa Cys	Xaa Xaa	Xaa Xaa	Asp Pro	Xaa Xaa	Pro Gly	Leu Asp	Arg	7880	7885	7890
Glu Xaa	Leu Tyr	Trp Glu	Leu Ser	Xaa Leu	Thr Xaa	Xaa Ile	Xaa	7895	7900	7905
Glu Leu	Gly Pro	Tyr Xaa	Leu Asp	Arg Xaa	Ser Leu	Tyr Val	Asn	7910	7915	7920
Gly Phe	Thr His	Arg Ser	Phe Gly	Leu Thr	Thr Ser	Thr Pro	Trp	7925	7930	7935
Thr Ser	Thr Val	Asp Leu	Gly Thr	Ser Gly	Thr Pro	Ser Pro	Val	7940	7945	7950
Pro Ser	Pro Thr	Thr Ala	Gly Pro	Leu Leu	Val Pro	Phe Thr	Leu	7955	7960	7965
Asn Phe	Thr Ile	Thr Asn	Leu Gln	Tyr Glu	Glu Asp	Met His	Arg	7970	7975	7980
Pro Gly	Ser Arg	Lys Phe	Asn Thr	Thr Glu	Arg Val	Leu Gln	Gly	7985	7990	7995

215

Leu	Leu	Thr	Pro	Leu	Phe	Arg	Asn	Thr	Ser	Val	Ser	Ser	Leu	Tyr
8000						8005					8010			
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Ala
8015						8020					8025			
Ala	Thr	Arg	Val	Asp	Ala	Val	Cys	Thr	His	Arg	Pro	Asp	Pro	Lys
8030						8035					8040			
Ser	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
8045						8050					8055			
Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
8060						8065					8070			
Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
8075						8080					8085			
Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa	Val	Xaa	Leu	Xaa	Thr	Ser
8090						8095					8100			
Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Pro	Leu
8105						8110					8115			
Leu	Xaa	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Xaa	Tyr
8120						8125					8130			
Glu	Glu	Xaa	Met	Xaa	Xaa	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
8135						8140					8145			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Xaa	Pro	Xaa	Phe	Lys	Xaa	Thr
8150						8155					8160			
Ser	Val	Gly	Xaa	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
8165						8170					8175			
Xaa	Glu	Lys	Xaa	Xaa	Ala	Ala	Thr	Xaa	Val	Asp	Xaa	Xaa	Cys	Xaa
8180						8185					8190			
Xaa	Xaa	Xaa	Asp	Pro	Xaa	Xaa	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu
8195						8200					8205			

Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly
8210						8215					8220			
Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
8225						8230					8235			
His	Trp	Ile	Pro	Val	Pro	Thr	Ser	Ser	Thr	Pro	Gly	Thr	Ser	Thr
8240						8245					8250			
Val	Asp	Leu	Gly	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser	Pro	Thr
8255						8260					8265			
Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile
8270						8275					8280			
Thr	Asn	Leu	Gln	Tyr	Gly	Glu	Asp	Met	Gly	His	Pro	Gly	Ser	Arg
8285						8290					8295			
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro
8300						8305					8310			
Ile	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg
8315						8320					8325			
Leu	Thr	Ser	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val
8330						8335					8340			
Asp	Ala	Ile	Cys	Ile	His	His	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu
8345						8350					8355			
Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa
8360						8365					8370			
Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr
8375						8380					8385			
Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Ser	Thr
8390						8395					8400			

217

Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa
8405 8410 8415

Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
8420 8425 8430

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
8435 8440 8445

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
8450 8455 8460

Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa
8465 8470 8475

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa
8480 8485 8490

Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp
8495 8500 8505

Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu
8510 8515 8520

Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu
8525 8530 8535

Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Phe
8540 8545 8550

Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
8555 8560 8565

Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly
8570 8575 8580

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
8585 8590 8595

Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe Asn
8600 8605 8610

Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Met	Phe	Lys
8615						8620					8625			
Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu
8630						8635					8640			
Leu	Arg	Pro	Glu	Lys	Asn	Gly	Ala	Ala	Thr	Arg	Val	Asp	Ala	Val
8645						8650					8655			
Cys	Thr	His	Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu
8660						8665					8670			
Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu
8675						8680					8685			
Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly
8690						8695					8700			
Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Ser	Thr	Pro	Gly	Thr
8705						8710					8715			
Ser	Xaa	Val	Xaa	Leu	Xaa	Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro
8720						8725					8730			
Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu	Asn
8735						8740					8745			
Phe	Thr	Ile	Thr	Asn	Leu	Xaa	Tyr	Glu	Glu	Xaa	Met	Xaa	Xaa	Pro
8750						8755					8760			
Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu
8765						8770					8775			
Leu	Lys	Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser
8780						8785					8790			
Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Val	Ala
8795						8800					8805			

219

Thr Arg	Val Asp	Ala Ile	Cys	Thr His	Arg Pro	Asp	Pro Lys	Ile
8810			8815			8820		
Pro Gly	Leu Asp	Arg Gln	Gln	Leu Tyr	Trp Glu	Leu	Ser Gln	Leu
8825			8830			8835		
Thr His	Ser Ile	Thr Glu	Leu	Gly Pro	Tyr Thr	Leu	Asp Arg	Asp
8840			8845			8850		
Ser Leu	Tyr Val	Asn Gly	Phe	Thr Gln	Arg Ser	Ser	Val Pro	Thr
8855			8860			8865		
Thr Ser	Thr Pro	Gly Thr	Phe	Thr Val	Gln Pro	Glu	Thr Ser	Glu
8870			8875			8880		
Thr Pro	Ser Ser	Leu Pro	Gly	Pro Thr	Ala Thr	Gly	Pro Val	Leu
8885			8890			8895		
Leu Pro	Phe Thr	Leu Asn	Phe	Thr Ile	Thr Asn	Leu	Gln Tyr	Glu
8900			8905			8910		
Glu Asp	Met His	Arg Pro	Gly	Ser Arg	Lys Phe	Asn	Thr Thr	Glu
8915			8920			8925		
Arg Val	Leu Gln	Gly Leu	Leu	Met Pro	Leu Phe	Lys	Asn Thr	Ser
8930			8935			8940		
Val Ser	Ser Leu	Tyr Ser	Gly	Cys Arg	Leu Thr	Leu	Leu Arg	Pro
8945			8950			8955		
Glu Lys	Asp Gly	Ala Ala	Thr	Arg Val	Asp Ala	Val	Cys Thr	His
8960			8965			8970		
Arg Pro	Asp Pro	Lys Ser	Pro	Gly Leu	Asp Arg	Glu	Arg Leu	Tyr
8975			8980			8985		
Trp Lys	Leu Ser	Gln Leu	Thr	His Gly	Ile Thr	Glu	Leu Gly	Pro
8990			8995			9000		
Tyr Thr	Leu Asp	Arg His	Ser	Leu Tyr	Val Asn	Gly	Phe Thr	His
9005			9010			9015		

Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr Met		
9020	9025	9030
His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr		
9035	9040	9045
Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile		
9050	9055	9060
Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg		
9065	9070	9075
Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro		
9080	9085	9090
Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg		
9095	9100	9105
Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val		
9110	9115	9120
Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu		
9125	9130	9135
Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser		
9140	9145	9150
Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr		
9155	9160	9165
Asn Val Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Val		
9170	9175	9180
Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val		
9185	9190	9195
Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val Leu Phe		
9200	9205	9210

221

Thr Leu Asn Gly Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met
9215 9220 9225

Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
9230 9235 9240

Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro
9245 9250 9255

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
9260 9265 9270

Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp
9275 9280 9285

Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
9290 9295 9300

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala Leu
9305 9310 9315

Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser
9320 9325 9330

Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly
9335 9340 9345

Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser
9350 9355 9360

His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
9365 9370 9375

Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
9380 9385 9390

Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn
9395 9400 9405

Thr Ser Val Gly Pro Leu Tyr Ser Gly Ser Arg Leu Thr Leu Leu
9410 9415 9420

222

Arg	Pro	Glu	Lys	Asp	Gly	Glu	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys
9425						9430					9435			
Thr	His	Arg	Pro	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Gln
9440						9445					9450			
Leu	Tyr	Leu	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu
9455						9460					9465			
Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe
9470						9475					9480			
Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr	Gly	Val	Val	Ser
9485						9490					9495			
Glu	Glu	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu	Arg	Tyr
9500						9505					9510			
Met	Ala	Asp	Met	Gly	Gln	Pro	Gly	Ser	Leu	Lys	Phe	Asn	Ile	Thr
9515						9520					9525			
Asp	Asn	Val	Met	Lys	His	Leu	Leu	Ser	Pro	Leu	Phe	Gln	Arg	Ser
9530						9535					9540			
Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Cys	Arg	Val	Ile	Ala	Leu	Arg
9545						9550					9555			
Ser	Val	Lys	Asn	Gly	Ala	Glu	Thr	Arg	Val	Asp	Leu	Leu	Cys	Thr
9560						9565					9570			
Tyr	Leu	Gln	Pro	Leu	Ser	Gly	Pro	Gly	Leu	Pro	Ile	Lys	Gln	Val
9575						9580					9585			
Phe	His	Glu	Leu	Ser	Gln	Gln	Thr	His	Gly	Ile	Thr	Arg	Leu	Gly
9590						9595					9600			
Pro	Tyr	Ser	Leu	Asp	Lys	Asp	Ser	Leu	Tyr	Leu	Asn	Gly	Tyr	Asn
9605						9610					9615			

223

Glu Pro Gly Leu Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
 9620 9625 9630
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr
 9635 9640 9645
 His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln
 9650 9655 9660
 Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr
 9665 9670 9675
 Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser
 9680 9685 9690
 Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg
 9695 9700 9705
 Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr
 9710 9715 9720
 Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu
 9725 9730 9735
 Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly
 9740 9745 9750
 Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala
 9755 9760 9765
 Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
 9770 9775 9780
 Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu
 9785 9790 9795

Tyr

<210> 147

224

<211> 1422

<212> DNA

<213> Homo sapiens

<400> 147

gccatgggg	accacctgaa	gaccctcaca	ctcaacttca	ccatctccaa	tctccagtat	60
tcaccagata	tgggcaagg	ctcagctaca	ttcaactcca	ccgaggggg	ccttcagcac	120
ctgctcagac	ccttgttcca	gaagagcagc	atgggcccct	tctacttggg	ttgccaactg	180
atctccctca	ggcctgagaa	ggatggggca	gccactgggt	tggacaccac	ctgcacctac	240
cacctgacc	ctgtggggcc	cgggctggac	atacagcagc	tttactggga	gctgagtcag	300
ctgacctatg	gtgtcaccca	actgggcttc	tatgtcctgg	acagggatag	cctcttcac	360
aattggctatg	caccccagaa	tttatcaatc	cggggcgagt	accagataaa	tttcacatt	420
gtcaactgga	acctcagtaa	tccagacccc	acatcctcag	agtacatcac	cctgctgagg	480
gacatccagg	acaaggtcac	cacactctac	aaaggcagtc	aactacatga	cacattccgc	540
ttctgcctgg	tcaccaactt	gacgatggac	tccgtgttgg	tcactgtcaa	ggcattgttc	600
tcctccaatt	tggaccccag	cctgggtggag	caagtctttc	tagataagac	cctgaatgcc	660
tcattccatt	ggctgggctc	cacctaccag	ttggtggaca	tccatgtgac	agaaatggag	720
tcacagttt	atcaaccaac	aagcagctcc	agcaccacgc	acttctacct	gaatttcacc	780
atcaccaacc	taccatattc	ccaggacaaa	gccagccag	gcaccaccaa	ttaccagagg	840
aacaaaagga	atattgagga	tgcgctcaac	caactcttcc	gaaacagcag	catcaagagt	900
tatTTTTctg	actgtcaagt	ttcaacattc	aggtctgtcc	ccaacaggca	ccacaccggg	960
gtggactccc	tgtgtaactt	ctcgccactg	gctcggagag	tagacagagt	tgccatctat	1020
gaggaatttc	tgcggatgac	ccggaatggt	accagctgc	agaacttcac	cctggacagg	1080
agcagtgtcc	ttgtggatgg	gtattctccc	aacagaaatg	agcccttaac	tgggaattct	1140
gaccttccct	tctgggctgt	catcctcatc	ggcttggcag	gactcctggg	actcatcaca	1200
tgcctgatct	gcggtgtcct	ggtgaccacc	cgccggcgga	agaaggaagg	agaatacaac	1260
gtccagcaac	agtgcccagg	ctactaccag	tcacacctag	acctggagga	tctgcaatga	1320
ctggaacttg	cgggtgcctg	gggtgccttt	ccccagcca	gggtccaaag	aagcttggct	1380

225

ggggcagaaa taaaccatat tggtcggaaa aaaaaaaaaa aa

1422

<210> 148

<211> 439

<212> PRT

<213> Homo sapiens

<400> 148

Ala	Met	Gly	Tyr	His	Leu	Lys	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Ile	Ser
1				5					10					15	

Asn	Leu	Gln	Tyr	Ser	Pro	Asp	Met	Gly	Lys	Gly	Ser	Ala	Thr	Phe	Asn
			20					25					30		

Ser	Thr	Glu	Gly	Val	Leu	Gln	His	Leu	Leu	Arg	Pro	Leu	Phe	Gln	Lys
		35					40					45			

Ser	Ser	Met	Gly	Pro	Phe	Tyr	Leu	Gly	Cys	Gln	Leu	Ile	Ser	Leu	Arg
	50					55					60				

Pro	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Thr	Thr	Cys	Thr	Tyr
65					70					75					80

His	Pro	Asp	Pro	Val	Gly	Pro	Gly	Leu	Asp	Ile	Gln	Gln	Leu	Tyr	Trp
				85					90					95	

Glu	Leu	Ser	Gln	Leu	Thr	His	Gly	Val	Thr	Gln	Leu	Gly	Phe	Tyr	Val
			100					105					110		

Leu	Asp	Arg	Asp	Ser	Leu	Phe	Ile	Asn	Gly	Tyr	Ala	Pro	Gln	Asn	Leu
		115					120					125			

Ser	Ile	Arg	Gly	Glu	Tyr	Gln	Ile	Asn	Phe	His	Ile	Val	Asn	Trp	Asn
	130					135					140				

Leu	Ser	Asn	Pro	Asp	Pro	Thr	Ser	Ser	Glu	Tyr	Ile	Thr	Leu	Leu	Arg
145					150					155					160

226

Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His
 165 170 175

Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val
 180 185 190

Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu
 195 200 205

Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp
 210 215 220

Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu
 225 230 235 240

Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr
 245 250 255

Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln
 260 265 270

Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala
 275 280 285

Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp
 290 295 300

Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly
 305 310 315 320

Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg
 325 330 335

Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln
 340 345 350

Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr
 355 360 365

227

Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe
 370 375 380

Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr
 385 390 395 400

Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu
 405 410 415

Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His
 420 425 430

Leu Asp Leu Glu Asp Leu Gln
 435

<210> 149

<211> 1799

<212> PRT

<213> Homo sapiens

<400> 149

Arg Thr Asp Gly Ile Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala
 1 5 10 15

Ala His Arg Gly Thr Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr
 20 25 30

Ser Pro Ala Ser Pro Lys Gly Leu His Thr Gly Gly Thr Lys Arg Met
 35 40 45

Glu Thr Thr Thr Thr Ala Leu Lys Thr Thr Thr Thr Ala Leu Lys Thr
 50 55 60

Thr Ser Arg Ala Thr Leu Thr Thr Ser Val Tyr Thr Pro Thr Leu Gly
 65 70 75 80

Thr Leu Thr Pro Leu Asn Ala Ser Arg Gln Met Ala Ser Thr Ile Leu
 85 90 95

228

Thr Glu Met Met Ile Thr Thr Pro Tyr Val Phe Pro Asp Val Pro Glu
 100 105 110

Thr Thr Ser Ser Leu Ala Thr Ser Leu Gly Ala Glu Thr Ser Thr Ala
 115 120 125

Leu Pro Arg Thr Thr Pro Ser Val Leu Asn Arg Glu Ser Glu Thr Thr
 130 135 140

Ala Ser Leu Val Ser Arg Ser Gly Ala Glu Arg Ser Pro Val Ile Gln
 145 150 155 160

Thr Leu Asp Val Ser Ser Ser Glu Pro Asp Thr Thr Ala Ser Trp Val
 165 170 175

Ile His Pro Ala Glu Thr Ile Pro Thr Val Ser Lys Thr Thr Pro Asn
 180 185 190

Phe Phe His Ser Glu Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His
 195 200 205

Gly Ala Asp Val Ser Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu
 210 215 220

Leu Asp Ala Leu Thr Pro Leu Val Thr Ile Ser Gly Thr Asp Thr Ser
 225 230 235 240

Thr Thr Phe Pro Thr Leu Thr Lys Ser Pro His Glu Thr Glu Thr Arg
 245 250 255

Thr Thr Trp Leu Thr His Pro Ala Glu Thr Ser Ser Thr Ile Pro Arg
 260 265 270

Thr Ile Pro Asn Phe Ser His His Glu Ser Asp Ala Thr Pro Ser Ile
 275 280 285

Ala Thr Ser Pro Gly Ala Glu Thr Ser Ser Ala Ile Pro Ile Met Thr
 290 295 300

229

Val Ser Pro Gly Ala Glu Asp Leu Val Thr Ser Gln Val Thr Ser Ser
305 310 315 320

Gly Thr Asp Arg Asn Met Thr Ile Pro Thr Leu Thr Leu Ser Pro Gly
325 330 335

Glu Pro Lys Thr Ile Ala Ser Leu Val Thr His Pro Glu Ala Gln Thr
340 345 350

Ser Ser Ala Ile Pro Thr Ser Thr Ile Ser Pro Ala Val Ser Arg Leu
355 360 365

Val Thr Ser Met Val Thr Ser Leu Ala Ala Lys Thr Ser Thr Thr Asn
370 375 380

Arg Ala Leu Thr Asn Ser Pro Gly Glu Pro Ala Thr Thr Val Ser Leu
385 390 395 400

Val Thr His Pro Ala Gln Thr Ser Pro Thr Val Pro Trp Thr Thr Ser
405 410 415

Ile Phe Phe His Ser Lys Ser Asp Thr Thr Pro Ser Met Thr Thr Ser
420 425 430

His Gly Ala Glu Ser Ser Ser Ala Val Pro Thr Pro Thr Val Ser Thr
435 440 445

Glu Val Pro Gly Val Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val
450 455 460

Ile Ser Thr Thr Ile Pro Ile Leu Thr Leu Ser Pro Gly Glu Pro Glu
465 470 475 480

Thr Thr Pro Ser Met Ala Thr Ser His Gly Glu Glu Ala Ser Ser Ala
485 490 495

Ile Pro Thr Pro Thr Val Ser Pro Gly Val Pro Gly Val Val Thr Ser
500 505 510

Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu
515 520 525

230

Thr Phe Ser Leu Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser
 530 535 540

His Gly Thr Glu Ala Gly Ser Ala Val Pro Thr Val Leu Pro Glu Val
 545 550 555 560

Pro Gly Met Val Thr Ser Leu Val Ala Ser Ser Arg Ala Val Thr Ser
 565 570 575

Thr Thr Leu Pro Thr Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr
 580 585 590

Pro Ser Met Ala Thr Ser His Gly Ala Glu Ala Ser Ser Thr Val Pro
 595 600 605

Thr Val Ser Pro Glu Val Pro Gly Val Val Thr Ser Leu Val Thr Ser
 610 615 620

Ser Ser Gly Val Asn Ser Thr Ser Ile Pro Thr Leu Ile Leu Ser Pro
 625 630 635 640

Gly Glu Leu Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu
 645 650 655

Ala Ser Ser Ala Val Pro Thr Pro Thr Val Ser Pro Gly Val Ser Gly
 660 665 670

Val Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr
 675 680 685

Ile Pro Ile Leu Thr Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser
 690 695 700

Met Ala Thr Ser His Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val
 705 710 715 720

Ser Pro Glu Val Pro Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg
 725 730 735

231

Ala Val Thr Ser Thr Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu
740 745 750

Pro Glu Thr Thr Thr Ser Leu Val Thr His Ser Glu Ala Lys Met Ile
755 760 765

Ser Ala Ile Pro Thr Leu Ala Val Ser Pro Thr Val Gln Gly Leu Val
770 775 780

Thr Ser Leu Val Thr Ser Ser Gly Ser Glu Thr Ser Ala Phe Ser Asn
785 790 795 800

Leu Thr Val Ala Ser Ser Gln Pro Glu Thr Ile Asp Ser Trp Val Ala
805 810 815

His Pro Gly Thr Glu Ala Ser Ser Val Val Pro Thr Leu Thr Val Ser
820 825 830

Thr Gly Glu Pro Phe Thr Asn Ile Ser Leu Val Thr His Pro Ala Glu
835 840 845

Ser Ser Ser Thr Leu Pro Arg Thr Thr Ser Arg Phe Ser His Ser Glu
850 855 860

Leu Asp Thr Met Pro Ser Thr Val Thr Ser Pro Glu Ala Glu Ser Ser
865 870 875 880

Ser Ala Ile Ser Thr Thr Ile Ser Pro Gly Ile Pro Gly Val Leu Thr
885 890 895

Ser Leu Val Thr Ser Ser Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr
900 905 910

Val Pro Glu Ser Pro His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr
915 920 925

His Pro Ala Val Thr Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr
930 935 940

Ser His Ser Glu Pro Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly
945 950 955 960

232

Ala Glu Ala Thr Ser Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val
 965 970 975

Pro Asp Met Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser
 980 985 990

Ile Thr Ile Pro Thr Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr Thr
 995 1000 1005

Thr Ser Phe Ile Thr Tyr Ser Glu Thr His Thr Ser Ser Ala Ile
 1010 1015 1020

Pro Thr Leu Pro Val Ser Pro Gly Ala Ser Lys Met Leu Thr Ser
 1025 1030 1035

Leu Val Ile Ser Ser Gly Thr Asp Ser Thr Thr Thr Phe Pro Thr
 1040 1045 1050

Leu Thr Glu Thr Pro Tyr Glu Pro Glu Thr Thr Ala Ile Gln Leu
 1055 1060 1065

Ile His Pro Ala Glu Thr Asn Thr Met Val Pro Arg Thr Thr Pro
 1070 1075 1080

Lys Phe Ser His Ser Lys Ser Asp Thr Thr Leu Pro Val Ala Ile
 1085 1090 1095

Thr Ser Pro Gly Pro Glu Ala Ser Ser Ala Val Ser Thr Thr Thr
 1100 1105 1110

Ile Ser Pro Asp Met Ser Asp Leu Val Thr Ser Leu Val Pro Ser
 1115 1120 1125

Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr Leu Ser Glu Thr
 1130 1135 1140

Pro Tyr Glu Pro Glu Thr Thr Ala Thr Trp Leu Thr His Pro Ala
 1145 1150 1155

233

Glu Thr Ser Thr Thr Val Ser Gly Thr Ile Pro Asn Phe Ser His
 1160 1165 1170

Arg Gly Ser Asp Thr Ala Pro Ser Met Val Thr Ser Pro Gly Val
 1175 1180 1185

Asp Thr Arg Ser Gly Val Pro Thr Thr Thr Ile Pro Pro Ser Ile
 1190 1195 1200

Pro Gly Val Val Thr Ser Gln Val Thr Ser Ser Ala Thr Asp Thr
 1205 1210 1215

Ser Thr Ala Ile Pro Thr Leu Thr Pro Ser Pro Gly Glu Pro Glu
 1220 1225 1230

Thr Thr Ala Ser Ser Ala Thr His Pro Gly Thr Gln Thr Gly Phe
 1235 1240 1245

Thr Val Pro Ile Arg Thr Val Pro Ser Ser Glu Pro Asp Thr Met
 1250 1255 1260

Ala Ser Trp Val Thr His Pro Pro Gln Thr Ser Thr Pro Val Ser
 1265 1270 1275

Arg Thr Thr Ser Ser Phe Ser His Ser Ser Pro Asp Ala Thr Pro
 1280 1285 1290

Val Met Ala Thr Ser Pro Arg Thr Glu Ala Ser Ser Ala Val Leu
 1295 1300 1305

Thr Thr Ile Ser Pro Gly Ala Pro Glu Met Val Thr Ser Gln Ile
 1310 1315 1320

Thr Ser Ser Gly Ala Ala Thr Ser Thr Thr Val Pro Thr Leu Thr
 1325 1330 1335

His Ser Pro Gly Met Pro Glu Thr Thr Ala Leu Leu Ser Thr His
 1340 1345 1350

Pro Arg Thr Glu Thr Ser Lys Thr Phe Pro Ala Ser Thr Val Phe
 1355 1360 1365

234

Pro	Gln	Val	Ser	Glu	Thr	Thr	Ala	Ser	Leu	Thr	Ile	Arg	Pro	Gly
1370							1375					1380		
Ala	Glu	Thr	Ser	Thr	Ala	Leu	Pro	Thr	Gln	Thr	Thr	Ser	Ser	Leu
1385						1390						1395		
Phe	Thr	Leu	Leu	Val	Thr	Gly	Thr	Ser	Arg	Val	Asp	Leu	Ser	Pro
1400						1405					1410			
Thr	Ala	Ser	Pro	Gly	Val	Ser	Ala	Lys	Thr	Ala	Pro	Leu	Ser	Thr
1415						1420					1425			
His	Pro	Gly	Thr	Glu	Thr	Ser	Thr	Met	Ile	Pro	Thr	Ser	Thr	Leu
1430						1435					1440			
Ser	Leu	Gly	Leu	Leu	Glu	Thr	Thr	Gly	Leu	Leu	Ala	Thr	Ser	Ser
1445						1450					1455			
Ser	Ala	Glu	Thr	Ser	Thr	Ser	Thr	Leu	Thr	Leu	Thr	Val	Ser	Pro
1460						1465					1470			
Ala	Val	Ser	Gly	Leu	Ser	Ser	Ala	Ser	Ile	Thr	Thr	Asp	Lys	Pro
1475						1480					1485			
Gln	Thr	Val	Thr	Ser	Trp	Asn	Thr	Glu	Thr	Ser	Pro	Ser	Val	Thr
1490						1495					1500			
Ser	Val	Gly	Pro	Pro	Glu	Phe	Ser	Arg	Thr	Val	Thr	Gly	Thr	Thr
1505						1510					1515			
Met	Thr	Leu	Ile	Pro	Ser	Glu	Met	Pro	Thr	Pro	Pro	Lys	Thr	Ser
1520						1525					1530			
His	Gly	Glu	Gly	Val	Ser	Pro	Thr	Thr	Ile	Leu	Arg	Thr	Thr	Met
1535						1540					1545			
Val	Glu	Ala	Thr	Asn	Leu	Ala	Thr	Thr	Gly	Ser	Ser	Pro	Thr	Val
1550						1555					1560			

235

Ala Lys Thr Thr Thr Thr Phe Asn Thr Leu Ala Gly Ser Leu Phe 1565 1570 1575
Thr Pro Leu Thr Thr Pro Gly Met Ser Thr Leu Ala Ser Glu Ser 1580 1585 1590
Val Thr Ser Arg Thr Ser Tyr Asn His Arg Ser Trp Ile Ser Thr 1595 1600 1605
Thr Ser Ser Tyr Asn Arg Arg Tyr Trp Thr Pro Ala Thr Ser Thr 1610 1615 1620
Pro Val Thr Ser Thr Phe Ser Pro Gly Ile Ser Thr Ser Ser Ile 1625 1630 1635
Pro Ser Ser Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe Thr 1640 1645 1650
Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg 1655 1660 1665
His Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Glu Leu Gln 1670 1675 1680
Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu 1685 1690 1695
Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser 1700 1705 1710
Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro 1715 1720 1725
Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser 1730 1735 1740
Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp 1745 1750 1755
Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met 1760 1765 1770

236

Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr
 1775 1780 1785

Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr
 1790 1795

<210> 150

<211> 156

<212> PRT

<213> Homo sapiens

<400> 150

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
 1 5 10 15

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
 35 40 45

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 50 55 60

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
 65 70 75 80

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
 85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
 100 105 110

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
 115 120 125

237

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
 130 135 140

Thr Ser Gly Thr Pro Ser Ser Leu Pro Lys Leu Thr
 145 150 155

<210> 151

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(507)

<223>

<400> 151
 atg aga gga tcg cat cac cat cac cat cac gga tcc atg ggc cac aca 48
 Met Arg Gly Ser His His His His His His Gly Ser Met Gly His Thr
 1 5 10 15

gag cct ggc cct ctc ctg ata cca ttc act ttc aac ttt acc atc acc 96
 Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
 20 25 30

aac ctg cat tat gag gaa aac atg caa cac cct ggt tcc agg aag ttc 144
 Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
 35 40 45

aac acc acg gag agg gtt ctg cag ggt ctg ctc aag ccc ttg ttc aag 192
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
 50 55 60

aac acc agt gtt ggc cct ctg tac tct ggc tgc aga ctg acc ttg ctc 240
 Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 65 70 75 80

aga cct gag aag cat gag gca gcc act gga gtg gac acc atc tgt acc 288
 Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
 85 90 95

cac cgc gtt gat ccc atc gga cct gga ctg gac aga gag cgg cta tac 336

238

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
 100 105 110
 tgg gag ctg agc cag ctg acc aac agc atc aca gag ctg gga ccc tac 384
 Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
 115 120 125
 acc ctg gac agg gac agt ctc tat gtc aat ggc ttc aac cct cgg agc 432
 Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
 130 135 140
 tct gtg cca acc acc agc act cct ggg acc tcc aca gtg cac ctg gca 480
 Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
 145 150 155 160
 acc tct ggg act cca tcc tcc ctg cct 507
 Thr Ser Gly Thr Pro Ser Ser Leu Pro
 165

<210> 152

<211> 169

<212> PRT

<213> Homo sapiens

<400> 152

Met Arg Gly Ser His His His His His His Gly Ser Met Gly His Thr
 1 5 10 15
 Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
 20 25 30
 Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
 35 40 45
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
 50 55 60
 Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 65 70 75 80
 Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
 85 90 95

239

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
 100 105 110

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
 115 120 125

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
 130 135 140

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
 145 150 155 160

Thr Ser Gly Thr Pro Ser Ser Leu Pro
 165

<210> 153

<211> 507

<212> DNA

<213> Homo sapiens

<400> 153
 aggcaggggag gatggagtcc cagaggttgc caggtgcact gtggaggtcc caggagtgc 60
 ggtggttggc acagagctcc gagggttgaa gccattgaca tagagactgt ccctgtccag 120
 ggtgtagggc cccagctctg tgatgctgtt ggtcagctgg ctgagctccc agtatagccg 180
 ctctctgtcc agtccaggtc cgatgggata aacgcggtgg gtacagatgg tgtccactcc 240
 agtggctgcc tcatgcttct caggtctgag caaggtcagt ctgcagccag agtacagagg 300
 gccaaactg gtgttcttga acaagggtt gagcagaccc tgcagaaccc tctccgtggt 360
 gttgaacttc ctggaaccag ggtgttgcg gtttccctca taatgcaggt tggatgatgg 420
 aaagttgaaa gtgaatggtg tcaggagagg gccaggctct gtgtggccca tggatccgtg 480
 atggtgatgg tgatgcgata ctctcat 507

<210> 154

240

<211> 9

<212> PRT

<213> Homo sapiens

<400> 154

Arg Leu Tyr Trp Glu Leu Ser Gln Leu
1 5

<210> 155

<211> 9

<212> PRT

<213> Homo sapiens

<400> 155

Thr Leu Asp Arg Asp Ser Leu Tyr Val
1 5

<210> 156

<211> 9

<212> PRT

<213> Homo sapiens

<400> 156

Val Leu Gln Gly Leu Leu Lys Pro Leu
1 5

<210> 157

<211> 9

<212> PRT

<213> Homo sapiens

241

<400> 157

Gln Leu Thr Asn Ser Ile Thr Glu Leu
1 5

<210> 158

<211> 780

<212> PRT

<213> Homo sapiens

<400> 158

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg
35 40 45

Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu
50 55 60

Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr
65 70 75 80

His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr
85 90 95

Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
115 120 125

Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly
130 135 140

242

Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Ala Ala Gly Pro
145 150 155 160

Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
165 170 175

Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu
180 185 190

Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val
195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
210 215 220

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
225 230 235 240

Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser
245 250 255

Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg
260 265 270

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr
275 280 285

Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr
290 295 300

Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala Gly Pro Leu Leu Val
305 310 315 320

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp
325 330 335

Met Gly His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
340 345 350

243

Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu
 355 360 365

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly Ala
 370 375 380

Ala Thr Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser
 385 390 395 400

Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 405 410 415

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 420 425 430

Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Ser Ser Thr
 435 440 445

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser
 450 455 460

Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu
 465 470 475 480

Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro
 485 490 495

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Leu
 500 505 510

Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys
 515 520 525

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val
 530 535 540

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp
 545 550 555 560

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys
 565 570 575

244

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 580 585 590

Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser
 595 600 605

Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr
 610 615 620

Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 625 630 635 640

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
 645 650 655

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys
 660 665 670

Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 675 680 685

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
 690 695 700

His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr
 705 710 715 720

Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
 725 730 735

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr
 740 745 750

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
 755 760 765

Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr
 770 775 780

245

<210> 159

<211> 780

<212> PRT

<213> Homo sapiens

<400> 159

Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys
 35 40 45

Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 50 55 60

Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser
 65 70 75 80

His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr
 85 90 95

Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr
 100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
 115 120 125

Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
 130 135 140

Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro
 145 150 155 160

Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 165 170 175

246

Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
 180 185 190

Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val
 195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys
 210 215 220

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn
 225 230 235 240

Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser
 245 250 255

Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 260 265 270

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr
 275 280 285

Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr
 290 295 300

Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
 305 310 315 320

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
 325 330 335

His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln
 340 345 350

Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
 355 360 365

Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala
 370 375 380

247

Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro
385 390 395 400

Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
405 410 415

Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr
420 425 430

Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro
435 440 445

Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe
450 455 460

Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn
465 470 475 480

Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly
485 490 495

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys
500 505 510

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
515 520 525

Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp
530 535 540

Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg
545 550 555 560

Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu
565 570 575

Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
580 585 590

Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
595 600 605

248

Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr
610 615 620

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
625 630 635 640

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
645 650 655

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
660 665 670

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
675 680 685

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
690 695 700

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
705 710 715 720

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
725 730 735

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
740 745 750

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
755 760 765

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr
770 775 780

<210> 160

<211> 624

<212> PRT

<213> Homo sapiens

249

<400> 160

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Arg Phe
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys
 35 40 45

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 50 55 60

Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
 65 70 75 80

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
 85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
 100 105 110

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser
 115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
 130 135 140

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro
 145 150 155 160

Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asp Leu His Tyr
 165 170 175

Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
 180 185 190

Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val
 195 200 205

250

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
 210 215 220

His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp
 225 230 235 240

Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser
 245 250 255

Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 260 265 270

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr
 275 280 285

Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr
 290 295 300

Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro
 305 310 315 320

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
 325 330 335

Arg His Pro Gly Ser Arg Lys Phe Ser Thr Thr Glu Arg Val Leu Gln
 340 345 350

Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr
 355 360 365

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala
 370 375 380

Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro
 385 390 395 400

Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His
 405 410 415

251

Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr
 420 425 430

Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro
 435 440 445

Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu
 450 455 460

Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn
 465 470 475 480

Phe Thr Ile Thr Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly
 485 490 495

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
 500 505 510

Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 515 520 525

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp
 530 535 540

Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
 545 550 555 560

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu
 565 570 575

Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
 580 585 590

Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala
 595 600 605

Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr
 610 615 620

<210> 161

252

<211> 468

<212> PRT

<213> Homo sapiens

<400> 161

Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe Lys
35 40 45

Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
50 55 60

Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr
65 70 75 80

His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr
85 90 95

Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser
115 120 125

Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala
130 135 140

Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro
145 150 155 160

Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr
165 170 175

253

Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
 180 185 190

Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val
 195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys
 210 215 220

Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp
 225 230 235 240

Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
 245 250 255

Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg
 260 265 270

Asp Ser Leu Tyr Asn Val Gly Phe Thr Gln Arg Ser Ser Val Pro Thr
 275 280 285

Thr Ser Val Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr
 290 295 300

Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val Leu
 305 310 315 320

Phe Thr Leu Asn Gly Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met
 325 330 335

Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
 340 345 350

Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr
 355 360 365

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala
 370 375 380

Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser Pro
 385 390 395 400

254

Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
 405 410 415

Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu Phe
 420 425 430

Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro
 435 440 445

Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile
 450 455 460

Phe Gly Pro Ser
 465

<210> 162

<211> 11721

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(11721)

<223> Any "X" = any amino acid

<400> 162

Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala Ala His Arg Gly Thr
 1 5 10 15

Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr Ser Pro Ala Ser Pro
 20 25 30

Lys Gly Leu His Thr Gly Gly Thr Lys Arg Met Glu Thr Thr Thr Thr
 35 40 45

255

Ala Leu Lys Thr Thr Thr Thr Ala Leu Lys Thr Thr Ser Arg Ala Thr
 50 55 60

Leu Thr Thr Ser Val Tyr Thr Pro Thr Leu Gly Thr Leu Thr Pro Leu
 65 70 75 80

Asn Ala Ser Arg Gln Met Ala Ser Thr Ile Leu Thr Glu Met Met Ile
 85 90 95

Thr Thr Pro Tyr Val Phe Pro Asp Val Pro Glu Thr Thr Ser Ser Leu
 100 105 110

Ala Thr Ser Leu Gly Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr
 115 120 125

Pro Ser Val Leu Asn Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser
 130 135 140

Arg Ser Gly Ala Glu Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser
 145 150 155 160

Ser Ser Glu Pro Asp Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu
 165 170 175

Thr Ile Pro Thr Val Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu
 180 185 190

Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His Gly Ala Asp Val Ser
 195 200 205

Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu Leu Asp Ala Leu Thr
 210 215 220

Pro Leu Val Thr Ile Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr
 225 230 235 240

Leu Thr Lys Ser Pro His Glu Thr Glu Thr Arg Thr Thr Trp Leu Thr
 245 250 255

256

His Pro Ala Glu Thr Ser Ser Thr Ile Pro Arg Thr Ile Pro Asn Phe
 260 265 270

Ser His His Glu Ser Asp Ala Thr Pro Ser Ile Ala Thr Ser Pro Gly
 275 280 285

Ala Glu Thr Ser Ser Ala Ile Pro Ile Met Thr Val Ser Pro Gly Ala
 290 295 300

Glu Asp Leu Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Arg Asn
 305 310 315 320

Met Thr Ile Pro Thr Leu Thr Leu Ser Pro Gly Glu Pro Lys Thr Ile
 325 330 335

Ala Ser Leu Val Thr His Pro Glu Ala Gln Thr Ser Ser Ala Ile Pro
 340 345 350

Thr Ser Thr Ile Ser Pro Ala Val Ser Arg Leu Val Thr Ser Met Val
 355 360 365

Thr Ser Leu Ala Ala Lys Thr Ser Thr Thr Asn Arg Ala Leu Thr Asn
 370 375 380

Ser Pro Gly Glu Pro Ala Thr Thr Val Ser Leu Val Thr His Pro Ala
 385 390 395 400

Gln Thr Ser Pro Thr Val Pro Trp Thr Thr Ser Ile Phe Phe His Ser
 405 410 415

Lys Ser Asp Thr Thr Pro Ser Met Thr Thr Ser His Gly Ala Glu Ser
 420 425 430

Ser Ser Ala Val Pro Thr Pro Thr Val Ser Thr Glu Val Pro Gly Val
 435 440 445

Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val Ile Ser Thr Thr Ile
 450 455 460

Pro Ile Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met
 465 470 475 480

257

Ala Thr Ser His Gly Glu Glu Ala Ser Ser Ala Ile Pro Thr Pro Thr
485 490 495

Val Ser Pro Gly Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser
500 505 510

Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr Phe Ser Leu Gly
515 520 525

Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Thr Glu Ala
530 535 540

Gly Ser Ala Val Pro Thr Val Leu Pro Glu Val Pro Gly Met Val Thr
545 550 555 560

Ser Leu Val Ala Ser Ser Arg Ala Val Thr Ser Thr Thr Leu Pro Thr
565 570 575

Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr
580 585 590

Ser His Gly Ala Glu Ala Ser Ser Thr Val Pro Thr Val Ser Pro Glu
595 600 605

Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser Ser Gly Val Asn
610 615 620

Ser Thr Ser Ile Pro Thr Leu Ile Leu Ser Pro Gly Glu Leu Glu Thr
625 630 635 640

Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu Ala Ser Ser Ala Val
645 650 655

Pro Thr Pro Thr Val Ser Pro Gly Val Ser Gly Val Val Thr Pro Leu
660 665 670

Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr
675 680 685

258

Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His
 690 695 700

Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val Ser Pro Glu Val Pro
 705 710 715 720

Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr
 725 730 735

Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu Pro Glu Thr Thr Thr
 740 745 750

Ser Leu Val Thr His Ser Glu Ala Lys Met Ile Ser Ala Ile Pro Thr
 755 760 765

Leu Ala Val Ser Pro Thr Val Gln Gly Leu Val Thr Ser Leu Val Thr
 770 775 780

Ser Ser Gly Ser Glu Thr Ser Ala Phe Ser Asn Leu Thr Val Ala Ser
 785 790 795 800

Ser Gln Pro Glu Thr Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu
 805 810 815

Ala Ser Ser Val Val Pro Thr Leu Thr Val Ser Thr Gly Glu Pro Phe
 820 825 830

Thr Asn Ile Ser Leu Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu
 835 840 845

Pro Arg Thr Thr Ser Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro
 850 855 860

Ser Thr Val Thr Ser Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr
 865 870 875 880

Thr Ile Ser Pro Gly Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser
 885 890 895

Ser Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro
 900 905 910

259

His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr His Pro Ala Val Thr
 915 920 925

Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr Ser His Ser Glu Pro
 930 935 940

Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu Ala Thr Ser
 945 950 955 960

Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val Pro Asp Met Val Thr
 965 970 975

Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser Ile Thr Ile Pro Thr
 980 985 990

Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr Thr Thr Ser Phe Ile Thr
 995 1000 1005

Tyr Ser Glu Thr His Thr Ser Ser Ala Ile Pro Thr Leu Pro Val
 1010 1015 1020

Ser Pro Gly Ala Ser Lys Met Leu Thr Ser Leu Val Ile Ser Ser
 1025 1030 1035

Gly Thr Asp Ser Thr Thr Thr Phe Pro Thr Leu Thr Glu Thr Pro
 1040 1045 1050

Tyr Glu Pro Glu Thr Thr Ala Ile Gln Leu Ile His Pro Ala Glu
 1055 1060 1065

Thr Asn Thr Met Val Pro Arg Thr Thr Pro Lys Phe Ser His Ser
 1070 1075 1080

Lys Ser Asp Thr Thr Leu Pro Val Ala Ile Thr Ser Pro Gly Pro
 1085 1090 1095

Glu Ala Ser Ser Ala Val Ser Thr Thr Thr Ile Ser Pro Asp Met
 1100 1105 1110

260

Ser Asp Leu Val Thr Ser Leu Val Pro Ser Ser Gly Thr Asp Thr
 1115 1120 1125

Ser Thr Thr Phe Pro Thr Leu Ser Glu Thr Pro Tyr Glu Pro Glu
 1130 1135 1140

Thr Thr Ala Thr Trp Leu Thr His Pro Ala Glu Thr Ser Thr Thr
 1145 1150 1155

Val Ser Gly Thr Ile Pro Asn Phe Ser His Arg Gly Ser Asp Thr
 1160 1165 1170

Ala Pro Ser Met Val Thr Ser Pro Gly Val Asp Thr Arg Ser Gly
 1175 1180 1185

Val Pro Thr Thr Thr Ile Pro Pro Ser Ile Pro Gly Val Val Thr
 1190 1195 1200

Ser Gln Val Thr Ser Ser Ala Thr Asp Thr Ser Thr Ala Ile Pro
 1205 1210 1215

Thr Leu Thr Pro Ser Pro Gly Glu Pro Glu Thr Thr Ala Ser Ser
 1220 1225 1230

Ala Thr His Pro Gly Thr Gln Thr Gly Phe Thr Val Pro Ile Arg
 1235 1240 1245

Thr Val Pro Ser Ser Glu Pro Asp Thr Met Ala Ser Trp Val Thr
 1250 1255 1260

His Pro Pro Gln Thr Ser Thr Pro Val Ser Arg Thr Thr Ser Ser
 1265 1270 1275

Phe Ser His Ser Ser Pro Asp Ala Thr Pro Val Met Ala Thr Ser
 1280 1285 1290

Pro Arg Thr Glu Ala Ser Ser Ala Val Leu Thr Thr Ile Ser Pro
 1295 1300 1305

Gly Ala Pro Glu Met Val Thr Ser Gln Ile Thr Ser Ser Gly Ala
 1310 1315 1320

261

Ala Thr Ser Thr Thr Val Pro Thr Leu Thr His Ser Pro Gly Met 1325 1330 1335
Pro Glu Thr Thr Ala Leu Leu Ser Thr His Pro Arg Thr Glu Thr 1340 1345 1350
Ser Lys Thr Phe Pro Ala Ser Thr Val Phe Pro Gln Val Ser Glu 1355 1360 1365
Thr Thr Ala Ser Leu Thr Ile Arg Pro Gly Ala Glu Thr Ser Thr 1370 1375 1380
Ala Leu Pro Thr Gln Thr Thr Ser Ser Leu Phe Thr Leu Leu Val 1385 1390 1395
Thr Gly Thr Ser Arg Val Asp Leu Ser Pro Thr Ala Ser Pro Gly 1400 1405 1410
Val Ser Ala Lys Thr Ala Pro Leu Ser Thr His Pro Gly Thr Glu 1415 1420 1425
Thr Ser Thr Met Ile Pro Thr Ser Thr Leu Ser Leu Gly Leu Leu 1430 1435 1440
Glu Thr Thr Gly Leu Leu Ala Thr Ser Ser Ser Ala Glu Thr Ser 1445 1450 1455
Thr Ser Thr Leu Thr Leu Thr Val Ser Pro Ala Val Ser Gly Leu 1460 1465 1470
Ser Ser Ala Ser Ile Thr Thr Asp Lys Pro Gln Thr Val Thr Ser 1475 1480 1485
Trp Asn Thr Glu Thr Ser Pro Ser Val Thr Ser Val Gly Pro Pro 1490 1495 1500
Glu Phe Ser Arg Thr Val Thr Gly Thr Thr Met Thr Leu Ile Pro 1505 1510 1515

262

Ser Glu Met Pro Thr Pro Pro Lys Thr Ser His Gly Glu Gly Val
 1520 1525 1530

Ser Pro Thr Thr Ile Leu Arg Thr Thr Met Val Glu Ala Thr Asn
 1535 1540 1545

Leu Ala Thr Thr Gly Ser Ser Pro Thr Val Ala Lys Thr Thr Thr
 1550 1555 1560

Thr Phe Asn Thr Leu Ala Gly Ser Leu Phe Thr Pro Leu Thr Thr
 1565 1570 1575

Pro Gly Met Ser Thr Leu Ala Ser Glu Ser Val Thr Ser Arg Thr
 1580 1585 1590

Ser Tyr Asn His Arg Ser Trp Ile Ser Thr Thr Ser Ser Tyr Asn
 1595 1600 1605

Arg Arg Tyr Trp Thr Pro Ala Thr Ser Thr Pro Val Thr Ser Thr
 1610 1615 1620

Phe Ser Pro Gly Ile Ser Thr Ser Ser Ile Pro Ser Ser Thr Ala
 1625 1630 1635

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile
 1640 1645 1650

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
 1655 1660 1665

Lys Phe Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro
 1670 1675 1680

Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg
 1685 1690 1695

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
 1700 1705 1710

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
 1715 1720 1725

263

Asp Arg	Glu Arg	Leu Tyr	Trp	Glu Leu	Ser Asn	Leu	Thr Asn	Gly
1730			1735			1740		
Ile Gln	Glu Leu	Gly Pro	Tyr	Thr Leu	Asp Arg	Asn	Ser Leu	Tyr
1745			1750			1755		
Val Asn	Gly Phe	Thr His	Arg	Ser Ser	Met Pro	Thr	Thr Ser	Thr
1760			1765			1770		
Pro Gly	Thr Ser	Thr Val	Asp	Val Gly	Thr Ser	Gly	Thr Pro	Ser
1775			1780			1785		
Ser Ser	Pro Ser	Pro Thr	Ala	Ala Gly	Pro Leu	Leu	Met Pro	Phe
1790			1795			1800		
Thr Leu	Asn Phe	Thr Ile	Thr	Asn Leu	Gln Tyr	Glu	Glu Asp	Met
1805			1810			1815		
Arg Arg	Thr Gly	Ser Arg	Lys	Phe Asn	Thr Met	Glu	Ser Val	Leu
1820			1825			1830		
Gln Gly	Leu Leu	Lys Pro	Leu	Phe Lys	Asn Thr	Ser	Val Gly	Pro
1835			1840			1845		
Leu Tyr	Ser Gly	Cys Arg	Leu	Thr Leu	Leu Arg	Pro	Glu Lys	Asp
1850			1855			1860		
Gly Ala	Ala Thr	Gly Val	Asp	Ala Ile	Cys Thr	His	Arg Leu	Asp
1865			1870			1875		
Pro Lys	Ser Pro	Gly Leu	Asn	Arg Glu	Gln Leu	Tyr	Trp Glu	Leu
1880			1885			1890		
Ser Lys	Leu Thr	Asn Asp	Ile	Glu Glu	Leu Gly	Pro	Tyr Thr	Leu
1895			1900			1905		
Asp Arg	Asn Ser	Leu Tyr	Val	Asn Gly	Phe Thr	His	Gln Ser	Ser
1910			1915			1920		

264

Val 1925	Ser	Thr	Thr	Ser	Thr	Pro 1930	Gly	Thr	Ser	Thr	Val 1935	Asp	Leu	Arg
Thr 1940	Ser	Gly	Thr	Pro	Ser	Ser 1945	Leu	Ser	Ser	Pro	Thr 1950	Ile	Met	Ala
Ala 1955	Gly	Pro	Leu	Leu	Val	Pro 1960	Phe	Thr	Leu	Asn	Phe 1965	Thr	Ile	Thr
Asn 1970	Leu	Gln	Tyr	Gly	Glu	Asp 1975	Met	Gly	His	Pro	Gly 1980	Ser	Arg	Lys
Phe 1985	Asn	Thr	Thr	Glu	Arg	Val 1990	Leu	Gln	Gly	Leu	Leu 1995	Gly	Pro	Ile
Phe 2000	Lys	Asn	Thr	Ser	Val	Gly 2005	Pro	Leu	Tyr	Ser	Gly 2010	Cys	Arg	Leu
Thr 2015	Ser	Leu	Arg	Ser	Glu	Lys 2020	Asp	Gly	Ala	Ala	Thr 2025	Gly	Val	Asp
Ala 2030	Ile	Cys	Ile	His	His	Leu 2035	Asp	Pro	Lys	Ser	Pro 2040	Gly	Leu	Asn
Arg 2045	Glu	Arg	Leu	Tyr	Trp	Glu 2050	Leu	Ser	Gln	Leu	Thr 2055	Asn	Gly	Ile
Lys 2060	Glu	Leu	Gly	Pro	Tyr	Thr 2065	Leu	Asp	Arg	Asn	Ser 2070	Leu	Tyr	Val
Asn 2075	Gly	Phe	Thr	His	Arg	Thr 2080	Ser	Val	Pro	Thr	Ser 2085	Ser	Thr	Pro
Gly 2090	Thr	Ser	Thr	Val	Asp	Leu 2095	Gly	Thr	Ser	Gly	Thr 2100	Pro	Phe	Ser
Leu 2105	Pro	Ser	Pro	Ala	Thr	Ala 2110	Gly	Pro	Leu	Leu	Val 2115	Leu	Phe	Thr
Leu 2120	Asn	Phe	Thr	Ile	Thr	Asn 2125	Leu	Lys	Tyr	Glu	Glu 2130	Asp	Met	His

265

Arg	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln
2135						2140					2145			
Thr	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu
2150						2155					2160			
Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Ser	Glu	Lys	Asp	Gly
2165						2170					2175			
Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro
2180						2185					2190			
Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser
2195						2200					2205			
Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp
2210						2215					2220			
Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Trp	Ile	Pro	Val
2225						2230					2235			
Pro	Thr	Ser	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Gly	Ser
2240						2245					2250			
Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser	Pro	Thr	Ala	Ala	Gly	Pro	Leu
2255						2260					2265			
Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr
2270						2275					2280			
Glu	Glu	Asp	Met	His	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
2285						2290					2295			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr
2300						2305					2310			
Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
2315						2320					2325			

266

Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr
2330						2335					2340			
His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Val	Asp	Arg	Glu	Gln	Leu
2345						2350					2355			
Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly
2360						2365					2370			
Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
2375						2380					2385			
His	Gln	Thr	Ser	Ala	Pro	Asn	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr
2390						2395					2400			
Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser	Pro
2405						2410					2415			
Thr	Ser	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr
2420						2425					2430			
Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	Arg	His	Pro	Gly	Ser
2435						2440					2445			
Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys
2450						2455					2460			
Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys
2465						2470					2475			
Arg	Leu	Thr	Leu	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly
2480						2485					2490			
Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly
2495						2500					2505			
Val	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn
2510						2515					2520			
Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu
2525						2530					2535			

267

Tyr Val	Asn Gly Phe Thr His	Gln Thr Ser Ala Pro	Asn Thr Ser
2540	2545	2550	
Thr Pro	Gly Thr Ser Thr Val	Asp Leu Gly Thr Ser	Gly Thr Pro
2555	2560	2565	
Ser Ser	Leu Pro Ser Pro Thr	Ser Ala Gly Pro Leu	Leu Val Pro
2570	2575	2580	
Phe Thr	Leu Asn Phe Thr Ile	Thr Asn Leu Gln Tyr	Glu Glu Asp
2585	2590	2595	
Met His	His Pro Gly Ser Arg	Lys Phe Asn Thr Thr	Glu Arg Val
2600	2605	2610	
Leu Gln	Gly Leu Leu Gly Pro	Met Phe Lys Asn Thr	Ser Val Gly
2615	2620	2625	
Leu Leu	Tyr Ser Gly Cys Arg	Leu Thr Leu Leu Arg	Pro Glu Lys
2630	2635	2640	
Asn Gly	Ala Ala Thr Gly Met	Asp Ala Ile Cys Ser	His Arg Leu
2645	2650	2655	
Asp Pro	Lys Ser Pro Gly Leu	Asn Arg Glu Gln Leu	Tyr Trp Glu
2660	2665	2670	
Leu Ser	Gln Leu Thr His Gly	Ile Lys Glu Leu Gly	Pro Tyr Thr
2675	2680	2685	
Leu Asp	Arg Asn Ser Leu Tyr	Val Asn Gly Phe Thr	His Arg Ser
2690	2695	2700	
Ser Val	Ala Pro Thr Ser Thr	Pro Gly Thr Ser Thr	Val Asp Leu
2705	2710	2715	
Gly Thr	Ser Gly Thr Pro Ser	Ser Leu Pro Ser Pro	Thr Thr Ala
2720	2725	2730	

268

Val	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn
2735						2740					2745			
Leu	Gln	Tyr	Gly	Glu	Asp	Met	Arg	His	Pro	Gly	Ser	Arg	Lys	Phe
2750						2755					2760			
Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Leu	Phe
2765						2770					2775			
Lys	Asn	Ser	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Ile
2780						2785					2790			
Ser	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala
2795						2800					2805			
Ile	Cys	Thr	His	His	Leu	Asn	Pro	Gln	Ser	Pro	Gly	Leu	Asp	Arg
2810						2815					2820			
Glu	Gln	Leu	Tyr	Trp	Gln	Leu	Ser	Gln	Met	Thr	Asn	Gly	Ile	Lys
2825						2830					2835			
Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn
2840						2845					2850			
Gly	Phe	Thr	His	Arg	Ser	Ser	Gly	Leu	Thr	Thr	Ser	Thr	Pro	Trp
2855						2860					2865			
Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Ser	Pro	Val
2870						2875					2880			
Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu
2885						2890					2895			
Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	His	Arg
2900						2905					2910			
Pro	Gly	Ser	Arg	Lys	Phe	Asn	Ala	Thr	Glu	Arg	Val	Leu	Gln	Gly
2915						2920					2925			
Leu	Leu	Ser	Pro	Ile	Phe	Lys	Asn	Ser	Ser	Val	Gly	Pro	Leu	Tyr
2930						2935					2940			

269

Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
 2945 2950 2955

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys
 2960 2965 2970

Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln
 2975 2980 2985

Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
 2990 2995 3000

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
 3005 3010 3015

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr
 3020 3025 3030

Gly Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu
 3035 3040 3045

Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr
 3050 3055 3060

Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 3065 3070 3075

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr
 3080 3085 3090

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
 3095 3100 3105

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
 3110 3115 3120

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu
 3125 3130 3135

270

Tyr	Cys	Glu	Leu	Ser	Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	Gly
3140						3145					3150			
Pro	Tyr	Ser	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
3155						3160					3165			
His	Gln	Asn	Ser	Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr
3170						3175					3180			
Val	Tyr	Trp	Ala	Thr	Thr	Gly	Thr	Pro	Ser	Ser	Phe	Pro	Gly	His
3185						3190					3195			
Thr	Glu	Pro	Gly	Pro	Leu	Leu	Ile	Pro	Phe	Thr	Phe	Asn	Phe	Thr
3200						3205					3210			
Ile	Thr	Asn	Leu	His	Tyr	Glu	Glu	Asn	Met	Gln	His	Pro	Gly	Ser
3215						3220					3225			
Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys
3230						3235					3240			
Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys
3245						3250					3255			
Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	His	Glu	Ala	Ala	Thr	Gly
3260						3265					3270			
Val	Asp	Thr	Ile	Cys	Thr	His	Arg	Val	Asp	Pro	Ile	Gly	Pro	Gly
3275						3280					3285			
Leu	Asp	Arg	Glu	Arg	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn
3290						3295					3300			
Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu
3305						3310					3315			
Tyr	Val	Asn	Gly	Phe	Asn	Pro	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser
3320						3325					3330			
Thr	Pro	Gly	Thr	Ser	Thr	Val	His	Leu	Ala	Thr	Ser	Gly	Thr	Pro
3335						3340					3345			

271

Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro
 3350 3355 3360

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
 3365 3370 3375

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
 3380 3385 3390

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
 3395 3400 3405

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
 3410 3415 3420

His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
 3425 3430 3435

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
 3440 3445 3450

Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
 3455 3460 3465

Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa
 3470 3475 3480

Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu
 3485 3490 3495

Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Ser Ala
 3500 3505 3510

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
 3515 3520 3525

Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
 3530 3535 3540

272

Asn Thr	Thr Glu Arg Val	Leu	Gln Gly Leu Leu Gly	Pro Met Phe
3545		3550		3555
Lys Asn	Thr Ser Val Gly	Leu	Leu Tyr Ser Gly Cys	Arg Leu Thr
3560		3565		3570
Leu Leu	Arg Pro Glu Lys	Asn	Gly Ala Ala Thr Gly	Met Asp Ala
3575		3580		3585
Ile Cys	Ser His Arg Leu	Asp	Pro Lys Ser Pro Gly	Leu Asp Arg
3590		3595		3600
Glu Gln	Leu Tyr Trp Glu	Leu	Ser Gln Leu Thr His	Gly Ile Lys
3605		3610		3615
Glu Leu	Gly Pro Tyr Thr	Leu	Asp Arg Asn Ser Leu	Tyr Val Asn
3620		3625		3630
Gly Phe	Thr His Arg Ser	Ser	Val Ala Pro Thr Ser	Thr Pro Gly
3635		3640		3645
Thr Ser	Thr Val Asp Leu	Gly	Thr Ser Gly Thr Pro	Ser Ser Leu
3650		3655		3660
Pro Ser	Pro Thr Thr Ala	Val	Pro Leu Leu Val Pro	Phe Thr Leu
3665		3670		3675
Asn Phe	Thr Ile Thr Asn	Leu	Gln Tyr Gly Glu Asp	Met Arg His
3680		3685		3690
Pro Gly	Ser Arg Lys Phe	Asn	Thr Thr Glu Arg Val	Leu Gln Gly
3695		3700		3705
Leu Leu	Gly Pro Leu Phe	Lys	Asn Ser Ser Val Gly	Pro Leu Tyr
3710		3715		3720
Ser Gly	Cys Arg Leu Ile	Ser	Leu Arg Ser Glu Lys	Asp Gly Ala
3725		3730		3735
Ala Thr	Gly Val Asp Ala	Ile	Cys Thr His His Leu	Asn Pro Gln
3740		3745		3750

Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln
 3755 3760 3765

Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 3770 3775 3780

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
 3785 3790 3795

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser
 3800 3805 3810

Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu
 3815 3820 3825

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 3830 3835 3840

Glu Glu / Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr
 3845 3850 3855

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser
 3860 3865 3870

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
 3875 3880 3885

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
 3890 3895 3900

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu
 3905 3910 3915

Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 3920 3925 3930

Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
 3935 3940 3945

274

His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr
 3950 3955 3960

Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 3965 3970 3975

Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Cys Thr
 3980 3985 3990

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser
 3995 4000 4005

Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys
 4010 4015 4020

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 4025 4030 4035

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly
 4040 4045 4050

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
 4055 4060 4065

Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn
 4070 4075 4080

Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 4085 4090 4095

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser
 4100 4105 4110

Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro
 4115 4120 4125

Ser Ser Leu Ser Ser Pro Thr Ile Met Xaa Xaa Xaa Pro Leu Leu
 4130 4135 4140

Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu
 4145 4150 4155

275

Glu Xaa	Met Xaa Xaa	Pro Gly	Ser Arg Lys Phe	Asn Thr Thr	Glu
4160		4165		4170	
Arg Val	Leu Gln Gly Leu	Leu Arg Pro	Leu Phe Lys	Asn Thr Ser	
4175		4180		4185	
Val Ser	Ser Leu Tyr Ser	Gly Cys Arg	Leu Thr Leu	Leu Arg Pro	
4190		4195		4200	
Glu Lys	Asp Gly Ala Ala	Thr Arg Val	Asp Ala Ala	Cys Thr Tyr	
4205		4210		4215	
Arg Pro	Asp Pro Lys Ser	Pro Gly Leu	Asp Arg Glu	Gln Leu Tyr	
4220		4225		4230	
Trp Glu	Leu Ser Gln Leu	Thr His Ser	Ile Thr Glu	Leu Gly Pro	
4235		4240		4245	
Tyr Thr	Leu Asp Arg Val	Ser Leu Tyr	Val Asn Gly	Phe Asn Pro	
4250		4255		4260	
Arg Ser	Ser Val Pro Thr	Thr Ser Thr	Pro Gly Thr	Ser Thr Val	
4265		4270		4275	
His Leu	Ala Thr Ser Gly	Thr Pro Ser	Ser Leu Pro	Gly His Thr	
4280		4285		4290	
Xaa Xaa	Xaa Pro Leu Leu	Xaa Pro Phe	Thr Leu Asn	Phe Thr Ile	
4295		4300		4305	
Thr Asn	Leu Xaa Tyr Glu	Glu Xaa Met	Xaa Xaa Pro	Gly Ser Arg	
4310		4315		4320	
Lys Phe	Asn Thr Thr Glu	Arg Val Leu	Gln Gly Leu	Leu Lys Pro	
4325		4330		4335	
Leu Phe	Arg Asn Ser Ser	Leu Glu Tyr	Leu Tyr Ser	Gly Cys Arg	
4340		4345		4350	

276

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
 4355 4360 4365

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
 4370 4375 4380

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly
 4385 4390 4395

Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
 4400 4405 4410

Val Asn Gly Phe Thr His Arg Ser Ser Phe Leu Thr Thr Ser Thr
 4415 4420 4425

Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser
 4430 4435 4440

Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe
 4445 4450 4455

Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
 4460 4465 4470

His Arg Pro Gly Ser Arg Arg Phe Asn Thr Thr Glu Arg Val Leu
 4475 4480 4485

Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro
 4490 4495 4500

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln
 4505 4510 4515

Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp
 4520 4525 4530

Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 4535 4540 4545

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
 4550 4555 4560

277

Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Asn	Pro	Trp	Ser	Ser
4565						4570					4575			
Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	His	Leu	Ala
4580						4585					4590			
Thr	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Gly	His	Thr	Ala	Pro	Val
4595						4600					4605			
Pro	Leu	Leu	Ile	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asp	Leu
4610						4615					4620			
His	Tyr	Glu	Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn
4625						4630					4635			
Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys	Pro	Leu	Phe	Lys
4640						4645					4650			
Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu
4655						4660					4665			
Leu	Arg	Pro	Glu	Lys	His	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile
4670						4675					4680			
Cys	Thr	Leu	Arg	Leu	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu
4685						4690					4695			
Arg	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Ser	Val	Thr	Glu
4700						4705					4710			
Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly
4715						4720					4725			
Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr
4730						4735					4740			
Ser	Ala	Val	His	Leu	Glu	Thr	Ser	Gly	Thr	Pro	Ala	Ser	Leu	Pro
4745						4750					4755			

279

Val Gly 4970	Pro Leu Tyr Ser Gly 4975	Cys Arg Leu Thr Leu 4980	Leu Arg Pro
Lys Lys 4985	Asp Gly Ala Ala Thr 4990	Lys Val Asp Ala Ile 4995	Cys Thr Tyr
Arg Pro 5000	Asp Pro Lys Ser Pro 5005	Gly Leu Asp Arg Glu 5010	Gln Leu Tyr
Trp Glu 5015	Leu Ser Gln Leu Thr 5020	His Ser Ile Thr Glu 5025	Leu Gly Pro
Tyr Thr 5030	Gln Asp Arg Asp Ser 5035	Leu Tyr Val Asn Gly 5040	Phe Thr His
Arg Ser 5045	Ser Val Pro Thr Thr 5050	Ser Ile Pro Gly Thr 5055	Ser Ala Val
His Leu 5060	Glu Thr Ser Gly Thr 5065	Pro Ala Ser Leu Pro 5070	Gly His Thr
Ala Pro 5075	Gly Pro Leu Leu Val 5080	Pro Phe Thr Leu Asn 5085	Phe Thr Ile
Thr Asn 5090	Leu Gln Tyr Glu Glu 5095	Asp Met Arg His Pro 5100	Gly Ser Arg
Lys Phe 5105	Asn Thr Thr Glu Arg 5110	Val Leu Gln Gly Leu 5115	Leu Lys Pro
Leu Phe 5120	Lys Ser Thr Ser Val 5125	Gly Pro Leu Tyr Ser 5130	Gly Cys Arg
Leu Thr 5135	Leu Leu Arg Pro Glu 5140	Lys Arg Gly Ala Ala 5145	Thr Gly Val
Asp Thr 5150	Ile Cys Thr His Arg 5155	Leu Asp Pro Leu Asn 5160	Pro Gly Leu

280

Asp Arg	Glu Gln	Leu Tyr	Trp	Glu Leu	Ser Lys	Leu	Thr Arg	Gly	
5165			5170			5175			
Ile Ile	Glu Leu	Gly Pro	Tyr	Leu Leu	Asp Arg	Gly	Ser Leu	Tyr	
5180			5185			5190			
Val Asn	Gly Phe	Thr His	Arg	Thr Ser	Val Pro	Thr	Thr Ser	Thr	
5195			5200			5205			
Pro Gly	Thr Ser	Thr Val	Asp	Leu Gly	Thr Ser	Gly	Thr Pro	Phe	
5210			5215			5220			
Ser Leu	Pro Ser	Pro Ala	Xaa	Xaa Xaa	Pro Leu	Leu	Xaa Pro	Phe	
5225			5230			5235			
Thr Leu	Asn Phe	Thr Ile	Thr	Asn Leu	Xaa Tyr	Glu	Glu Xaa	Met	
5240			5245			5250			
Xaa Xaa	Pro Gly	Ser Arg	Lys	Phe Asn	Thr Thr	Glu	Arg Val	Leu	
5255			5260			5265			
Gln Thr	Leu Leu	Gly Pro	Met	Phe Lys	Asn Thr	Ser	Val Gly	Leu	
5270			5275			5280			
Leu Tyr	Ser Gly	Cys Arg	Leu	Thr Leu	Leu Arg	Ser	Glu Lys	Asp	
5285			5290			5295			
Gly Ala	Ala Thr	Gly Val	Asp	Ala Ile	Cys Thr	His	Arg Leu	Asp	
5300			5305			5310			
Pro Lys	Ser Pro	Gly Val	Asp	Arg Glu	Gln Leu	Tyr	Trp Glu	Leu	
5315			5320			5325			
Ser Gln	Leu Thr	Asn Gly	Ile	Lys Glu	Leu Gly	Pro	Tyr Thr	Leu	
5330			5335			5340			
Asp Arg	Asn Ser	Leu Tyr	Val	Asn Gly	Phe Thr	His	Trp Ile	Pro	
5345			5350			5355			
Val Pro	Thr Ser	Ser Thr	Pro	Gly Thr	Ser Thr	Val	Asp Leu	Gly	
5360			5365			5370			

281

Ser Gly	Thr Pro Ser Leu Pro	Ser Ser Pro Thr Thr	Ala Gly Pro
5375	5380	5385	
Leu Leu	Val Pro Phe Thr Leu	Asn Phe Thr Ile Thr	Asn Leu Lys
5390	5395	5400	
Tyr Glu	Glu Asp Met His Cys	Pro Gly Ser Arg Lys	Phe Asn Thr
5405	5410	5415	
Thr Glu	Arg Val Leu Gln Ser	Leu Leu Gly Pro Met	Phe Lys Asn
5420	5425	5430	
Thr Ser	Val Gly Pro Leu Tyr	Ser Gly Cys Arg Leu	Thr Leu Leu
5435	5440	5445	
Arg Ser	Glu Lys Asp Gly Ala	Ala Thr Gly Val Asp	Ala Ile Cys
5450	5455	5460	
Thr His	Arg Leu Asp Pro Lys	Ser Pro Gly Val Asp	Arg Glu Gln
5465	5470	5475	
Leu Tyr	Trp Glu Leu Ser Gln	Leu Thr Asn Gly Ile	Lys Glu Leu
5480	5485	5490	
Gly Pro	Tyr Thr Leu Asp Arg	Asn Ser Leu Tyr Val	Asn Gly Phe
5495	5500	5505	
Thr His	Gln Thr Ser Ala Pro	Asn Thr Ser Thr Pro	Gly Thr Ser
5510	5515	5520	
Thr Val	Asp Leu Gly Thr Ser	Gly Thr Pro Ser Ser	Leu Pro Ser
5525	5530	5535	
Pro Thr	Xaa Xaa Xaa Pro Leu	Leu Xaa Pro Phe Thr	Leu Asn Phe
5540	5545	5550	
Thr Ile	Thr Asn Leu Xaa Tyr	Glu Glu Xaa Met Xaa	Xaa Pro Gly
5555	5560	5565	

282

Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu
5570						5575					5580			
Xaa	Pro	Xaa	Phe	Lys	Xaa	Thr	Ser	Val	Gly	Xaa	Leu	Tyr	Ser	Gly
5585						5590					5595			
Cys	Arg	Leu	Thr	Leu	Leu	Arg	Xaa	Glu	Lys	Xaa	Xaa	Ala	Ala	Thr
5600						5605					5610			
Xaa	Val	Asp	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa	Xaa	Pro
5615						5620					5625			
Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa	Leu	Thr
5630						5635					5640			
Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg	Xaa	Ser
5645						5650					5655			
Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Trp	Ile	Pro	Val	Pro	Thr	Ser
5660						5665					5670			
Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Gly	Ser	Gly	Thr	Pro
5675						5680					5685			
Ser	Ser	Leu	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro
5690						5695					5700			
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Lys	Tyr	Glu	Glu	Asp
5705						5710					5715			
Met	His	Cys	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val
5720						5725					5730			
Leu	Gln	Ser	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr	Ser	Val	Gly
5735						5740					5745			
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Ser	Leu	Arg	Ser	Glu	Lys
5750						5755					5760			
Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Val
5765						5770					5775			

283

Asp Pro	Lys Ser	Pro Gly	Val	Asp Arg	Glu Gln	Leu	Tyr Trp	Glu
5780			5785			5790		
Leu Ser	Gln Leu	Thr Asn	Gly	Ile Lys	Glu Leu	Gly	Pro Tyr	Thr
5795			5800			5805		
Leu Asp	Arg Asn	Ser Leu	Tyr	Val Asn	Gly Phe	Thr	His Gln	Thr
5810			5815			5820		
Ser Ala	Pro Asn	Thr Ser	Thr	Pro Gly	Thr Ser	Thr	Val Asp	Leu
5825			5830			5835		
Gly Thr	Ser Gly	Thr Pro	Ser	Ser Leu	Pro Ser	Pro	Thr Ser	Ala
5840			5845			5850		
Gly Pro	Leu Leu	Val Pro	Phe	Thr Leu	Asn Phe	Thr	Ile Thr	Asn
5855			5860			5865		
Leu Gln	Tyr Glu	Glu Asp	Met	His His	Pro Gly	Ser	Arg Lys	Phe
5870			5875			5880		
Asn Thr	Thr Glu	Arg Val	Leu	Gln Gly	Leu Leu	Gly	Pro Met	Phe
5885			5890			5895		
Lys Asn	Thr Ser	Val Gly	Leu	Leu Tyr	Ser Gly	Cys	Arg Leu	Thr
5900			5905			5910		
Leu Leu	Arg Pro	Glu Lys	Asn	Gly Ala	Ala Thr	Gly	Met Asp	Ala
5915			5920			5925		
Ile Cys	Thr His	Arg Leu	Asp	Pro Lys	Ser Pro	Gly	Leu Asp	Arg
5930			5935			5940		
Glu Xaa	Leu Tyr	Trp Glu	Leu	Ser Xaa	Leu Thr	Xaa	Xaa Ile	Xaa
5945			5950			5955		
Glu Leu	Gly Pro	Tyr Xaa	Leu	Asp Arg	Xaa Ser	Leu	Tyr Val	Asn
5960			5965			5970		

284

Gly Phe	Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa Xaa Thr	Ser Thr Pro Gly
5975		5980	5985
Thr Ser	Xaa Val Xaa Leu Xaa	Thr Ser Gly Thr Pro	Xaa Xaa Xaa
5990		5995	6000
Pro Xaa	Xaa Thr Xaa Xaa Xaa	Pro Leu Leu Xaa Pro	Phe Thr Leu
6005		6010	6015
Asn Phe	Thr Ile Thr Asn Leu	Xaa Tyr Glu Glu Xaa	Met Xaa Xaa
6020		6025	6030
Pro Gly	Ser Arg Lys Phe Asn	Thr Thr Glu Arg Val	Leu Gln Gly
6035		6040	6045
Leu Leu	Lys Pro Leu Phe Arg	Asn Ser Ser Leu Glu	Tyr Leu Tyr
6050		6055	6060
Ser Gly	Cys Arg Leu Ala Ser	Leu Arg Pro Glu Lys	Asp Ser Ser
6065		6070	6075
Ala Met	Ala Val Asp Ala Ile	Cys Thr His Arg Pro	Asp Pro Glu
6080		6085	6090
Asp Leu	Gly Leu Asp Arg Glu	Arg Leu Tyr Trp Glu	Leu Ser Asn
6095		6100	6105
Leu Thr	Asn Gly Ile Gln Glu	Leu Gly Pro Tyr Thr	Leu Asp Arg
6110		6115	6120
Asn Ser	Leu Tyr Val Asn Gly	Phe Thr His Arg Ser	Ser Met Pro
6125		6130	6135
Thr Thr	Ser Thr Pro Gly Thr	Ser Thr Val Asp Val	Gly Thr Ser
6140		6145	6150
Gly Thr	Pro Ser Ser Ser Pro	Ser Pro Thr Thr Ala	Gly Pro Leu
6155		6160	6165
Leu Ile	Pro Phe Thr Leu Asn	Phe Thr Ile Thr Asn	Leu Gln Tyr
6170		6175	6180

285

Gly	Glu	Asp	Met	Gly	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
6185						6190					6195			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Ile	Phe	Lys	Asn	Thr
6200						6205					6210			
Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Ser	Leu	Arg
6215						6220					6225			
Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Ile
6230						6235					6240			
His	His	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Arg	Leu
6245						6250					6255			
Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly
6260						6265					6270			
Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
6275						6280					6285			
His	Arg	Thr	Ser	Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr
6290						6295					6300			
Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Phe	Ser	Leu	Pro	Ser	Pro
6305						6310					6315			
Ala	Thr	Ala	Gly	Pro	Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr
6320						6325					6330			
Ile	Thr	Asn	Leu	Lys	Tyr	Glu	Glu	Asp	Met	His	Arg	Pro	Gly	Ser
6335						6340					6345			
Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Thr	Leu	Leu	Gly
6350						6355					6360			
Pro	Met	Phe	Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys
6365						6370					6375			

286

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly	
6380	6385 6390
Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly	
6395	6400 6405
Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa	
6410	6415 6420
Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu	
6425	6430 6435
Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser	
6440	6445 6450
Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro	
6455	6460 6465
Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro	
6470	6475 6480
Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa	
6485	6490 6495
Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val	
6500	6505 6510
Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly	
6515	6520 6525
Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys	
6530	6535 6540
Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro	
6545	6550 6555
Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu	
6560	6565 6570
Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr	
6575	6580 6585

Gln Asp 6590	Arg Asp	Ser Leu	Tyr 6595	Val Asn	Gly Phe	Thr 6600	His Arg	Ser
Ser Val 6605	Pro Thr	Thr Ser	Ile 6610	Pro Gly	Thr Ser	Ala 6615	Val His	Leu
Glu Thr 6620	Thr Gly	Thr Pro	Ser 6625	Ser Phe	Pro Gly	His 6630	Thr Glu	Pro
Gly Pro 6635	Leu Leu	Ile Pro	Phe 6640	Thr Phe	Asn Phe	Thr 6645	Ile Thr	Asn
Leu Arg 6650	Tyr Glu	Glu Asn	Met 6655	Gln His	Pro Gly	Ser 6660	Arg Lys	Phe
Asn Thr 6665	Thr Glu	Arg Val	Leu 6670	Gln Gly	Leu Leu	Thr 6675	Pro Leu	Phe
Lys Asn 6680	Thr Ser	Val Gly	Pro 6685	Leu Tyr	Ser Gly	Cys 6690	Arg Leu	Thr
Leu Leu 6695	Arg Pro	Glu Lys	Gln 6700	Glu Ala	Ala Thr	Gly 6705	Val Asp	Thr
Ile Cys 6710	Thr His	Arg Val	Asp 6715	Pro Ile	Gly Pro	Gly 6720	Leu Asp	Arg
Glu Arg 6725	Leu Tyr	Trp Glu	Leu 6730	Ser Gln	Leu Thr	Asn 6735	Ser Ile	Thr
Glu Leu 6740	Gly Pro	Tyr Thr	Leu 6745	Asp Arg	Asp Ser	Leu 6750	Tyr Val	Asp
Gly Phe 6755	Asn Pro	Trp Ser	Ser 6760	Val Pro	Thr Thr	Ser 6765	Thr Pro	Gly
Thr Ser 6770	Thr Val	His Leu	Ala 6775	Thr Ser	Gly Thr	Pro 6780	Ser Pro	Leu

288

Pro Gly 6785	His Thr Ala	Pro Val 6790	Pro Leu Leu Ile	Pro Phe Thr Leu 6795
Asn Phe 6800	Thr Ile Thr Asp	Leu His Tyr Glu Glu 6805	Asn Met Gln His 6810	
Pro Gly 6815	Ser Arg Lys Phe	Asn Thr Thr Glu Arg 6820	Val Leu Gln Gly 6825	
Leu Leu 6830	Lys Pro Leu Phe	Lys Ser Thr Ser Val 6835	Gly Pro Leu Tyr 6840	
Ser Gly 6845	Cys Arg Leu Thr	Leu Leu Arg Pro Glu 6850	Lys His Gly Ala 6855	
Ala Thr 6860	Gly Val Asp Ala	Ile Cys Thr Leu Arg 6865	Leu Asp Pro Thr 6870	
Gly Pro 6875	Gly Leu Asp Arg	Glu Arg Leu Tyr Trp 6880	Glu Leu Ser Gln 6885	
Leu Thr 6890	Asn Ser Ile Thr	Glu Leu Gly Pro Tyr 6895	Thr Leu Asp Arg 6900	
Asp Ser 6905	Leu Tyr Val Asn	Gly Phe Asn Pro Trp 6910	Ser Ser Val Pro 6915	
Thr Thr 6920	Ser Thr Pro Gly	Thr Ser Thr Val His 6925	Leu Ala Thr Ser 6930	
Gly Thr 6935	Pro Ser Ser Leu	Pro Gly His Thr Thr 6940	Ala Gly Pro Leu 6945	
Leu Val 6950	Pro Phe Thr Leu	Asn Phe Thr Ile Thr 6955	Asn Leu Lys Tyr 6960	
Glu Glu 6965	Asp Met His Cys	Pro Gly Ser Arg Lys 6970	Phe Asn Thr Thr 6975	
Glu Arg 6980	Val Leu Gln Ser	Leu His Gly Pro Met 6985	Phe Lys Asn Thr 6990	

289

Ser Val 6995	Gly Pro Leu Tyr	Ser 7000	Gly Cys Arg Leu Thr	Leu Leu Arg 7005
Ser Glu 7010	Lys Asp Gly Ala	Ala 7015	Thr Gly Val Asp	Ala Ile Cys Thr 7020
His Arg 7025	Leu Asp Pro Lys	Ser 7030	Pro Gly Leu Asp	Arg Glu Xaa Leu 7035
Tyr Trp 7040	Glu Leu Ser Xaa	Leu 7045	Thr Xaa Xaa Ile	Xaa Glu Leu Gly 7050
Pro Tyr 7055	Xaa Leu Asp Arg	Xaa 7060	Ser Leu Tyr Val	Asn Gly Phe Xaa 7065
Xaa Xaa 7070	Xaa Xaa Xaa Xaa	Xaa 7075	Thr Ser Thr Pro	Gly Thr Ser Xaa 7080
Val Xaa 7085	Leu Xaa Thr Ser	Gly 7090	Thr Pro Xaa Xaa	Xaa Pro Xaa Xaa 7095
Thr Xaa 7100	Xaa Xaa Pro Leu	Leu 7105	Xaa Pro Phe Thr	Leu Asn Phe Thr 7110
Ile Thr 7115	Asn Leu Xaa Tyr	Glu 7120	Glu Xaa Met Xaa	Xaa Pro Gly Ser 7125
Arg Lys 7130	Phe Asn Thr Thr	Glu 7135	Arg Val Leu Gln	Gly Leu Leu Xaa 7140
Pro Xaa 7145	Phe Lys Xaa Thr	Ser 7150	Val Gly Xaa Leu	Tyr Ser Gly Cys 7155
Arg Leu 7160	Thr Leu Leu Arg	Xaa 7165	Glu Lys Xaa Xaa	Ala Ala Thr Xaa 7170
Val Asp 7175	Xaa Xaa Cys Xaa	Xaa 7180	Xaa Xaa Asp Pro	Xaa Xaa Pro Gly 7185

290

Leu Asp 7190	Arg Glu Xaa Leu Tyr 7195	Trp Glu Leu Ser Xaa 7200	Leu Thr Asn
Ser Ile 7205	Thr Glu Leu Gly Pro 7210	Tyr Thr Leu Asp Arg 7215	Asp Ser Leu
Tyr Val 7220	Asn Gly Phe Thr His 7225	Arg Ser Ser Met Pro 7230	Thr Thr Ser
Ile Pro 7235	Gly Thr Ser Ala Val 7240	His Leu Glu Thr Ser 7245	Gly Thr Pro
Ala Ser 7250	Leu Pro Gly His Thr 7255	Ala Pro Gly Pro Leu 7260	Leu Val Pro
Phe Thr 7265	Leu Asn Phe Thr Ile 7270	Thr Asn Leu Gln Tyr 7275	Glu Glu Asp
Met Arg 7280	His Pro Gly Ser Arg 7285	Lys Phe Asn Thr Thr 7290	Glu Arg Val
Leu Gln 7295	Gly Leu Leu Lys Pro 7300	Leu Phe Lys Ser Thr 7305	Ser Val Gly
Pro Leu 7310	Tyr Ser Gly Cys Arg 7315	Leu Thr Leu Leu Arg 7320	Pro Glu Lys
Arg Gly 7325	Ala Ala Thr Gly Val 7330	Asp Thr Ile Cys Thr 7335	His Arg Leu
Asp Pro 7340	Leu Asn Pro Gly Leu 7345	Asp Arg Glu Xaa Leu 7350	Tyr Trp Glu
Leu Ser 7355	Xaa Leu Thr Xaa Xaa 7360	Ile Xaa Glu Leu Gly 7365	Pro Tyr Xaa
Leu Asp 7370	Arg Xaa Ser Leu Tyr 7375	Val Asn Gly Phe Xaa 7380	Xaa Xaa Xaa
Xaa Xaa 7385	Xaa Xaa Thr Ser Thr 7390	Pro Gly Thr Ser Xaa 7395	Val Xaa Leu

Xaa Thr 7400	Ser Gly Thr Pro Xaa 7405	Xaa Xaa Pro Xaa Xaa 7410	Thr Xaa Xaa
Xaa Pro 7415	Leu Leu Xaa Pro Phe 7420	Thr Leu Asn Phe Thr 7425	Ile Thr Asn
Leu Xaa 7430	Tyr Glu Glu Xaa Met 7435	Xaa Xaa Pro Gly Ser 7440	Arg Lys Phe
Asn Thr 7445	Thr Glu Arg Val Leu 7450	Gln Gly Leu Leu Xaa 7455	Pro Xaa Phe
Lys Xaa 7460	Thr Ser Val Gly Xaa 7465	Leu Tyr Ser Gly Cys 7470	Arg Leu Thr
Leu Leu 7475	Arg Xaa Glu Lys Xaa 7480	Xaa Ala Ala Thr Xaa 7485	Val Asp Xaa
Xaa Cys 7490	Xaa Xaa Xaa Xaa Asp 7495	Pro Xaa Xaa Pro Gly 7500	Leu Asp Arg
Glu Xaa 7505	Leu Tyr Trp Glu Leu 7510	Ser Xaa Leu Thr Xaa 7515	Xaa Ile Xaa
Glu Leu 7520	Gly Pro Tyr Xaa Leu 7525	Asp Arg Xaa Ser Leu 7530	Tyr Val Asn
Gly Phe 7535	His Pro Arg Ser Ser 7540	Val Pro Thr Thr Ser 7545	Thr Pro Gly
Thr Ser 7550	Thr Val His Leu Ala 7555	Thr Ser Gly Thr Pro 7560	Ser Ser Leu
Pro Gly 7565	His Thr Ala Pro Val 7570	Pro Leu Leu Ile Pro 7575	Phe Thr Leu
Asn Phe 7580	Thr Ile Thr Asn Leu 7585	His Tyr Glu Glu Asn 7590	Met Gln His

Xaa Xaa Xaa Asp Pro Xaa Xaa	Pro Gly Leu Asp Arg	Glu Xaa Leu
7805	7810	7815
Tyr Trp Glu Leu Ser Xaa Leu	Thr Xaa Xaa Ile Xaa	Glu Leu Gly
7820	7825	7830
Pro Tyr Xaa Leu Asp Arg Xaa	Ser Leu Tyr Val Asn	Gly Phe Thr
7835	7840	7845
His Gln Asn Ser Val Pro Thr	Thr Ser Thr Pro Gly	Thr Ser Thr
7850	7855	7860
Val Tyr Trp Ala Thr Thr Gly	Thr Pro Ser Ser Phe	Pro Gly His
7865	7870	7875
Thr Glu Pro Gly Pro Leu Leu	Ile Pro Phe Thr Phe	Asn Phe Thr
7880	7885	7890
Ile Thr Asn Leu His Tyr Glu	Glu Asn Met Gln His	Pro Gly Ser
7895	7900	7905
Arg Lys Phe Asn Thr Thr Glu	Arg Val Leu Gln Gly	Leu Leu Thr
7910	7915	7920
Pro Leu Phe Lys Asn Thr Ser	Val Gly Pro Leu Tyr	Ser Gly Cys
7925	7930	7935
Arg Leu Thr Leu Leu Arg Pro	Glu Lys Gln Glu Ala	Ala Thr Gly
7940	7945	7950
Val Asp Thr Ile Cys Thr His	Arg Val Asp Pro Ile	Gly Pro Gly
7955	7960	7965
Leu Asp Arg Glu Xaa Leu Tyr	Trp Glu Leu Ser Xaa	Leu Thr Xaa
7970	7975	7980
Xaa Ile Xaa Glu Leu Gly Pro	Tyr Xaa Leu Asp Arg	Xaa Ser Leu
7985	7990	7995

294

Tyr Val 8000	Asn Gly Phe Xaa Xaa 8005	Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser 8010
Thr Pro 8015	Gly Thr Ser Xaa Val 8020	Xaa Leu Xaa Thr Ser Gly Thr Pro 8025
Xaa Xaa 8030	Xaa Pro Xaa Xaa Thr 8035	Xaa Xaa Xaa Pro Leu Leu Xaa Pro 8040
Phe Thr 8045	Leu Asn Phe Thr Ile 8050	Thr Asn Leu Xaa Tyr Glu Glu Xaa 8055
Met Xaa 8060	Xaa Pro Gly Ser Arg 8065	Lys Phe Asn Thr Thr Glu Arg Val 8070
Leu Gln 8075	Gly Leu Leu Xaa Pro 8080	Xaa Phe Lys Xaa Thr Ser Val Gly 8085
Xaa Leu 8090	Tyr Ser Gly Cys Arg 8095	Leu Thr Leu Leu Arg Xaa Glu Lys 8100
Xaa Xaa 8105	Ala Ala Thr Xaa Val 8110	Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa 8115
Asp Pro 8120	Xaa Xaa Pro Gly Leu 8125	Asp Arg Glu Xaa Leu Tyr Trp Glu 8130
Leu Ser 8135	Xaa Leu Thr Xaa Xaa 8140	Ile Xaa Glu Leu Gly Pro Tyr Xaa 8145
Leu Asp 8150	Arg Xaa Ser Leu Tyr 8155	Val Asn Gly Phe Thr His Arg Ser 8160
Ser Val 8165	Pro Thr Thr Ser Ser 8170	Pro Gly Thr Ser Thr Val His Leu 8175
Ala Thr 8180	Ser Gly Thr Pro Ser 8185	Ser Leu Pro Gly His Thr Ala Pro 8190
Val Pro 8195	Leu Leu Ile Pro Phe 8200	Thr Leu Asn Phe Thr Ile Thr Asn 8205

295

Leu His	Tyr Glu Glu Asn Met	Gln His Pro Gly Ser	Arg Lys Phe
8210	8215	8220	
Asn Thr	Thr Glu Arg Val Leu	Gln Gly Leu Leu Lys	Pro Leu Phe
8225	8230	8235	
Lys Ser	Thr Ser Val Gly Pro	Leu Tyr Ser Gly Cys	Arg Leu Thr
8240	8245	8250	
Leu Leu	Arg Pro Glu Lys His	Gly Ala Ala Thr Gly	Val Asp Ala
8255	8260	8265	
Ile Cys	Thr Leu Arg Leu Asp	Pro Thr Gly Pro Gly	Leu Asp Arg
8270	8275	8280	
Glu Xaa	Leu Tyr Trp Glu Leu	Ser Xaa Leu Thr Xaa	Xaa Ile Xaa
8285	8290	8295	
Glu Leu	Gly Pro Tyr Xaa Leu	Asp Arg Xaa Ser Leu	Tyr Val Asn
8300	8305	8310	
Gly Phe	Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa Thr Ser	Thr Pro Gly
8315	8320	8325	
Thr Ser	Xaa Val Xaa Leu Xaa	Thr Ser Gly Thr Pro	Xaa Xaa Xaa
8330	8335	8340	
Pro Xaa	Xaa Thr Xaa Xaa Xaa	Pro Leu Leu Xaa Pro	Phe Thr Leu
8345	8350	8355	
Asn Phe	Thr Ile Thr Asn Leu	Xaa Tyr Glu Glu Xaa	Met Xaa Xaa
8360	8365	8370	
Pro Gly	Ser Arg Lys Phe Asn	Thr Thr Glu Arg Val	Leu Gln Gly
8375	8380	8385	
Leu Leu	Xaa Pro Xaa Phe Lys	Xaa Thr Ser Val Gly	Xaa Leu Tyr
8390	8395	8400	

296

Ser Gly 8405	Cys Arg Leu Thr	Leu 8410	Leu Arg Xaa Glu	Lys 8415	Xaa Xaa Ala
Ala Thr 8420	Xaa Val Asp Xaa	Xaa 8425	Cys Xaa Xaa Xaa	Xaa 8430	Asp Pro Xaa
Xaa Pro 8435	Gly Leu Asp Arg	Glu 8440	Xaa Leu Tyr Trp	Glu 8445	Leu Ser Xaa
Leu Thr 8450	Xaa Xaa Ile Xaa	Glu 8455	Leu Gly Pro Tyr	Xaa 8460	Leu Asp Arg
Xaa Ser 8465	Leu Tyr Val Asn	Gly 8470	Phe Thr His Arg	Thr 8475	Ser Val Pro
Thr Thr 8480	Ser Thr Pro Gly	Thr 8485	Ser Thr Val His	Leu 8490	Ala Thr Ser
Gly Thr 8495	Pro Ser Ser Leu	Pro 8500	Gly His Thr Ala	Pro 8505	Val Pro Leu
Leu Ile 8510	Pro Phe Thr Leu	Asn 8515	Phe Thr Ile Thr	Asn 8520	Leu Gln Tyr
Glu Glu 8525	Asp Met His Arg	Pro 8530	Gly Ser Arg Lys	Phe 8535	Asn Thr Thr
Glu Arg 8540	Val Leu Gln Gly	Leu 8545	Leu Ser Pro Ile	Phe 8550	Lys Asn Ser
Ser Val 8555	Gly Pro Leu Tyr	Ser 8560	Gly Cys Arg Leu	Thr 8565	Ser Leu Arg
Pro Glu 8570	Lys Asp Gly Ala	Ala 8575	Thr Gly Met Asp	Ala 8580	Val Cys Leu
Tyr His 8585	Pro Asn Pro Lys	Arg 8590	Pro Gly Leu Asp	Arg 8595	Glu Gln Leu
Tyr Cys 8600	Glu Leu Ser Gln	Leu 8605	Thr His Asn Ile	Thr 8610	Glu Leu Gly

Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
8615 8620 8625

His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
8630 8635 8640

Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
8645 8650 8655

Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr
8660 8665 8670

Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser
8675 8680 8685

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa
8690 8695 8700

Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys
8705 8710 8715

Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa
8720 8725 8730

Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly
8735 8740 8745

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
8750 8755 8760

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
8765 8770 8775

Tyr Val Asn Gly Phe Thr His Trp Ser Ser Gly Leu Thr Thr Ser
8780 8785 8790

Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
8795 8800 8805

298

Ser	Pro	Val	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro
8810						8815					8820			
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp
8825						8830					8835			
Met	His	Arg	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Ala	Thr	Glu	Arg	Val
8840						8845					8850			
Leu	Gln	Gly	Leu	Leu	Ser	Pro	Ile	Phe	Lys	Asn	Thr	Ser	Val	Gly
8855						8860					8865			
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys
8870						8875					8880			
Gln	Glu	Ala	Ala	Thr	Gly	Val	Asp	Thr	Ile	Cys	Thr	His	Arg	Val
8885						8890					8895			
Asp	Pro	Ile	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu
8900						8905					8910			
Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa
8915						8920					8925			
Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa
8930						8935					8940			
Xaa	Xaa	Xaa	Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa	Val	Xaa	Leu
8945						8950					8955			
Xaa	Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Xaa	Xaa
8960						8965					8970			
Xaa	Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn
8975						8980					8985			
Leu	Xaa	Tyr	Glu	Glu	Xaa	Met	Xaa	Xaa	Pro	Gly	Ser	Arg	Lys	Phe
8990						8995					9000			
Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Xaa	Pro	Xaa	Phe
9005						9010					9015			

Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr
 9020 9025 9030

Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa
 9035 9040 9045

Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg
 9050 9055 9060

Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
 9065 9070 9075

Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
 9080 9085 9090

Gly Phe Thr His Arg Ser Phe Gly Leu Thr Thr Ser Thr Pro Trp
 9095 9100 9105

Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
 9110 9115 9120

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu
 9125 9130 9135

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg
 9140 9145 9150

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 9155 9160 9165

Leu Leu Thr Pro Leu Phe Arg Asn Thr Ser Val Ser Ser Leu Tyr
 9170 9175 9180

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
 9185 9190 9195

Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys
 9200 9205 9210

300

Ser Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
 9215 9220 9225

Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
 9230 9235 9240

Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 9245 9250 9255

Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser
 9260 9265 9270

Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu
 9275 9280 9285

Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr
 9290 9295 9300

Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr
 9305 9310 9315

Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr
 9320 9325 9330

Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
 9335 9340 9345

Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa
 9350 9355 9360

Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu
 9365 9370 9375

Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
 9380 9385 9390

Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr
 9395 9400 9405

His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr
 9410 9415 9420

Val Asp 9425	Leu Gly Ser Gly Thr 9430	Pro Ser Ser Leu Pro 9435	Ser Pro Thr
Thr Ala 9440	Gly Pro Leu Leu Val 9445	Pro Phe Thr Leu Asn 9450	Phe Thr Ile
Thr Asn 9455	Leu Gln Tyr Gly Glu 9460	Asp Met Gly His Pro 9465	Gly Ser Arg
Lys Phe 9470	Asn Thr Thr Glu Arg 9475	Val Leu Gln Gly Leu 9480	Leu Gly Pro
Ile Phe 9485	Lys Asn Thr Ser Val 9490	Gly Pro Leu Tyr Ser 9495	Gly Cys Arg
Leu Thr 9500	Ser Leu Arg Ser Glu 9505	Lys Asp Gly Ala Ala 9510	Thr Gly Val
Asp Ala 9515	Ile Cys Ile His His 9520	Leu Asp Pro Lys Ser 9525	Pro Gly Leu
Asp Arg 9530	Glu Xaa Leu Tyr Trp 9535	Glu Leu Ser Xaa Leu 9540	Thr Xaa Xaa
Ile Xaa 9545	Glu Leu Gly Pro Tyr 9550	Xaa Leu Asp Arg Xaa 9555	Ser Leu Tyr
Val Asn 9560	Gly Phe Xaa Xaa Xaa 9565	Xaa Xaa Xaa Xaa Xaa 9570	Thr Ser Thr
Pro Gly 9575	Thr Ser Xaa Val Xaa 9580	Leu Xaa Thr Ser Gly 9585	Thr Pro Xaa
Xaa Xaa 9590	Pro Xaa Xaa Thr Xaa 9595	Xaa Xaa Pro Leu Leu 9600	Xaa Pro Phe
Thr Leu 9605	Asn Phe Thr Ile Thr 9610	Asn Leu Xaa Tyr Glu 9615	Glu Xaa Met

302

Xaa Xaa	Pro Gly Ser Arg	Lys	Phe Asn Thr Thr	Glu	Arg Val Leu
9620		9625		9630	
Gln Gly	Leu Leu Xaa Pro	Xaa	Phe Lys Xaa Thr	Ser	Val Gly Xaa
9635		9640		9645	
Leu Tyr	Ser Gly Cys Arg	Leu	Thr Leu Leu Arg	Xaa	Glu Lys Xaa
9650		9655		9660	
Xaa Ala	Ala Thr Xaa Val	Asp	Xaa Xaa Cys Xaa	Xaa	Xaa Xaa Asp
9665		9670		9675	
Pro Xaa	Xaa Pro Gly Leu	Asp	Arg Glu Xaa Leu	Tyr	Trp Glu Leu
9680		9685		9690	
Ser Xaa	Leu Thr Xaa Xaa	Ile	Xaa Glu Leu Gly	Pro	Tyr Xaa Leu
9695		9700		9705	
Asp Arg	Xaa Ser Leu Tyr	Val	Asn Gly Phe Thr	His	Gln Thr Phe
9710		9715		9720	
Ala Pro	Asn Thr Ser Thr	Pro	Gly Thr Ser Thr	Val	Asp Leu Gly
9725		9730		9735	
Thr Ser	Gly Thr Pro Ser	Ser	Leu Pro Ser Pro	Thr	Ser Ala Gly
9740		9745		9750	
Pro Leu	Leu Val Pro Phe	Thr	Leu Asn Phe Thr	Ile	Thr Asn Leu
9755		9760		9765	
Gln Tyr	Glu Glu Asp Met	His	His Pro Gly Ser	Arg	Lys Phe Asn
9770		9775		9780	
Thr Thr	Glu Arg Val Leu	Gln	Gly Leu Leu Gly	Pro	Met Phe Lys
9785		9790		9795	
Asn Thr	Ser Val Gly Leu	Leu	Tyr Ser Gly Cys	Arg	Leu Thr Leu
9800		9805		9810	
Leu Arg	Pro Glu Lys Asn	Gly	Ala Ala Thr Arg	Val	Asp Ala Val
9815		9820		9825	

303

Cys Thr	His Arg	Pro Asp	Pro Lys	Ser Pro	Gly Leu	Asp Arg	Glu
9830			9835		9840		
Xaa Leu	Tyr Trp	Glu Leu	Ser Xaa	Leu Thr	Xaa Xaa	Ile Xaa	Glu
9845			9850		9855		
Leu Gly	Pro Tyr	Xaa Leu	Asp Arg	Xaa Ser	Leu Tyr	Val Asn	Gly
9860			9865		9870		
Phe Xaa	Xaa Xaa	Xaa Xaa	Xaa Xaa	Xaa Thr	Ser Thr	Pro Gly	Thr
9875			9880		9885		
Ser Xaa	Val Xaa	Leu Xaa	Thr Ser	Gly Thr	Pro Xaa	Xaa Xaa	Pro
9890			9895		9900		
Xaa Xaa	Thr Ala	Pro Val	Pro Leu	Leu Ile	Pro Phe	Thr Leu	Asn
9905			9910		9915		
Phe Thr	Ile Thr	Asn Leu	His Tyr	Glu Glu	Asn Met	Gln His	Pro
9920			9925		9930		
Gly Ser	Arg Lys	Phe Asn	Thr Thr	Glu Arg	Val Leu	Gln Gly	Leu
9935			9940		9945		
Leu Arg	Pro Leu	Phe Lys	Ser Thr	Ser Val	Gly Pro	Leu Tyr	Ser
9950			9955		9960		
Gly Cys	Arg Leu	Thr Leu	Leu Arg	Pro Glu	Lys His	Gly Ala	Ala
9965			9970		9975		
Thr Gly	Val Asp	Ala Ile	Cys Thr	Leu Arg	Leu Asp	Pro Thr	Gly
9980			9985		9990		
Pro Gly	Leu Asp	Arg Glu	Arg Leu	Tyr Trp	Glu Leu	Ser Gln	Leu
9995			10000		10005		
Thr Asn	Ser Val	Thr Glu	Leu Gly	Pro Tyr	Thr Leu	Asp Arg	Asp
10010			10015		10020		

304

Ser Leu 10025	Tyr Val Asn Gly Phe 10030	Thr Gln Arg Ser Ser 10035	Val Pro Thr
Thr Ser 10040	Ile Pro Gly Thr Ser 10045	Ala Val His Leu Glu 10050	Thr Ser Gly
Thr Pro 10055	Ala Ser Leu Pro Gly 10060	His Thr Ala Pro Gly 10065	Pro Leu Leu
Val Pro 10070	Phe Thr Leu Asn Phe 10075	Thr Ile Thr Asn Leu 10080	Gln Tyr Glu
Val Asp 10085	Met Arg His Pro Gly 10090	Ser Arg Lys Phe Asn 10095	Thr Thr Glu
Arg Val 10100	Leu Gln Gly Leu Leu 10105	Lys Pro Leu Phe Lys 10110	Ser Thr Ser
Val Gly 10115	Pro Leu Tyr Ser Gly 10120	Cys Arg Leu Thr Leu 10125	Leu Arg Pro
Glu Lys 10130	Arg Gly Ala Ala Thr 10135	Gly Val Asp Thr Ile 10140	Cys Thr His
Arg Leu 10145	Asp Pro Leu Asn Pro 10150	Gly Leu Asp Arg Glu 10155	Gln Leu Tyr
Trp Glu 10160	Leu Ser Lys Leu Thr 10165	Arg Gly Ile Ile Glu 10170	Leu Gly Pro
Tyr Leu 10175	Leu Asp Arg Gly Ser 10180	Leu Tyr Val Asn Gly 10185	Phe Thr His
Arg Asn 10190	Phe Val Pro Ile Thr 10195	Ser Thr Pro Gly Thr 10200	Ser Thr Val
His Leu 10205	Gly Thr Ser Glu Thr 10210	Pro Ser Ser Leu Pro 10215	Arg Pro Ile
Val Pro 10220	Gly Pro Leu Leu Val 10225	Pro Phe Thr Leu Asn 10230	Phe Thr Ile

305

Thr Asn 10235	Leu Gln Tyr Glu Glu 10240	Ala Met Arg His Pro 10245	Gly Ser Arg
Lys Phe 10250	Asn Thr Thr Glu Arg 10255	Val Leu Gln Gly Leu 10260	Leu Arg Pro
Leu Phe 10265	Lys Asn Thr Ser Ile 10270	Gly Pro Leu Tyr Ser 10275	Ser Cys Arg
Leu Thr 10280	Leu Leu Arg Pro Glu 10285	Lys Asp Lys Ala Ala 10290	Thr Arg Val
Asp Ala 10295	Ile Cys Thr His His 10300	Pro Asp Pro Gln Ser 10305	Pro Gly Leu
Asn Arg 10310	Glu Gln Leu Tyr Trp 10315	Glu Leu Ser Gln Leu 10320	Thr His Gly
Ile Thr 10325	Glu Leu Gly Pro Tyr 10330	Thr Leu Asp Arg Asp 10335	Ser Leu Tyr
Val Asp 10340	Gly Phe Thr His Trp 10345	Ser Pro Ile Pro Thr 10350	Thr Ser Thr
Pro Gly 10355	Thr Ser Ile Val Asn 10360	Leu Gly Thr Ser Gly 10365	Ile Pro Pro
Ser Leu 10370	Pro Glu Thr Thr Xaa 10375	Xaa Xaa Pro Leu Leu 10380	Xaa Pro Phe
Thr Leu 10385	Asn Phe Thr Ile Thr 10390	Asn Leu Xaa Tyr Glu 10395	Glu Xaa Met
Xaa Xaa 10400	Pro Gly Ser Arg Lys 10405	Phe Asn Thr Thr Glu 10410	Arg Val Leu
Gln Gly 10415	Leu Leu Lys Pro Leu 10420	Phe Lys Ser Thr Ser 10425	Val Gly Pro

306

Leu Tyr 10430	Ser Gly Cys Arg 10435	Leu Thr Leu Leu Arg Pro 10440	Glu Lys Asp
Gly Val 10445	Ala Thr Arg Val Asp 10450	Ala Ile Cys Thr His 10455	Arg Pro Asp
Pro Lys 10460	Ile Pro Gly Leu Asp 10465	Arg Gln Gln Leu Tyr 10470	Trp Glu Leu
Ser Gln 10475	Leu Thr His Ser Ile 10480	Thr Glu Leu Gly Pro 10485	Tyr Thr Leu
Asp Arg 10490	Asp Ser Leu Tyr Val 10495	Asn Gly Phe Thr Gln 10500	Arg Ser Ser
Val Pro 10505	Thr Thr Ser Thr Pro 10510	Gly Thr Phe Thr Val 10515	Gln Pro Glu
Thr Ser 10520	Glu Thr Pro Ser Ser 10525	Leu Pro Gly Pro Thr 10530	Ala Thr Gly
Pro Val 10535	Leu Leu Pro Phe Thr 10540	Leu Asn Phe Thr Ile 10545	Thr Asn Leu
Gln Tyr 10550	Glu Glu Asp Met His 10555	Arg Pro Gly Ser Arg 10560	Lys Phe Asn
Thr Thr 10565	Glu Arg Val Leu Gln 10570	Gly Leu Leu Met Pro 10575	Leu Phe Lys
Asn Thr 10580	Ser Val Ser Ser Leu 10585	Tyr Ser Gly Cys Arg 10590	Leu Thr Leu
Leu Arg 10595	Pro Glu Lys Asp Gly 10600	Ala Ala Thr Arg Val 10605	Asp Ala Val
Cys Thr 10610	His Arg Pro Asp Pro 10615	Lys Ser Pro Gly Leu 10620	Asp Arg Glu
Arg Leu 10625	Tyr Trp Lys Leu Ser 10630	Gln Leu Thr His Gly 10635	Ile Thr Glu

307

Leu Gly 10640	Pro Tyr Thr Leu Asp 10645	Arg His Ser Leu Tyr 10650	Val Asn Gly
Phe Thr 10655	His Gln Ser Ser Met 10660	Thr Thr Thr Arg Thr 10665	Pro Asp Thr
Ser Thr 10670	Met His Leu Ala Thr 10675	Ser Arg Thr Pro Ala 10680	Ser Leu Ser
Gly Pro 10685	Thr Thr Ala Ser Pro 10690	Leu Leu Val Leu Phe 10695	Thr Ile Asn
Phe Thr 10700	Ile Thr Asn Leu Arg 10705	Tyr Glu Glu Asn Met 10710	His His Pro
Gly Ser 10715	Arg Lys Phe Asn Thr 10720	Thr Glu Arg Val Leu 10725	Gln Gly Leu
Leu Arg 10730	Pro Val Phe Lys Asn 10735	Thr Ser Val Gly Pro 10740	Leu Tyr Ser
Gly Cys 10745	Arg Leu Thr Leu Leu 10750	Arg Pro Lys Lys Asp 10755	Gly Ala Ala
Thr Lys 10760	Val Asp Ala Ile Cys 10765	Thr Tyr Arg Pro Asp 10770	Pro Lys Ser
Pro Gly 10775	Leu Asp Arg Glu Gln 10780	Leu Tyr Trp Glu Leu 10785	Ser Gln Leu
Thr His 10790	Ser Ile Thr Glu Leu 10795	Gly Pro Tyr Thr Gln 10800	Asp Arg Asp
Ser Leu 10805	Tyr Asn Val Gly Phe 10810	Thr Gln Arg Ser Ser 10815	Val Pro Thr
Thr Ser 10820	Val Pro Gly Thr Pro 10825	Thr Val Asp Leu Gly 10830	Thr Ser Gly

308

Thr Pro	Val Ser Lys Pro Gly	Pro Ser Ala Ala Ser	Pro Leu Leu
10835	10840	10845	
Val Leu	Phe Thr Leu Asn Gly	Thr Ile Thr Asn Leu	Arg Tyr Glu
10850	10855	10860	
Glu Asn	Met Gln His Pro Gly	Ser Arg Lys Phe Asn	Thr Thr Glu
10865	10870	10875	
Arg Val	Leu Gln Gly Leu Leu	Arg Ser Leu Phe Lys	Ser Thr Ser
10880	10885	10890	
Val Gly	Pro Leu Tyr Ser Gly	Cys Arg Leu Thr Leu	Leu Arg Pro
10895	10900	10905	
Glu Lys	Asp Gly Thr Ala Thr	Gly Val Asp Ala Ile	Cys Thr His
10910	10915	10920	
His Pro	Asp Pro Lys Ser Pro	Arg Leu Asp Arg Glu	Gln Leu Tyr
10925	10930	10935	
Trp Glu	Leu Ser Gln Leu Thr	His Asn Ile Thr Glu	Leu Gly His
10940	10945	10950	
Tyr Ala	Leu Asp Asn Asp Ser	Leu Phe Val Asn Gly	Phe Thr His
10955	10960	10965	
Arg Ser	Ser Val Ser Thr Thr	Ser Thr Pro Gly Thr	Pro Thr Val
10970	10975	10980	
Tyr Leu	Gly Ala Ser Lys Thr	Pro Ala Ser Ile Phe	Gly Pro Ser
10985	10990	10995	
Ala Ala	Ser His Leu Leu Ile	Leu Phe Thr Leu Asn	Phe Thr Ile
11000	11005	11010	
Thr Asn	Leu Arg Tyr Glu Glu	Asn Met Trp Pro Gly	Ser Arg Lys
11015	11020	11025	
Phe Asn	Thr Thr Glu Arg Val	Leu Gln Gly Leu Leu	Arg Pro Leu
11030	11035	11040	

Phe Lys	Asn Thr Ser Val Gly	Pro Leu Tyr Ser Gly	Ser Arg Leu
11045	11050	11055	
Thr Leu	Leu Arg Pro Glu Lys	Asp Gly Glu Ala Thr	Gly Val Asp
11060	11065	11070	
Ala Ile	Cys Thr His Arg Pro	Asp Pro Thr Gly Pro	Gly Leu Asp
11075	11080	11085	
Arg Glu	Gln Leu Tyr Leu Glu	Leu Ser Gln Leu Thr	His Ser Ile
11090	11095	11100	
Thr Glu	Leu Gly Pro Tyr Thr	Leu Asp Arg Asp Ser	Leu Tyr Val
11105	11110	11115	
Asn Gly	Phe Thr His Arg Ser	Ser Val Pro Thr Thr	Ser Thr Gly
11120	11125	11130	
Val Val	Ser Glu Glu Pro Phe	Thr Leu Asn Phe Thr	Ile Asn Asn
11135	11140	11145	
Leu Arg	Tyr Met Ala Asp Met	Gly Gln Pro Gly Ser	Leu Lys Phe
11150	11155	11160	
Asn Ile	Thr Asp Asn Val Met	Lys His Leu Leu Ser	Pro Leu Phe
11165	11170	11175	
Gln Arg	Ser Ser Leu Gly Ala	Arg Tyr Thr Gly Cys	Arg Val Ile
11180	11185	11190	
Ala Leu	Arg Ser Val Lys Asn	Gly Ala Glu Thr Arg	Val Asp Leu
11195	11200	11205	
Leu Cys	Thr Tyr Leu Gln Pro	Leu Ser Gly Pro Gly	Leu Pro Ile
11210	11215	11220	
Lys Gln	Val Phe His Glu Leu	Ser Gln Gln Thr His	Gly Ile Thr
11225	11230	11235	

310

Arg Leu 11240	Gly Pro Tyr Ser Leu 11245	Asp Lys Asp Ser Leu 11250	Tyr Leu Asn
Gly Tyr 11255	Asn Glu Pro Gly Leu 11260	Asp Glu Pro Pro Thr 11265	Thr Pro Lys
Pro Ala 11270	Thr Thr Phe Leu Pro 11275	Pro Leu Ser Glu Ala 11280	Thr Thr Ala
Met Gly 11285	Tyr His Leu Lys Thr 11290	Leu Thr Leu Asn Phe 11295	Thr Ile Ser
Asn Leu 11300	Gln Tyr Ser Pro Asp 11305	Met Gly Lys Gly Ser 11310	Ala Thr Phe
Asn Ser 11315	Thr Glu Gly Val Leu 11320	Gln His Leu Leu Arg 11325	Pro Leu Phe
Gln Lys 11330	Ser Ser Met Gly Pro 11335	Phe Tyr Leu Gly Cys 11340	Gln Leu Ile
Ser Leu 11345	Arg Pro Glu Lys Asp 11350	Gly Ala Ala Thr Gly 11355	Val Asp Thr
Thr Cys 11360	Thr Tyr His Pro Asp 11365	Pro Val Gly Pro Gly 11370	Leu Asp Ile
Gln Gln 11375	Leu Tyr Trp Glu Leu 11380	Ser Gln Leu Thr His 11385	Gly Val Thr
Gln Leu 11390	Gly Phe Tyr Val Leu 11395	Asp Arg Asp Ser Leu 11400	Phe Ile Asn
Gly Tyr 11405	Ala Pro Gln Asn Leu 11410	Ser Ile Arg Gly Glu 11415	Tyr Gln Ile
Asn Phe 11420	His Ile Val Asn Trp 11425	Asn Leu Ser Asn Pro 11430	Asp Pro Thr
Ser Ser 11435	Glu Tyr Ile Thr Leu 11440	Leu Arg Asp Ile Gln 11445	Asp Lys Val

311

Thr Thr 11450	Leu Tyr Lys Gly Ser 11455	Gln Leu His Asp Thr 11460	Phe Arg Phe
Cys Leu 11465	Val Thr Asn Leu Thr 11470	Met Asp Ser Val Leu 11475	Val Thr Val
Lys Ala 11480	Leu Phe Ser Ser Asn 11485	Leu Asp Pro Ser Leu 11490	Val Glu Gln
Val Phe 11495	Leu Asp Lys Thr Leu 11500	Asn Ala Ser Phe His 11505	Trp Leu Gly
Ser Thr 11510	Tyr Gln Leu Val Asp 11515	Ile His Val Thr Glu 11520	Met Glu Ser
Ser Val 11525	Tyr Gln Pro Thr Ser 11530	Ser Ser Ser Thr Gln 11535	His Phe Tyr
Leu Asn 11540	Phe Thr Ile Thr Asn 11545	Leu Pro Tyr Ser Gln 11550	Asp Lys Ala
Gln Pro 11555	Gly Thr Thr Asn Tyr 11560	Gln Arg Asn Lys Arg 11565	Asn Ile Glu
Asp Ala 11570	Leu Asn Gln Leu Phe 11575	Arg Asn Ser Ser Ile 11580	Lys Ser Tyr
Phe Ser 11585	Asp Cys Gln Val Ser 11590	Thr Phe Arg Ser Val 11595	Pro Asn Arg
His His 11600	Thr Gly Val Asp Ser 11605	Leu Cys Asn Phe Ser 11610	Pro Leu Ala
Arg Arg 11615	Val Asp Arg Val Ala 11620	Ile Tyr Glu Glu Phe 11625	Leu Arg Met
Thr Arg 11630	Asn Gly Thr Gln Leu 11635	Gln Asn Phe Thr Leu 11640	Asp Arg Ser

313

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 85 90 95

Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr
 100 105 110

Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn
 115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala
 130 135 140

Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr
 145 150 155

<210> 164

<211> 42

<212> PRT

<213> Homo sapiens

<400> 164

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu
 35 40

<210> 165

<211> 42

<212> PRT

<213> Homo sapiens

314

<400> 165

Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 166

<211> 42

<212> PRT

<213> Homo sapiens

<400> 166

Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 167

<211> 42

<212> PRT

<213> Homo sapiens

<400> 167

Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

316

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 170

<211> 42

<212> PRT

<213> Homo sapiens

<400> 170

Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 171

<211> 42

<212> PRT

<213> Homo sapiens

<400> 171

Ala Ala Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe
20 25 30

Asn Thr Met Glu Ser Val Leu Gln Gly Leu
35 40

<210> 172

317

<211> 42

<212> PRT

<213> Homo sapiens

<400> 172

Thr	Ala	Ser	Pro	Leu	Leu	Val	Leu	Phe	Thr	Ile	Asn	Cys	Thr	Ile	Thr
1				5					10					15	

Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	Arg	Arg	Thr	Gly	Ser	Arg	Lys	Phe
			20					25					30		

Asn	Thr	Met	Glu	Ser	Val	Leu	Gln	Gly	Leu
		35						40	

<210> 173

<211> 42

<212> PRT

<213> Homo sapiens

<400> 173

Ala	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr
1				5					10					15	

Asn	Leu	Gln	Tyr	Gly	Glu	Asp	Met	Gly	His	Pro	Gly	Ser	Arg	Lys	Phe
			20					25					30		

Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu
		35						40	

<210> 174

<211> 42

<212> PRT

<213> Homo sapiens

318

<400> 174

Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 175

<211> 42

<212> PRT

<213> Homo sapiens

<400> 175

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 176

<211> 42

<212> PRT

<213> Homo sapiens

<400> 176

Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

320

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 179

<211> 42

<212> PRT

<213> Homo sapiens

<400> 179

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 180

<211> 42

<212> PRT

<213> Homo sapiens

<400> 180

Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 181

321

<211> 42

<212> PRT

<213> Homo sapiens

<400> 181

Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 182

<211> 42

<212> PRT

<213> Homo sapiens

<400> 182

Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 183

<211> 42

<212> PRT

<213> Homo sapiens

322

<400> 183

Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
 35 40

<210> 184

<211> 42

<212> PRT

<213> Homo sapiens

<400> 184

Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr
 1 5 10 15

Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
 35 40

<210> 185

<211> 42

<212> PRT

<213> Homo sapiens

<400> 185

Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr
 1 5 10 15

324

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 188

<211> 42

<212> PRT

<213> Homo sapiens

<400> 188

Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 189

<211> 42

<212> PRT

<213> Homo sapiens

<400> 189

Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asp Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 190

325

<211> 42

<212> PRT

<213> Homo sapiens

<400> 190

Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Gly Thr Ile Thr
1 5 10 15

Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 191

<211> 42

<212> PRT

<213> Homo sapiens

<400> 191

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Ser Leu
35 40

<210> 192

<211> 41

<212> PRT

<213> Homo sapiens

326

<400> 192

Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn
20 25 30

Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 193

<211> 42

<212> PRT

<213> Homo sapiens

<400> 193

Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn
1 5 10 15

Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe
20 25 30

Asn Ile Thr Asp Asn Val Met Lys His Leu
35 40

<210> 194

<211> 42

<212> PRT

<213> Homo sapiens

<400> 194

Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser
1 5 10 15

327

Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn
 20 25 30

Ser Thr Glu Gly Val Leu Gln His Leu Leu
 35 40

<210> 195

<211> 23

<212> PRT

<213> Homo sapiens

<400> 195

Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly
 1 5 10 15

Cys Arg Leu Ala Ser Leu Arg
 20

<210> 196

<211> 23

<212> PRT

<213> Homo sapiens

<400> 196

Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
 1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
 20

<210> 197

<211> 23

328

<212> PRT

<213> Homo sapiens

<400> 197

Leu	Lys	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Leu	Leu	Arg
			20			

<210> 198

<211> 23

<212> PRT

<213> Homo sapiens

<400> 198

Leu	Lys	Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Leu	Leu	Arg
			20			

<210> 199

<211> 23

<212> PRT

<213> Homo sapiens

<400> 199

Leu	Lys	Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Ser
1				5					10					15	

Cys	Arg	Leu	Thr	Leu	Leu	Arg
			20			

329

<210> 200

<211> 23

<212> PRT

<213> Homo sapiens

<400> 200

Leu	Lys	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Ser	Leu	Arg
			20			

<210> 201

<211> 23

<212> PRT

<213> Homo sapiens

<400> 201

Leu	Gly	Pro	Ile	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Ser	Leu	Arg
			20			

<210> 202

<211> 23

<212> PRT

<213> Homo sapiens

<400> 202

330

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
 20

<210> 203

<211> 23

<212> PRT

<213> Homo sapiens

<400> 203

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
 20

<210> 204

<211> 23

<212> PRT

<213> Homo sapiens

<400> 204

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
 20

<210> 205

<211> 23

<212> PRT

331

<213> Homo sapiens

<400> 205

Leu	Gly	Pro	Leu	Phe	Lys	Asn	Ser	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Ile	Ser	Leu	Arg
		20				

<210> 206

<211> 23

<212> PRT

<213> Homo sapiens

<400> 206

Leu	Gly	Pro	Leu	Phe	Lys	Asn	Ser	Ser	Val	Asp	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Ser	Leu	Arg
		20				

<210> 207

<211> 23

<212> PRT

<213> Homo sapiens

<400> 207

Leu	Ser	Pro	Ile	Phe	Lys	Asn	Ser	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Ser	Leu	Arg
		20				

332

<210> 208

<211> 23

<212> PRT

<213> Homo sapiens

<400> 208

Leu	Ser	Pro	Ile	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly
1				5					10					15	

Cys	Arg	Leu	Thr	Leu	Leu	Arg
			20			

<210> 209

<211> 23

<212> PRT

<213> Homo sapiens

<400> 209

Leu	Ser	Pro	Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly
1				5					10					15	

Cys	Arg	Val	Ile	Ala	Leu	Arg
			20			

<210> 210

<211> 23

<212> PRT

<213> Homo sapiens

<400> 210

Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Ser	Ser	Leu	Tyr	Ser	Gly
1				5					10					15	

333

Cys Arg Leu Thr Leu Leu Arg
20

<210> 211

<211> 23

<212> PRT

<213> Homo sapiens

<400> 211

Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Ser Arg Leu Thr Leu Leu Arg
20

<210> 212

<211> 23

<212> PRT

<213> Homo sapiens

<400> 212

Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 213

<211> 23

<212> PRT

<213> Homo sapiens

334

<400> 213

Leu Arg Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 214

<211> 23

<212> PRT

<213> Homo sapiens

<400> 214

Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 215

<211> 23

<212> PRT

<213> Homo sapiens

<400> 215

Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 216

335

<211> 23

<212> PRT

<213> Homo sapiens

<400> 216

Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 217

<211> 23

<212> PRT

<213> Homo sapiens

<400> 217

Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 218

<211> 23

<212> PRT

<213> Homo sapiens

<400> 218

Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

336

Cys Arg Leu Thr Leu Leu Arg
20

<210> 219

<211> 23

<212> PRT

<213> Homo sapiens

<400> 219

Leu Thr Pro Leu Phe Arg Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 220

<211> 23

<212> PRT

<213> Homo sapiens

<400> 220

Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 221

<211> 22

<212> PRT

<213> Homo sapiens

337

<400> 221

Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys
1 5 10 15

Gln Leu Ile Ser Leu Arg
20

<210> 222

<211> 58

<212> PRT

<213> Homo sapiens

<400> 222

Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 223

<211> 58

<212> PRT

<213> Homo sapiens

<400> 223

Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

338

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 224

<211> 58

<212> PRT

<213> Homo sapiens

<400> 224

Pro Lys Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 225

<211> 58

<212> PRT

<213> Homo sapiens

<400> 225

Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

339

His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala
 35 40 45

Leu Asp Asn Asp Ser Leu Phe Val Asn Gly
 50 55

<210> 226

<211> 58

<212> PRT

<213> Homo sapiens

<400> 226

Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His
 1 5 10 15

Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu
 20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 227

<211> 58

<212> PRT

<213> Homo sapiens

<400> 227

340

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr
 1 5 10 15

His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
 35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 228

<211> 58

<212> PRT

<213> Homo sapiens

<400> 228

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr
 1 5 10 15

His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys
 20 25 30

Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
 35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 229

<211> 58

<212> PRT

<213> Homo sapiens

341

<400> 229

Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Ala Cys Thr Tyr
 1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Val Ser Leu Tyr Val Asn Gly
 50 55

<210> 230

<211> 58

<212> PRT

<213> Homo sapiens

<400> 230

Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
 1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 35 40 45

Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 231

<211> 58

<212> PRT

<213> Homo sapiens

342

<400> 231

Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Gln Asp Arg Asp Ser Leu Tyr Asn Val Gly
50 55

<210> 232

<211> 58

<212> PRT

<213> Homo sapiens

<400> 232

Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr His
1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg His Ser Leu Tyr Val Asn Gly
50 55

<210> 233

<211> 58

<212> PRT

343

<213> Homo sapiens

<400> 233

Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His
 1 5 10 15

Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 234

<211> 58

<212> PRT

<213> Homo sapiens

<400> 234

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His
 1 5 10 15

His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 50 55

<210> 235

<211> 58

344

<212> PRT

<213> Homo sapiens

<400> 235

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
 1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 50 55

<210> 236

<211> 58

<212> PRT

<213> Homo sapiens

<400> 236

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
 1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 50 55

<210> 237

345

<211> 58

<212> PRT

<213> Homo sapiens

<400> 237

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 238

<211> 58

<212> PRT

<213> Homo sapiens

<400> 238

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

346

<210> 239

<211> 58

<212> PRT

<213> Homo sapiens

<400> 239

Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu
35 40 45

Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly
50 55

<210> 240

<211> 58

<212> PRT

<213> Homo sapiens

<400> 240

Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

347

<210> 241

<211> 58

<212> PRT

<213> Homo sapiens

<400> 241

Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 242

<211> 58

<212> PRT

<213> Homo sapiens

<400> 242

Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu
1 5 10 15

Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr
35 40 45

348

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 243

<211> 58

<212> PRT

<213> Homo sapiens

<400> 243

Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu
 1 5 10 15

Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 50 55

<210> 244

<211> 58

<212> PRT

<213> Homo sapiens

<400> 244

Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
 1 5 10 15

Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 35 40 45

349

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 245

<211> 58

<212> PRT

<213> Homo sapiens

<400> 245

Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 246

<211> 58

<212> PRT

<213> Homo sapiens

<400> 246

Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

350

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly
50 55

<210> 247

<211> 58

<212> PRT

<213> Homo sapiens

<400> 247

Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His
1 5 10 15

His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly
50 55

<210> 248

<211> 58

<212> PRT

<213> Homo sapiens

<400> 248

Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr
1 5 10 15

Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His
20 25 30

351

Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser
 35 40 45

Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly
 50 55

<210> 249

<211> 58

<212> PRT

<213> Homo sapiens

<400> 249

Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr
 1 5 10 15

His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp
 20 25 30

Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val
 35 40 45

Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly
 50 55

<210> 250

<211> 12

<212> PRT

<213> Homo sapiens

<400> 250

Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
 1 5 10

352

<210> 251

<211> 12

<212> PRT

<213> Homo sapiens

<400> 251

Phe	Thr	His	Arg	Ser	Ser	Met	Pro	Thr	Thr	Ser	Ile
1				5					10		

<210> 252

<211> 12

<212> PRT

<213> Homo sapiens

<400> 252

Phe	Thr	His	Arg	Thr	Ser	Val	Pro	Thr	Ser	Ser	Thr
1				5					10		

<210> 253

<211> 12

<212> PRT

<213> Homo sapiens

<400> 253

Phe	Thr	His	Arg	Thr	Ser	Val	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 254

<211> 12

<212> PRT

353

<213> Homo sapiens

<400> 254

Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ser
1				5					10		

<210> 255

<211> 12

<212> PRT

<213> Homo sapiens

<400> 255

Phe	Thr	His	Arg	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr
1				5					10		

<210> 256

<211> 12

<212> PRT

<213> Homo sapiens

<400> 256

Phe	Thr	His	Arg	Ser	Ser	Val	Ala	Pro	Thr	Ser	Thr
1				5					10		

<210> 257

<211> 12

<212> PRT

<213> Homo sapiens

<400> 257

354

Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr
1 5 10

<210> 258

<211> 12

<212> PRT

<213> Homo sapiens

<400> 258

Phe Thr His Arg Ser Phe Gly Leu Thr Thr Ser Thr
1 5 10

<210> 259

<211> 12

<212> PRT

<213> Homo sapiens

<400> 259

Phe Thr His Arg Ser Ser Phe Leu Thr Thr Ser Thr
1 5 10

<210> 260

<211> 12

<212> PRT

<213> Homo sapiens

<400> 260

Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
1 5 10

<210> 261

355

<211> 12

<212> PRT

<213> Homo sapiens

<400> 261

Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile
1				5					10		

<210> 262

<211> 12

<212> PRT

<213> Homo sapiens

<400> 262

Phe	Thr	His	Gln	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr
1				5					10		

<210> 263

<211> 12

<212> PRT

<213> Homo sapiens

<400> 263

Phe	Thr	His	Gln	Thr	Ser	Ala	Pro	Asn	Thr	Ser	Thr
1				5					10		

<210> 264

<211> 12

<212> PRT

<213> Homo sapiens

356

<400> 264

Phe	Thr	His	Gln	Thr	Phe	Ala	Pro	Asn	Thr	Ser	Thr
1				5					10		

<210> 265

<211> 12

<212> PRT

<213> Homo sapiens

<400> 265

Phe	Thr	His	Gln	Asn	Ser	Val	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 266

<211> 12

<212> PRT

<213> Homo sapiens

<400> 266

Phe	Thr	His	Gln	Ser	Ser	Met	Thr	Thr	Thr	Arg	Thr
1				5					10		

<210> 267

<211> 12

<212> PRT

<213> Homo sapiens

<400> 267

Phe	Thr	His	Trp	Ile	Pro	Val	Pro	Thr	Ser	Ser	Thr
1				5					10		

357

<210> 268

<211> 12

<212> PRT

<213> Homo sapiens

<400> 268

Phe	Thr	His	Trp	Ser	Pro	Ile	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 269

<211> 12

<212> PRT

<213> Homo sapiens

<400> 269

Phe	Thr	His	Trp	Ser	Ser	Gly	Leu	Thr	Thr	Ser	Thr
1				5					10		

<210> 270

<211> 12

<212> PRT

<213> Homo sapiens

<400> 270

Phe	His	Pro	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 271

<211> 12

358

<212> PRT

<213> Homo sapiens

<400> 271

Phe	Asn	Pro	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 272

<211> 12

<212> PRT

<213> Homo sapiens

<400> 272

Phe	Asn	Pro	Trp	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 273

<211> 12

<212> PRT

<213> Homo sapiens

<400> 273

Phe	Thr	Gln	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile
1				5					10		

<210> 274

<211> 12

<212> PRT

<213> Homo sapiens

359

<400> 274

Phe	Thr	Gln	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr
1				5					10		

<210> 275

<211> 12

<212> PRT

<213> Homo sapiens

<400> 275

Phe	Thr	Gln	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Val
1				5					10		

<210> 276

<211> 12

<212> PRT

<213> Homo sapiens

<400> 276

Tyr	Asn	Glu	Pro	Gly	Leu	Asp	Glu	Pro	Pro	Thr	Thr
1				5					10		

<210> 277

<211> 12

<212> PRT

<213> Homo sapiens

<400> 277

Tyr	Ala	Pro	Gln	Asn	Leu	Ser	Ile	Arg	Gly	Glu	Tyr
1				5					10		

360

<210> 278

<211> 21

<212> PRT

<213> Homo sapiens

<400> 278

Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
1 5 10 15

Ser Pro Ser Pro Thr
20

<210> 279

<211> 23

<212> PRT

<213> Homo sapiens

<400> 279

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
1 5 10 15

Leu Ser Ser Pro Thr Ile Met
20

<210> 280

<211> 21

<212> PRT

<213> Homo sapiens

<400> 280

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser
1 5 10 15

361

Leu Pro Ser Pro Ala
20

<210> 281

<211> 20

<212> PRT

<213> Homo sapiens

<400> 281

Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
1 5 10 15

Pro Ser Pro Thr
20

<210> 282

<211> 20

<212> PRT

<213> Homo sapiens

<400> 282

Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Leu Pro
1 5 10 15

Ser Ser Pro Thr
20

<210> 283

<211> 21

<212> PRT

<213> Homo sapiens

362

<400> 283

Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Ser	Ser
1				5					10					15	

Leu	Pro	Ser	Pro	Thr
			20	

<210> 284

<211> 21

<212> PRT

<213> Homo sapiens

<400> 284

Pro	Gly	Thr	Pro	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Val	Ser
1				5					10					15	

Lys	Pro	Gly	Pro	Ser
			20	

<210> 285

<211> 21

<212> PRT

<213> Homo sapiens

<400> 285

Pro	Trp	Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Ser	Pro
1				5					10					15	

Val	Pro	Ser	Pro	Thr
			20	

<210> 286

363

<211> 21

<212> PRT

<213> Homo sapiens

<400> 286

Pro	Gly	Thr	Ser	Thr	Val	Tyr	Trp	Ala	Thr	Thr	Gly	Thr	Pro	Ser	Ser
1				5					10					15	

Phe	Pro	Gly	His	Thr
			20	

<210> 287

<211> 21

<212> PRT

<213> Homo sapiens

<400> 287

Pro	Gly	Thr	Ser	Thr	Val	His	Leu	Ala	Thr	Ser	Gly	Thr	Pro	Ser	Ser
1				5					10					15	

Leu	Pro	Gly	His	Thr
			20	

<210> 288

<211> 21

<212> PRT

<213> Homo sapiens

<400> 288

Pro	Gly	Thr	Ser	Thr	Val	His	Leu	Ala	Thr	Ser	Gly	Thr	Pro	Ser	Pro
1				5					10					15	

364

Leu Pro Gly His Thr
20

<210> 289

<211> 21

<212> PRT

<213> Homo sapiens

<400> 289

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
1 5 10 15

Leu Ser Gly Pro Thr
20

<210> 290

<211> 21

<212> PRT

<213> Homo sapiens

<400> 290

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser
1 5 10 15

Leu Pro Gly His Thr
20

<210> 291

<211> 21

<212> PRT

<213> Homo sapiens

365

<400> 291

Pro Gly Thr Ser Ala Val His Leu Glu Thr Thr Gly Thr Pro Ser Ser
1 5 10 15

Phe Pro Gly His Thr
20

<210> 292

<211> 21

<212> PRT

<213> Homo sapiens

<400> 292

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
1 5 10 15

Leu Pro Arg Pro Ile
20

<210> 293

<211> 21

<212> PRT

<213> Homo sapiens

<400> 293

Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly Ile Pro Pro Ser
1 5 10 15

Leu Pro Glu Thr Thr
20

<210> 294

<211> 21

366

<212> PRT

<213> Homo sapiens

<400> 294

Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser
1 5 10 15

Leu Pro Gly Pro Thr
20

<210> 295

<211> 21

<212> PRT

<213> Homo sapiens

<400> 295

Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser
1 5 10 15

Lys Pro Gly Pro Ser
20

<210> 296

<211> 21

<212> PRT

<213> Homo sapiens

<400> 296

Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser
1 5 10 15

Ile Phe Gly Pro Ser
20

367

<210> 297

<211> 16

<212> PRT

<213> Homo sapiens

<400> 297

Pro	Lys	Pro	Ala	Thr	Thr	Phe	Leu	Pro	Pro	Leu	Ser	Glu	Ala	Thr	Thr
1				5				10						15	

<210> 298

<211> 21

<212> PRT

<213> Homo sapiens

<400> 298

Gln	Ile	Asn	Phe	His	Ile	Val	Asn	Trp	Asn	Leu	Ser	Asn	Pro	Asp	Pro
1				5				10						15	

Thr	Ser	Ser	Glu	Tyr
			20	

<210> 299

<211> 1794

<212> PRT

<213> Homo sapiens

<400> 299

Met	Glu	His	Ile	Thr	Lys	Ile	Pro	Asn	Glu	Ala	Ala	His	Arg	Gly	Thr
1				5				10						15	

368

Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr Ser Pro Ala Ser Pro
 20 25 30

Lys Gly Leu His Thr Gly Gly Thr Lys Arg Met Glu Thr Thr Thr Thr
 35 40 45

Ala Leu Lys Thr Thr Thr Thr Ala Leu Lys Thr Thr Ser Arg Ala Thr
 50 55 60

Leu Thr Thr Ser Val Tyr Thr Pro Thr Leu Gly Thr Leu Thr Pro Leu
 65 70 75 80

Asn Ala Ser Arg Gln Met Ala Ser Thr Ile Leu Thr Glu Met Met Ile
 85 90 95

Thr Thr Pro Tyr Val Phe Pro Asp Val Pro Glu Thr Thr Ser Ser Leu
 100 105 110

Ala Thr Ser Leu Gly Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr
 115 120 125

Pro Ser Val Leu Asn Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser
 130 135 140

Arg Ser Gly Ala Glu Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser
 145 150 155 160

Ser Ser Glu Pro Asp Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu
 165 170 175

Thr Ile Pro Thr Val Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu
 180 185 190

Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His Gly Ala Asp Val Ser
 195 200 205

Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu Leu Asp Ala Leu Thr
 210 215 220

Pro Leu Val Thr Ile Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr
 225 230 235 240

370

Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val Ile Ser Thr Thr Ile
 450 455 460

Pro Ile Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met
 465 470 475 480

Ala Thr Ser His Gly Glu Glu Ala Ser Ser Ala Ile Pro Thr Pro Thr
 485 490 495

Val Ser Pro Gly Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser
 500 505 510

Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr Phe Ser Leu Gly
 515 520 525

Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Thr Glu Ala
 530 535 540

Gly Ser Ala Val Pro Thr Val Leu Pro Glu Val Pro Gly Met Val Thr
 545 550 555 560

Ser Leu Val Ala Ser Ser Arg Ala Val Thr Ser Thr Thr Leu Pro Thr
 565 570 575

Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr
 580 585 590

Ser His Gly Ala Glu Ala Ser Ser Thr Val Pro Thr Val Ser Pro Glu
 595 600 605

Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser Ser Gly Val Asn
 610 615 620

Ser Thr Ser Ile Pro Thr Leu Ile Leu Ser Pro Gly Glu Leu Glu Thr
 625 630 635 640

Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu Ala Ser Ser Ala Val
 645 650 655

Pro Thr Pro Thr Val Ser Pro Gly Val Ser Gly Val Val Thr Pro Leu
 660 665 670

371

Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr
 675 680 685

Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His
 690 695 700

Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val Ser Pro Glu Val Pro
 705 710 715 720

Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr
 725 730 735

Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu Pro Glu Thr Thr Thr
 740 745 750

Ser Leu Val Thr His Ser Glu Ala Lys Met Ile Ser Ala Ile Pro Thr
 755 760 765

Leu Ala Val Ser Pro Thr Val Gln Gly Leu Val Thr Ser Leu Val Thr
 770 775 780

Ser Ser Gly Ser Glu Thr Ser Ala Phe Ser Asn Leu Thr Val Ala Ser
 785 790 795 800

Ser Gln Pro Glu Thr Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu
 805 810 815

Ala Ser Ser Val Val Pro Thr Leu Thr Val Ser Thr Gly Glu Pro Phe
 820 825 830

Thr Asn Ile Ser Leu Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu
 835 840 845

Pro Arg Thr Thr Ser Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro
 850 855 860

Ser Thr Val Thr Ser Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr
 865 870 875 880

372

Thr Ile Ser Pro Gly Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser
 885 890 895

Ser Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro
 900 905 910

His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr His Pro Ala Val Thr
 915 920 925

Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr Ser His Ser Glu Pro
 930 935 940

Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu Ala Thr Ser
 945 950 955 960

Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val Pro Asp Met Val Thr
 965 970 975

Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser Ile Thr Ile Pro Thr
 980 985 990

Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr Thr Thr Ser Phe Ile Thr
 995 1000 1005

Tyr Ser Glu Thr His Thr Ser Ser Ala Ile Pro Thr Leu Pro Val
 1010 1015 1020

Ser Pro Gly Ala Ser Lys Met Leu Thr Ser Leu Val Ile Ser Ser
 1025 1030 1035

Gly Thr Asp Ser Thr Thr Thr Phe Pro Thr Leu Thr Glu Thr Pro
 1040 1045 1050

Tyr Glu Pro Glu Thr Thr Ala Ile Gln Leu Ile His Pro Ala Glu
 1055 1060 1065

Thr Asn Thr Met Val Pro Arg Thr Thr Pro Lys Phe Ser His Ser
 1070 1075 1080

Lys Ser Asp Thr Thr Leu Pro Val Ala Ile Thr Ser Pro Gly Pro
 1085 1090 1095

373

Glu Ala	Ser Ser	Ala Val	Ser	Thr Thr Thr	Ile Ser	Pro Asp Met
1100			1105		1110	
Ser Asp	Leu Val	Thr Ser	Leu	Val Pro Ser	Ser Gly	Thr Asp Thr
1115			1120		1125	
Ser Thr	Thr Phe	Pro Thr	Leu	Ser Glu Thr	Pro Tyr	Glu Pro Glu
1130			1135		1140	
Thr Thr	Ala Thr	Trp Leu	Thr	His Pro Ala	Glu Thr	Ser Thr Thr
1145			1150		1155	
Val Ser	Gly Thr	Ile Pro	Asn	Phe Ser His	Arg Gly	Ser Asp Thr
1160			1165		1170	
Ala Pro	Ser Met	Val Thr	Ser	Pro Gly Val	Asp Thr	Arg Ser Gly
1175			1180		1185	
Val Pro	Thr Thr	Thr Ile	Pro	Pro Ser Ile	Pro Gly	Val Val Thr
1190			1195		1200	
Ser Gln	Val Thr	Ser Ser	Ala	Thr Asp Thr	Ser Thr	Ala Ile Pro
1205			1210		1215	
Thr Leu	Thr Pro	Ser Pro	Gly	Glu Pro Glu	Thr Thr	Ala Ser Ser
1220			1225		1230	
Ala Thr	His Pro	Gly Thr	Gln	Thr Gly Phe	Thr Val	Pro Ile Arg
1235			1240		1245	
Thr Val	Pro Ser	Ser Glu	Pro	Asp Thr Met	Ala Ser	Trp Val Thr
1250			1255		1260	
His Pro	Pro Gln	Thr Ser	Thr	Pro Val Ser	Arg Thr	Thr Ser Ser
1265			1270		1275	
Phe Ser	His Ser	Ser Pro	Asp	Ala Thr Pro	Val Met	Ala Thr Ser
1280			1285		1290	

374

Pro Arg	Thr Glu	Ala Ser	Ser	Ala Val	Leu Thr	Thr	Ile Ser	Pro	1295	1300	1305
Gly Ala	Pro Glu	Met Val	Thr	Ser Gln	Ile Thr	Ser	Ser Gly	Ala	1310	1315	1320
Ala Thr	Ser Thr	Thr Val	Pro	Thr Leu	Thr His	Ser	Pro Gly	Met	1325	1330	1335
Pro Glu	Thr Thr	Ala Leu	Leu	Ser Thr	His Pro	Arg	Thr Glu	Thr	1340	1345	1350
Ser Lys	Thr Phe	Pro Ala	Ser	Thr Val	Phe Pro	Gln	Val Ser	Glu	1355	1360	1365
Thr Thr	Ala Ser	Leu Thr	Ile	Arg Pro	Gly Ala	Glu	Thr Ser	Thr	1370	1375	1380
Ala Leu	Pro Thr	Gln Thr	Thr	Ser Ser	Leu Phe	Thr	Leu Leu	Val	1385	1390	1395
Thr Gly	Thr Ser	Arg Val	Asp	Leu Ser	Pro Thr	Ala	Ser Pro	Gly	1400	1405	1410
Val Ser	Ala Lys	Thr Ala	Pro	Leu Ser	Thr His	Pro	Gly Thr	Glu	1415	1420	1425
Thr Ser	Thr Met	Ile Pro	Thr	Ser Thr	Leu Ser	Leu	Gly Leu	Leu	1430	1435	1440
Glu Thr	Thr Gly	Leu Leu	Ala	Thr Ser	Ser Ser	Ala	Glu Thr	Ser	1445	1450	1455
Thr Ser	Thr Leu	Thr Leu	Thr	Val Ser	Pro Ala	Val	Ser Gly	Leu	1460	1465	1470
Ser Ser	Ala Ser	Ile Thr	Thr	Asp Lys	Pro Gln	Thr	Val Thr	Ser	1475	1480	1485
Trp Asn	Thr Glu	Thr Ser	Pro	Ser Val	Thr Ser	Val	Gly Pro	Pro	1490	1495	1500

also be employed in the present invention.

water and water absorbing, and the like. Combinations of such polymers may

synthetic hydrophobic polymers modified by making these polymers insoluble in

melamine resin, polyurethane, polyester, and sodium polyacrylate, natural or

polyamide, polyacrylamide, polyethylene oxide, polyvinyl pyridine, polyvinyl

casein, cation starch, natural resins such as gum arabic and sodium alginate,

groups such as hydroxy or carboxy, cellulose polymers, starch, gelatin, albumin,

polyvinyl alcohol, acrylic polymers, copolymers which possess hydrophilic

be natural or synthetic and include, but are not limited to, polyvinyl pyrrolidone,

at least one cationic resin, or a combination thereof. Hydrophilic polymers may

wound rod, or any conventional coating method.

can be applied to the substrate by means of a roller coater, a knife coater, or

substantially non-porous layer. Coating compositions of the first coating layer

and/or dye or pigment components of the ink and are capable of forming a

may not be particularly limited if they function to absorb and capture the ink

properties compatible to the ink. The polymers comprising the first coating layer

and/or a light-transmissive polymer or resin having solubility and swelling

comprise a light-transmissive polymer or resin capable of absorbing the ink

be either transparent or translucent. Additionally, the first coating layer should

be view through the substrate, both the substrate and the first coating layer should

absorption are employed in the first coating layer. When the printed image is to

dye or pigment in the ink. Organic polymers with good water and solvent

commonly employed in backlit printing, and avoid or minimize bleeding of the

coating layer has the ability to quickly absorb relatively large amounts of ink,

porous and comprises at least one hydrophilic polymer. Accordingly, the first

As indicated above, the first coating layer is substantially non-

FIRST COATING LAYER

Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg
1685 1690 1695

25

20

15

10

5

376

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
 1700 1705 1710

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
 1715 1720 1725

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly
 1730 1735 1740

Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
 1745 1750 1755

Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
 1760 1765 1770

Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser
 1775 1780 1785

Ser Ser Pro Ser Pro Thr
 1790

<210> 300

<211> 284

<212> PRT

<213> Homo sapiens

<400> 300

Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
 1 5 10 15

Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
 20 25 30

Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
 35 40 45

Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
 50 55 60

0

377

Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
65 70 75 80

Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
85 90 95

Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
100 105 110

Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
115 120 125

Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
130 135 140

Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn
145 150 155 160

Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
165 170 175

Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr
180 185 190

Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val
195 200 205

Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn
210 215 220

Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu
225 230 235 240

Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg
245 250 255

Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly
260 265 270

378

Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
275 280

<210> 301

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 301
gtctctatgt caatggtttc accc

24

<210> 302

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 302
tagctgctct ctgtccagtc c

21

<210> 303

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

379

<400> 303
ggacaaggtc accacactct ac 22

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 304
gcagatcctc caggtctagg tgtg 24

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 305
gtctctatgt caatggtttc accc 24

<210> 306

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

380

<400> 306

tagctgctct ctgtccagtc c

21

<210> 307

<211> 468

<212> DNA

<213> Homo sapiens

<400> 307

actgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtat	60
gaggaggaca tgcacgccc tggatctagg aagttcaaca ccacagagag ggtcctgcag	120
ggtctgctta gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga	180
ctgacctctc tcaggtctga gaaggatgga gcagccactg gagggatgc catctgcac	240
catcatcttg accccaaaag ccctggactc aacagagagc ggctgtactg ggagctgagc	300
cgactgacca atggcatcaa agagctgggc ccctacacc tggacaggaa cagtctctat	360
gtcaatggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca	420
gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca	468

<210> 308

<211> 156

<212> PRT

<213> Homo sapiens

<400> 308

Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr
1				5				10						15	

Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	His	Arg	Pro	Gly	Ser	Arg	Lys	Phe
		20						25					30		

Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Ser	Pro	Ile	Phe	Lys
	35						40					45			

381

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu
 50 55 60

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile
 65 70 75 80

His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr
 85 90 95

Trp Glu Leu Ser Arg Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
 100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr
 115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
 130 135 140

Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro Ala
 145 150 155

<210> 309

<211> 31497

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (205)..(31497)

<223>

<400> 309
 aagcgttgca caattccccc aacctccata catacggcag ctcttctaga cacaggtttt 60
 cccaggtcaa atgcggggac cccagccata tctcccaccc tgagaaattt tggagtttca 120

382

gggagctcag aagctctgca gaggccaccc tctctgaggg gattcttctt agacctccat	180
ccagaggcaa atgttgacct gtcc atg ctg aaa ccc tca ggc ctt cct ggg	231
Met Leu Lys Pro Ser Gly Leu Pro Gly	
1 5	
tca tct tct ccc acc cgc tcc ttg atg aca ggg agc agg agc act aaa	279
Ser Ser Ser Pro Thr Arg Ser Leu Met Thr Gly Ser Arg Ser Thr Lys	
10 15 20 25	
gcc aca cca gaa atg gat tca gga ctg aca gga gcc acc ttg tca cct	327
Ala Thr Pro Glu Met Asp Ser Gly Leu Thr Gly Ala Thr Leu Ser Pro	
30 35 40	
aag aca tct aca ggt gca atc gtg gtg aca gaa cat act ctg ccc ttt	375
Lys Thr Ser Thr Gly Ala Ile Val Val Thr Glu His Thr Leu Pro Phe	
45 50 55	
act tcc cca gat aag acc ttg gcc agt cct aca tct tcg gtt gtg gga	423
Thr Ser Pro Asp Lys Thr Leu Ala Ser Pro Thr Ser Ser Val Val Gly	
60 65 70	
aga acc acc cag tct ttg ggg gtg atg tcc tct gct ctc cct gag tca	471
Arg Thr Thr Gln Ser Leu Gly Val Met Ser Ser Ala Leu Pro Glu Ser	
75 80 85	
acc tct aga gga atg aca cac tcc gag caa aga acc agc cca tcg ctg	519
Thr Ser Arg Gly Met Thr His Ser Glu Gln Arg Thr Ser Pro Ser Leu	
90 95 100 105	
agt ccc cag gtc aat gga act ccc tct agg aac tac cct gct aca agc	567
Ser Pro Gln Val Asn Gly Thr Pro Ser Arg Asn Tyr Pro Ala Thr Ser	
110 115 120	
atg gtt tca gga ttg agt tcc cca agg acc agg acc agt tcc aca gaa	615
Met Val Ser Gly Leu Ser Ser Pro Arg Thr Arg Thr Ser Ser Thr Glu	
125 130 135	
gga aat ttt acc aaa gaa gca tct aca tac aca ctc act gta gag acc	663
Gly Asn Phe Thr Lys Glu Ala Ser Thr Tyr Thr Leu Thr Val Glu Thr	
140 145 150	
aca agt ggc cca gtc act gag aag tac aca gtc ccc act gag acc tca	711
Thr Ser Gly Pro Val Thr Glu Lys Tyr Thr Val Pro Thr Glu Thr Ser	
155 160 165	
aca act gaa ggt gac agc aca gag acc ccc tgg gac aca aga tat att	759
Thr Thr Glu Gly Asp Ser Thr Glu Thr Pro Trp Asp Thr Arg Tyr Ile	
170 175 180 185	
cct gta aaa atc aca tct cca atg aaa aca ttt gca gat tca act gca	807
Pro Val Lys Ile Thr Ser Pro Met Lys Thr Phe Ala Asp Ser Thr Ala	
190 195 200	

383

tcc aag gaa aat gcc cca gtg tct atg act cca gct gag acc aca gtt Ser Lys Glu Asn Ala Pro Val Ser Met Thr Pro Ala Glu Thr Thr Val 205 210 215	855
act gac tca cat act cca gga agg aca aac cca tca ttt ggg aca ctt Thr Asp Ser His Thr Pro Gly Arg Thr Asn Pro Ser Phe Gly Thr Leu 220 225 230	903
tat tct tcc ttc ctt gac cta tca cct aaa ggg acc cca aat tcc aga Tyr Ser Ser Phe Leu Asp Leu Ser Pro Lys Gly Thr Pro Asn Ser Arg 235 240 245	951
ggt gaa aca agc ctg gaa ctg att cta tca acc act gga tat ccc ttc Gly Glu Thr Ser Leu Glu Leu Ile Leu Ser Thr Thr Gly Tyr Pro Phe 250 255 260 265	999
tcc tct cct gaa cct ggc tct gca gga cac agc aga ata agt acc agt Ser Ser Pro Glu Pro Gly Ser Ala Gly His Ser Arg Ile Ser Thr Ser 270 275 280	1047
gcg cct ttg tca tca tct gct tca gtt ctc gat aat aaa ata tca gag Ala Pro Leu Ser Ser Ser Ala Ser Val Leu Asp Asn Lys Ile Ser Glu 285 290 295	1095
acc agc ata ttc tca ggc cag agt ctc acc tcc cct ctg tct cct ggg Thr Ser Ile Phe Ser Gly Gln Ser Leu Thr Ser Pro Leu Ser Pro Gly 300 305 310	1143
gtg ccc gag gcc aga gcc agc aca atg ccc aac tca gct atc cct ttt Val Pro Glu Ala Arg Ala Ser Thr Met Pro Asn Ser Ala Ile Pro Phe 315 320 325	1191
tcc atg aca cta agc aat gca gaa aca agt gcc gaa agg gtc aga agc Ser Met Thr Leu Ser Asn Ala Glu Thr Ser Ala Glu Arg Val Arg Ser 330 335 340 345	1239
aca att tcc tct ctg ggg act cca tca ata tcc aca aag cag aca gca Thr Ile Ser Ser Leu Gly Thr Pro Ser Ile Ser Thr Lys Gln Thr Ala 350 355 360	1287
gag act atc ctt acc ttc cat gcc ttc gct gag acc atg gat ata ccc Glu Thr Ile Leu Thr Phe His Ala Phe Ala Glu Thr Met Asp Ile Pro 365 370 375	1335
agc acc cac ata gcc aag act ttg gct tca gaa tgg ttg gga agt cca Ser Thr His Ile Ala Lys Thr Leu Ala Ser Glu Trp Leu Gly Ser Pro 380 385 390	1383
ggt acc ctt ggt ggc acc agc act tca gcg ctg aca acc aca tct cca Gly Thr Leu Gly Gly Thr Ser Thr Ser Ala Leu Thr Thr Thr Ser Pro 395 400 405	1431
tct acc act tta gtc tca gag gag acc aac acc cat cac tcc acg agt	1479

384

Ser Thr Thr Leu Val	Ser Glu Glu Thr Asn Thr His His Ser Thr Ser	
410	415 420 425	
gga aag gaa aca gaa gga act ttg aat aca tct atg act cca ctt gag		1527
Gly Lys Glu Thr Glu Gly Thr Leu Asn Thr Ser Met Thr Pro Leu Glu		
430	435 440	
acc tct gct cct gga gaa gag tcc gaa atg act gcc acc ttg gtc ccc		1575
Thr Ser Ala Pro Gly Glu Glu Ser Glu Met Thr Ala Thr Leu Val Pro		
445	450 455	
act cta ggt ttt aca act ctt gac agc aag atc aga agt cca tct cag		1623
Thr Leu Gly Phe Thr Thr Leu Asp Ser Lys Ile Arg Ser Pro Ser Gln		
460	465 470	
gtc tct tca tcc cac cca aca aga gag ctc aga acc aca ggc agc acc		1671
Val Ser Ser Ser His Pro Thr Arg Glu Leu Arg Thr Thr Gly Ser Thr		
475	480 485	
tct ggg agg cag agt tcc agc aca gct gcc cac ggg agc tct gac atc		1719
Ser Gly Arg Gln Ser Ser Ser Thr Ala Ala His Gly Ser Ser Asp Ile		
490	495 500 505	
ctg agg gca acc act tcc agc acc tca aaa gca tca tca tgg acc agt		1767
Leu Arg Ala Thr Thr Ser Ser Thr Ser Lys Ala Ser Ser Trp Thr Ser		
510	515 520	
gaa agc aca gct cag caa ttt agt gaa ccc cag cac aca cag tgg gtg		1815
Glu Ser Thr Ala Gln Gln Phe Ser Glu Pro Gln His Thr Gln Trp Val		
525	530 535	
gag aca agt cct agc atg aaa aca gag aga ccc cca gca tca acc agt		1863
Glu Thr Ser Pro Ser Met Lys Thr Glu Arg Pro Pro Ala Ser Thr Ser		
540	545 550	
gtg gca gcc cct atc acc act tct gtt ccc tca gtg gtc tct ggc ttc		1911
Val Ala Ala Pro Ile Thr Thr Ser Val Pro Ser Val Val Ser Gly Phe		
555	560 565	
acc acc ctg aag acc agc tcc aca aaa ggg att tgg ctt gaa gaa aca		1959
Thr Thr Leu Lys Thr Ser Ser Thr Lys Gly Ile Trp Leu Glu Glu Thr		
570	575 580 585	
tct gca gac aca ctc atc gga gaa tcc aca gct ggc cca acc acc cat		2007
Ser Ala Asp Thr Leu Ile Gly Glu Ser Thr Ala Gly Pro Thr Thr His		
590	595 600	
cag ttt gct gtt ccc act ggg att tca atg aca gga ggc agc agc acc		2055
Gln Phe Ala Val Pro Thr Gly Ile Ser Met Thr Gly Gly Ser Ser Thr		
605	610 615	
agg gga agc cag ggc aca acc cac cta ctc acc aga gcc aca gca tca		2103
Arg Gly Ser Gln Gly Thr Thr His Leu Leu Thr Arg Ala Thr Ala Ser		
620	625 630	

385

tct gag aca tcc gca gat ttg act ctg gcc acg aac ggt gtc cca gtc	2151
Ser Glu Thr Ser Ala Asp Leu Thr Leu Ala Thr Asn Gly Val Pro Val	
635 640 645	
tcc gtg tct cca gca gtg agc aag acg gct gct ggc tca agt cct cca	2199
Ser Val Ser Pro Ala Val Ser Lys Thr Ala Ala Gly Ser Ser Pro Pro	
650 655 660 665	
gga ggg aca aag cca tca tat aca atg gtt tct tct gtc atc cct gag	2247
Gly Gly Thr Lys Pro Ser Tyr Thr Met Val Ser Ser Val Ile Pro Glu	
670 675 680	
aca tca tct cta cag tcc tca gct ttc agg gaa gga acc agc ctg gga	2295
Thr Ser Ser Leu Gln Ser Ser Ala Phe Arg Glu Gly Thr Ser Leu Gly	
685 690 695	
ctg act cca tta aac act aga cat ccc ttc tct tcc cct gaa cca gac	2343
Leu Thr Pro Leu Asn Thr Arg His Pro Phe Ser Ser Pro Glu Pro Asp	
700 705 710	
tct gca gga cac acc aag ata agc acc agc att cct ctg ttg tca tct	2391
Ser Ala Gly His Thr Lys Ile Ser Thr Ser Ile Pro Leu Leu Ser Ser	
715 720 725	
gct tca gtt ctt gag gat aaa gtg tca gcg acc agc aca ttc tca cac	2439
Ala Ser Val Leu Glu Asp Lys Val Ser Ala Thr Ser Thr Phe Ser His	
730 735 740 745	
cac aaa gcc acc tca tct att acc aca ggg act cct gaa atc tca aca	2487
His Lys Ala Thr Ser Ser Ile Thr Thr Gly Thr Pro Glu Ile Ser Thr	
750 755 760	
aag aca aag ccc agc tca gcc gtt ctt tcc tcc atg acc cta agc aat	2535
Lys Thr Lys Pro Ser Ser Ala Val Leu Ser Ser Met Thr Leu Ser Asn	
765 770 775	
gca gca aca agt cct gaa aga gtc aga aat gca act tcc cct ctg act	2583
Ala Ala Thr Ser Pro Glu Arg Val Arg Asn Ala Thr Ser Pro Leu Thr	
780 785 790	
cat cca tct cca tca ggg gaa gag aca gca ggg agt gtc ctc act ctc	2631
His Pro Ser Pro Ser Gly Glu Glu Thr Ala Gly Ser Val Leu Thr Leu	
795 800 805	
agc acc tct gct gag act aca gac tca cct aac atc cac cca act ggg	2679
Ser Thr Ser Ala Glu Thr Thr Asp Ser Pro Asn Ile His Pro Thr Gly	
810 815 820 825	
aca ctg act tca gaa tcg tca gag agt cct agc act ctc agc ctc cca	2727
Thr Leu Thr Ser Glu Ser Ser Glu Ser Pro Ser Thr Leu Ser Leu Pro	
830 835 840	
agt gtc tct gga gtc aaa acc aca ttt tct tca tct act cct tcc act	2775

386

Ser Val Ser Gly Val Lys Thr Thr Phe Ser Ser Ser Thr Pro Ser Thr	
845 850 855	
cat cta ttt act agt gga gaa gaa aca gag gaa act tcg aat cca tct	2823
His Leu Phe Thr Ser Gly Glu Glu Thr Glu Glu Thr Ser Asn Pro Ser	
860 865 870	
gtg tct caa cct gag act tct gtt tcc aga gta agg acc acc ttg gcc	2871
Val Ser Gln Pro Glu Thr Ser Val Ser Arg Val Arg Thr Thr Leu Ala	
875 880 885	
agc acc tct gtc cct acc cca gta ttc ccc acc atg gac acc tgg cct	2919
Ser Thr Ser Val Pro Thr Pro Val Phe Pro Thr Met Asp Thr Trp Pro	
890 895 900 905	
aca cgt tca gct cag ttc tct tca tcc cac cta gtg agt gag ctc aga	2967
Thr Arg Ser Ala Gln Phe Ser Ser Ser His Leu Val Ser Glu Leu Arg	
910 915 920	
gct acg agc agt acc tca gtt aca aac tca act ggt tca gct ctt cct	3015
Ala Thr Ser Ser Thr Ser Val Thr Asn Ser Thr Gly Ser Ala Leu Pro	
925 930 935	
aaa ata tct cac ctc act ggg acg gca aca atg tca cag acc aat aga	3063
Lys Ile Ser His Leu Thr Gly Thr Ala Thr Met Ser Gln Thr Asn Arg	
940 945 950	
gac acg ttt aat gac tct gct gca ccc caa agc aca act tgg cca gag	3111
Asp Thr Phe Asn Asp Ser Ala Ala Pro Gln Ser Thr Thr Trp Pro Glu	
955 960 965	
act agt ccc aga ttc aag aca ggg tta cct tca gca aca acc act gtt	3159
Thr Ser Pro Arg Phe Lys Thr Gly Leu Pro Ser Ala Thr Thr Thr Val	
970 975 980 985	
tca acc tct gcc act tct ctc tct gct act gta atg gtc tct aaa ttc	3207
Ser Thr Ser Ala Thr Ser Leu Ser Ala Thr Val Met Val Ser Lys Phe	
990 995 1000	
act tct cca gca act agt tcc atg gaa gca act tct atc agg gaa	3252
Thr Ser Pro Ala Thr Ser Ser Met Glu Ala Thr Ser Ile Arg Glu	
1005 1010 1015	
cca tca aca acc atc ctc aca aca gag acc acg aat ggc cca ggc	3297
Pro Ser Thr Thr Ile Leu Thr Thr Glu Thr Thr Asn Gly Pro Gly	
1020 1025 1030	
tct atg gct gtg gct tct acc aac atc cca att gga aag ggc tac	3342
Ser Met Ala Val Ala Ser Thr Asn Ile Pro Ile Gly Lys Gly Tyr	
1035 1040 1045	
att act gaa gga aga ttg gac aca agc cat ctg ccc att gga acc	3387
Ile Thr Glu Gly Arg Leu Asp Thr Ser His Leu Pro Ile Gly Thr	
1050 1055 1060	

387

aca gct tcc tct	gag aca tct atg gat	ttt acc atg gcc aaa gaa	3432
Thr Ala Ser Ser	Glu Thr Ser Met Asp	Phe Thr Met Ala Lys Glu	
1065	1070	1075	
agt gtc tca atg	tca gta tct cca tct	cag tcc atg gat gct gct	3477
Ser Val Ser Met	Ser Val Ser Pro Ser	Gln Ser Met Asp Ala Ala	
1080	1085	1090	
ggc tca agc act	cca gga agg aca agc	caa ttc gtt gac aca ttt	3522
Gly Ser Ser Thr	Pro Gly Arg Thr Ser	Gln Phe Val Asp Thr Phe	
1095	1100	1105	
tct gat gat gtc	tat cat tta aca tcc	aga gaa att aca ata cct	3567
Ser Asp Asp Val	Tyr His Leu Thr Ser	Arg Glu Ile Thr Ile Pro	
1110	1115	1120	
aga gat gga aca	agc tca gct ctg act	cca caa atg act gca act	3612
Arg Asp Gly Thr	Ser Ser Ala Leu Thr	Pro Gln Met Thr Ala Thr	
1125	1130	1135	
cac cct cca tct	cct gat cct ggc tct	gct aga agc acc tgg ctt	3657
His Pro Pro Ser	Pro Asp Pro Gly Ser	Ala Arg Ser Thr Trp Leu	
1140	1145	1150	
ggc atc ttg tcc	tca tct cct tct tct	cct act ccc aaa gtc aca	3702
Gly Ile Leu Ser	Ser Ser Pro Ser Ser	Pro Thr Pro Lys Val Thr	
1155	1160	1165	
atg agc tcc aca	ttt tca act cag aga	gtc acc aca agc atg ata	3747
Met Ser Ser Thr	Phe Ser Thr Gln Arg	Val Thr Thr Ser Met Ile	
1170	1175	1180	
atg gac aca gtt	gaa act agt cgg tgg	aac atg ccc aac tta cct	3792
Met Asp Thr Val	Glu Thr Ser Arg Trp	Asn Met Pro Asn Leu Pro	
1185	1190	1195	
tcc acg act tcc	ctg aca cca agt aat	att cca aca agt ggt gcc	3837
Ser Thr Thr Ser	Leu Thr Pro Ser Asn	Ile Pro Thr Ser Gly Ala	
1200	1205	1210	
ata gga aaa agc	acc ctg gtt ccc ttg	gac act cca tct cca gcc	3882
Ile Gly Lys Ser	Thr Leu Val Pro Leu	Asp Thr Pro Ser Pro Ala	
1215	1220	1225	
aca tca ttg gag	gca tca gaa ggg gga	ctt cca acc ctc agc acc	3927
Thr Ser Leu Glu	Ala Ser Glu Gly Gly	Leu Pro Thr Leu Ser Thr	
1230	1235	1240	
tac cct gaa tca	aca aac aca ccc agc	atc cac ctc gga gca cac	3972
Tyr Pro Glu Ser	Thr Asn Thr Pro Ser	Ile His Leu Gly Ala His	
1245	1250	1255	
gct agt tca gaa	agt cca agc acc atc	aaa ctt acc atg gct tca	4017

388

Ala Ser Ser Glu	Ser Pro Ser Thr	Ile	Lys Leu Thr Met	Ala Ser	
1260		1265		1270	
gta gta aaa cct	ggc tct tac aca	cct	ctc acc ttc ccc	tca ata	4062
Val Val Lys Pro	Gly Ser Tyr Thr	Pro	Leu Thr Phe Pro	Ser Ile	
1275		1280		1285	
gag acc cac att	cat gta tca aca	gcc	aga atg gct tac	tct tct	4107
Glu Thr His Ile	His Val Ser Thr	Ala	Arg Met Ala Tyr	Ser Ser	
1290		1295		1300	
ggg tct tca cct	gag atg aca gct	cct	gga gag act aac	act ggt	4152
Gly Ser Ser Pro	Glu Met Thr Ala	Pro	Gly Glu Thr Asn	Thr Gly	
1305		1310		1315	
agt acc tgg gac	ccc acc acc tac	atc	acc act acg gat	cct aag	4197
Ser Thr Trp Asp	Pro Thr Thr Tyr	Ile	Thr Thr Thr Asp	Pro Lys	
1320		1325		1330	
gat aca agt tca	gct cag gtc tct	aca	ccc cac tca gtg	agg aca	4242
Asp Thr Ser Ser	Ala Gln Val Ser	Thr	Pro His Ser Val	Arg Thr	
1335		1340		1345	
ctc aga acc aca	gaa aac cat cca	aag	aca gag tcc gcc	acc cca	4287
Leu Arg Thr Thr	Glu Asn His Pro	Lys	Thr Glu Ser Ala	Thr Pro	
1350		1355		1360	
gct gct tac tct	gga agt cct aaa	atc	tca agt tca ccc	aat ctc	4332
Ala Ala Tyr Ser	Gly Ser Pro Lys	Ile	Ser Ser Ser Pro	Asn Leu	
1365		1370		1375	
acc agt ccg gcc	aca aaa gca tgg	acc	atc aca gac aca	act gaa	4377
Thr Ser Pro Ala	Thr Lys Ala Trp	Thr	Ile Thr Asp Thr	Thr Glu	
1380		1385		1390	
cac tcc act caa	tta cat tac aca	aaa	ttg gca gaa aaa	tca tct	4422
His Ser Thr Gln	Leu His Tyr Thr	Lys	Leu Ala Glu Lys	Ser Ser	
1395		1400		1405	
gga ttt gag aca	cag tca gct cca	gga	cct gtc tct gta	gta atc	4467
Gly Phe Glu Thr	Gln Ser Ala Pro	Gly	Pro Val Ser Val	Val Ile	
1410		1415		1420	
cct acc tcc cct	acc att gga agc	agc	aca ttg gaa cta	act tct	4512
Pro Thr Ser Pro	Thr Ile Gly Ser	Ser	Thr Leu Glu Leu	Thr Ser	
1425		1430		1435	
gat gtc cca ggg	gaa ccc ctg gtc	ctt	gct ccc agt gag	cag acc	4557
Asp Val Pro Gly	Glu Pro Leu Val	Leu	Ala Pro Ser Glu	Gln Thr	
1440		1445		1450	
aca atc act ctc	ccc atg gca aca	tgg	ctg agt acc agt	ttg aca	4602
Thr Ile Thr Leu	Pro Met Ala Thr	Trp	Leu Ser Thr Ser	Leu Thr	
1455		1460		1465	

389

gag gaa atg gct	tca aca gac ctt gat	att tca agt cca agt tca	4647
Glu Glu Met Ala	Ser Thr Asp Leu Asp	Ile Ser Ser Pro Ser Ser	
1470	1475	1480	
ccc atg agt aca	ttt gct att ttt cca	cct atg tcc aca cct tct	4692
Pro Met Ser Thr	Phe Ala Ile Phe Pro	Pro Met Ser Thr Pro Ser	
1485	1490	1495	
cat gaa ctt tca	aag tca gag gca gat	acc agt gcc att aga aat	4737
His Glu Leu Ser	Lys Ser Glu Ala Asp	Thr Ser Ala Ile Arg Asn	
1500	1505	1510	
aca gat tca aca	acg ttg gat cag cac	cta gga atc agg agt ttg	4782
Thr Asp Ser Thr	Thr Leu Asp Gln His	Leu Gly Ile Arg Ser Leu	
1515	1520	1525	
ggc aga act ggg	gac tta aca act gtt	cct atc acc cca ctg aca	4827
Gly Arg Thr Gly	Asp Leu Thr Thr Val	Pro Ile Thr Pro Leu Thr	
1530	1535	1540	
acc acg tgg acc	agt gtg att gaa cac	tca aca caa gca cag gac	4872
Thr Thr Trp Thr	Ser Val Ile Glu His	Ser Thr Gln Ala Gln Asp	
1545	1550	1555	
acc ctt tct gca	acg atg agt cct act	cac gtg aca cag tca ctc	4917
Thr Leu Ser Ala	Thr Met Ser Pro Thr	His Val Thr Gln Ser Leu	
1560	1565	1570	
aaa gat caa aca	tct ata cca gcc tca	gca tcc cct tcc cat ctt	4962
Lys Asp Gln Thr	Ser Ile Pro Ala Ser	Ala Ser Pro Ser His Leu	
1575	1580	1585	
act gaa gtc tac	cct gag ctc ggg aca	caa ggg aga agc tcc tct	5007
Thr Glu Val Tyr	Pro Glu Leu Gly Thr	Gln Gly Arg Ser Ser Ser	
1590	1595	1600	
gag gca acc act	ttt tgg aaa cca tct	aca gac aca ctg tcc aga	5052
Glu Ala Thr Thr	Phe Trp Lys Pro Ser	Thr Asp Thr Leu Ser Arg	
1605	1610	1615	
gag att gag act	ggc cca aca aac att	caa tcc act cca ccc atg	5097
Glu Ile Glu Thr	Gly Pro Thr Asn Ile	Gln Ser Thr Pro Pro Met	
1620	1625	1630	
gac aac aca aca	aca ggg agc agt agt	agt gga gtc acc ctg ggc	5142
Asp Asn Thr Thr	Thr Gly Ser Ser Ser	Ser Gly Val Thr Leu Gly	
1635	1640	1645	
ata gcc cac ctt	ccc ata gga aca tcc	tcc cca gct gag aca tcc	5187
Ile Ala His Leu	Pro Ile Gly Thr Ser	Ser Pro Ala Glu Thr Ser	
1650	1655	1660	
aca aac atg gca	ctg gaa aga aga agt	tct aca gcc act gtc tct	5232

390

Thr Asn Met	Ala	Leu Glu Arg Arg	Ser	Ser Thr Ala Thr Val	Ser	
	1665		1670		1675	
atg gct ggg	aca	atg gga ctc ctt gtt	act agt gct cca gga	aga		5277
Met Ala Gly	Thr	Met Gly Leu Leu Val	Thr Ser Ala Pro Gly	Arg		
	1680		1685	1690		
agc atc agc	cag	tca tta gga aga gtt	tcc tct gtc ctt tct	gag		5322
Ser Ile Ser	Gln	Ser Leu Gly Arg Val	Ser Ser Val Leu Ser	Glu		
	1695		1700	1705		
tca act act	gaa	gga gtc aca gat tct	agt aag gga agc agc	cca		5367
Ser Thr Thr	Glu	Gly Val Thr Asp Ser	Ser Lys Gly Ser Ser	Pro		
	1710		1715	1720		
agg ctg aac	aca	cag gga aat aca gct	ctc tcc tcc tct ctt	gaa		5412
Arg Leu Asn	Thr	Gln Gly Asn Thr Ala	Leu Ser Ser Ser Leu	Glu		
	1725		1730	1735		
ccc agc tat	gct	gaa gga agc cag atg	agc aca agc atc cct	cta		5457
Pro Ser Tyr	Ala	Glu Gly Ser Gln Met	Ser Thr Ser Ile Pro	Leu		
	1740		1745	1750		
acc tca tct	cct	aca act cct gat gtg	gaa ttc ata ggg ggc	agc		5502
Thr Ser Ser	Pro	Thr Thr Pro Asp Val	Glu Phe Ile Gly Gly	Ser		
	1755		1760	1765		
aca ttt tgg	acc	aag gag gtc acc aca	gtt atg acc tca gac	atc		5547
Thr Phe Trp	Thr	Lys Glu Val Thr Thr	Val Met Thr Ser Asp	Ile		
	1770		1775	1780		
tcc aag tct	tca	gca agg aca gag tcc	agc tca gct acc ctt	atg		5592
Ser Lys Ser	Ser	Ala Arg Thr Glu Ser	Ser Ser Ala Thr Leu	Met		
	1785		1790	1795		
tcc aca gct	ttg	gga agc act gaa aat	aca gga aaa gaa aaa	ctc		5637
Ser Thr Ala	Leu	Gly Ser Thr Glu Asn	Thr Gly Lys Glu Lys	Leu		
	1800		1805	1810		
aga act gcc	tct	atg gat ctt cca tct	cca act cca tca atg	gag		5682
Arg Thr Ala	Ser	Met Asp Leu Pro Ser	Pro Thr Pro Ser Met	Glu		
	1815		1820	1825		
gtg aca cca	tgg	att tct ctc act ctc	agt aat gcc ccc aat	acc		5727
Val Thr Pro	Trp	Ile Ser Leu Thr Leu	Ser Asn Ala Pro Asn	Thr		
	1830		1835	1840		
aca gat tca	ctt	gac ctc agc cat ggg	gtg cac acc agc tct	gca		5772
Thr Asp Ser	Leu	Asp Leu Ser His Gly	Val His Thr Ser Ser	Ala		
	1845		1850	1855		
ggg act ttg	gcc	act gac agg tca ttg	aat act ggt gtc act	aga		5817
Gly Thr Leu	Ala	Thr Asp Arg Ser Leu	Asn Thr Gly Val Thr	Arg		
	1860		1865	1870		

391

gcc tcc aga ttg	gaa aac ggc tct gat	acc tct tct aag tcc ctg	5862
Ala Ser Arg Leu	Glu Asn Gly Ser Asp	Thr Ser Ser Lys Ser Leu	
1875	1880	1885	
tct atg gga aac	agc act cac act tcc	atg act gac aca gag aag	5907
Ser Met Gly Asn	Ser Thr His Thr Ser	Met Thr Asp Thr Glu Lys	
1890	1895	1900	
agt gaa gtg tct	tct tca atc cat ccc	cga cct gag acc tca gct	5952
Ser Glu Val Ser	Ser Ser Ile His Pro	Arg Pro Glu Thr Ser Ala	
1905	1910	1915	
cct gga gca gag	acc act ttg act tcc	act cct gga aac agg gcc	5997
Pro Gly Ala Glu	Thr Thr Leu Thr Ser	Thr Pro Gly Asn Arg Ala	
1920	1925	1930	
ata agc tta aca	ttg cct ttt tca tcc	att cca gtg gaa gaa gtc	6042
Ile Ser Leu Thr	Leu Pro Phe Ser Ser	Ile Pro Val Glu Glu Val	
1935	1940	1945	
att tct aca ggc	ata acc tca gga cca	gac atc aac tca gca ccc	6087
Ile Ser Thr Gly	Ile Thr Ser Gly Pro	Asp Ile Asn Ser Ala Pro	
1950	1955	1960	
atg aca cat tct	ccc atc acc cca cca	aca att gta tgg acc agt	6132
Met Thr His Ser	Pro Ile Thr Pro Pro	Thr Ile Val Trp Thr Ser	
1965	1970	1975	
aca ggc aca att	gaa cag tcc act caa	cca cta cat gca gtt tct	6177
Thr Gly Thr Ile	Glu Gln Ser Thr Gln	Pro Leu His Ala Val Ser	
1980	1985	1990	
tca gaa aaa gtt	tct gtg cag aca cag	tca act cca tat gtc aac	6222
Ser Glu Lys Val	Ser Val Gln Thr Gln	Ser Thr Pro Tyr Val Asn	
1995	2000	2005	
tct gtg gca gtg	tct gct tcc cct acc	cat gag aat tca gtc tct	6267
Ser Val Ala Val	Ser Ala Ser Pro Thr	His Glu Asn Ser Val Ser	
2010	2015	2020	
tct gga agc agc	aca tcc tct cca tat	tcc tca gcc tca ctt gaa	6312
Ser Gly Ser Ser	Thr Ser Ser Pro Tyr	Ser Ser Ala Ser Leu Glu	
2025	2030	2035	
tcc ttg gat tcc	aca atc agt agg agg	aat gca atc act tcc tgg	6357
Ser Leu Asp Ser	Thr Ile Ser Arg Arg	Asn Ala Ile Thr Ser Trp	
2040	2045	2050	
cta tgg gac ctc	act aca tct ctc ccc	act aca act tgg cca agt	6402
Leu Trp Asp Leu	Thr Thr Ser Leu Pro	Thr Thr Thr Trp Pro Ser	
2055	2060	2065	
act agt tta tct	gag gca ctg tcc tca	ggc cat tct ggg gtt tca	6447

392

Thr	Ser	Leu	Ser	Glu	Ala	Leu	Ser	Ser	Gly	His	Ser	Gly	Val	Ser	
			2070					2075					2080		
aac	cca	agt	tca	act	acg	act	gaa	ttt	cca	ctc	ttt	tca	gct	gca	6492
Asn	Pro	Ser	Ser	Thr	Thr	Thr	Glu	Phe	Pro	Leu	Phe	Ser	Ala	Ala	
			2085					2090					2095		
tcc	aca	tct	gct	gct	aag	caa	aga	aat	cca	gaa	aca	gag	acc	cat	6537
Ser	Thr	Ser	Ala	Ala	Lys	Gln	Arg	Asn	Pro	Glu	Thr	Glu	Thr	His	
			2100					2105					2110		
ggt	ccc	cag	aat	aca	gcc	gcg	agt	act	ttg	aac	act	gat	gca	tcc	6582
Gly	Pro	Gln	Asn	Thr	Ala	Ala	Ser	Thr	Leu	Asn	Thr	Asp	Ala	Ser	
			2115					2120					2125		
tcg	gtc	aca	ggt	ctt	tct	gag	act	cct	gtg	ggg	gca	agt	atc	agc	6627
Ser	Val	Thr	Gly	Leu	Ser	Glu	Thr	Pro	Val	Gly	Ala	Ser	Ile	Ser	
			2130					2135					2140		
tct	gaa	gtc	cct	ctt	cca	atg	gcc	ata	act	tct	aga	tca	gat	gtt	6672
Ser	Glu	Val	Pro	Leu	Pro	Met	Ala	Ile	Thr	Ser	Arg	Ser	Asp	Val	
			2145					2150					2155		
tct	ggc	ctt	aca	tct	gag	agt	act	gct	aac	ccg	agt	tta	ggc	aca	6717
Ser	Gly	Leu	Thr	Ser	Glu	Ser	Thr	Ala	Asn	Pro	Ser	Leu	Gly	Thr	
			2160					2165					2170		
gcc	tct	tca	gca	ggg	acc	aaa	tta	act	agg	aca	ata	tcc	ctg	ccc	6762
Ala	Ser	Ser	Ala	Gly	Thr	Lys	Leu	Thr	Arg	Thr	Ile	Ser	Leu	Pro	
			2175					2180					2185		
act	tca	gag	tct	ttg	gtt	tcc	ttt	aga	atg	aac	aag	gat	cca	tgg	6807
Thr	Ser	Glu	Ser	Leu	Val	Ser	Phe	Arg	Met	Asn	Lys	Asp	Pro	Trp	
			2190					2195					2200		
aca	gtg	tca	atc	cct	ttg	ggg	tcc	cat	cca	act	act	aat	aca	gaa	6852
Thr	Val	Ser	Ile	Pro	Leu	Gly	Ser	His	Pro	Thr	Thr	Asn	Thr	Glu	
			2205					2210					2215		
aca	agc	atc	cca	gta	aac	agc	gca	ggt	cca	cct	ggc	ttg	tcc	aca	6897
Thr	Ser	Ile	Pro	Val	Asn	Ser	Ala	Gly	Pro	Pro	Gly	Leu	Ser	Thr	
			2220					2225					2230		
gta	gca	tca	gat	gta	att	gac	aca	cct	tca	gat	ggg	gct	gag	agt	6942
Val	Ala	Ser	Asp	Val	Ile	Asp	Thr	Pro	Ser	Asp	Gly	Ala	Glu	Ser	
			2235					2240					2245		
att	ccc	act	gtc	tcc	ttt	tcc	ccc	tcc	cct	gat	act	gaa	gtg	aca	6987
Ile	Pro	Thr	Val	Ser	Phe	Ser	Pro	Ser	Pro	Asp	Thr	Glu	Val	Thr	
			2250					2255					2260		
act	atc	tca	cat	ttc	cca	gaa	aag	aca	act	cat	tca	ttt	aga	acc	7032
Thr	Ile	Ser	His	Phe	Pro	Glu	Lys	Thr	Thr	His	Ser	Phe	Arg	Thr	
			2265					2270					2275		

393

att tca tct ctc act cat gag ttg act tca aga gtg aca cct att Ile Ser Ser Leu Thr His Glu Leu Thr Ser Arg Val Thr Pro Ile 2280 2285 2290	7077
cct ggg gat tgg atg agt tca gct atg tct aca aag ccc aca gga Pro Gly Asp Trp Met Ser Ser Ala Met Ser Thr Lys Pro Thr Gly 2295 2300 2305	7122
gcc agt ccc tcc att aca ctg gga gag aga agg aca atc acc tct Ala Ser Pro Ser Ile Thr Leu Gly Glu Arg Arg Thr Ile Thr Ser 2310 2315 2320	7167
gct gct cca acc act tcc ccc ata gtt ctc act gct agt ttc aca Ala Ala Pro Thr Thr Ser Pro Ile Val Leu Thr Ala Ser Phe Thr 2325 2330 2335	7212
gag acc agc aca gtt tca ctg gat aat gaa act aca gta aaa acc Glu Thr Ser Thr Val Ser Leu Asp Asn Glu Thr Thr Val Lys Thr 2340 2345 2350	7257
tca gat atc ctt gac gca cgg aaa aca aat gag ctc ccc tca gat Ser Asp Ile Leu Asp Ala Arg Lys Thr Asn Glu Leu Pro Ser Asp 2355 2360 2365	7302
agc agt tct tct tct gat ctg atc aac acc tcc ata gct tct tca Ser Ser Ser Ser Ser Asp Leu Ile Asn Thr Ser Ile Ala Ser Ser 2370 2375 2380	7347
act atg gat gtc act aaa aca gcc tcc atc agt ccc act agc atc Thr Met Asp Val Thr Lys Thr Ala Ser Ile Ser Pro Thr Ser Ile 2385 2390 2395	7392
tca gga atg aca gca agt tcc tcc cca tct ctc ttc tct tca gat Ser Gly Met Thr Ala Ser Ser Ser Pro Ser Leu Phe Ser Ser Asp 2400 2405 2410	7437
aga ccc cag gtt ccc aca tct aca aca gag aca aat aca gcc acc Arg Pro Gln Val Pro Thr Ser Thr Thr Glu Thr Asn Thr Ala Thr 2415 2420 2425	7482
tct cca tct gtt tcc agt aac acc tat tct ctt gat ggg ggc tcc Ser Pro Ser Val Ser Ser Asn Thr Tyr Ser Leu Asp Gly Gly Ser 2430 2435 2440	7527
aat gtg ggt ggc act cca tcc act tta cca ccc ttt aca atc acc Asn Val Gly Gly Thr Pro Ser Thr Leu Pro Pro Phe Thr Ile Thr 2445 2450 2455	7572
cac cct gtc gag aca agc tcg gcc cta tta gcc tgg tct aga cca His Pro Val Glu Thr Ser Ser Ala Leu Leu Ala Trp Ser Arg Pro 2460 2465 2470	7617
gta aga act ttc agc acc atg gtc agc act gac act gcc tcc gga	7662

394

Val Arg Thr Phe	Ser Thr Met Val	Ser Thr Asp Thr Ala	Ser Gly	
2475		2480	2485	
gaa aat cct acc	tct agc aat tct	gtg act tct gtt	cca gca	7707
Glu Asn Pro Thr	Ser Ser Asn Ser	Val Val Thr Ser	Val Pro Ala	
2490		2495	2500	
cca ggt aca tgg	acc agt gta ggc	agt act act gac	tta cct gcc	7752
Pro Gly Thr Trp	Thr Ser Val Gly	Ser Thr Thr Asp	Leu Pro Ala	
2505		2510	2515	
atg ggc ttt ctc	aag aca agt cct	gca gga gag gca	cac tca ctt	7797
Met Gly Phe Leu	Lys Thr Ser Pro	Ala Gly Glu Ala	His Ser Leu	
2520		2525	2530	
cta gca tca act	att gaa cca gcc	act gcc ttc act	ccc cat ctc	7842
Leu Ala Ser Thr	Ile Glu Pro Ala	Thr Ala Phe Thr	Pro His Leu	
2535		2540	2545	
tca gca gca gtg	gtc act gga tcc	agt gct aca tca	gaa gcc agt	7887
Ser Ala Ala Val	Val Thr Gly Ser	Ser Ala Thr Ser	Glu Ala Ser	
2550		2555	2560	
ctt ctc act acg	agt gaa agc aaa	gcc att cat tct	tca cca cag	7932
Leu Leu Thr Thr	Ser Glu Ser Lys	Ala Ile His Ser	Ser Pro Gln	
2565		2570	2575	
acc cca act aca	ccc acc tct gga	gca aac tgg gaa	act tca gct	7977
Thr Pro Thr Thr	Pro Thr Ser Gly	Ala Asn Trp Glu	Thr Ser Ala	
2580		2585	2590	
act cct gag agc	ctt ttg gta gtc	act gag act tca	gac aca aca	8022
Thr Pro Glu Ser	Leu Leu Val Val	Thr Glu Thr Ser	Asp Thr Thr	
2595		2600	2605	
ctt acc tca aag	att ttg gtc aca	gat acc atc ttg	ttt tca act	8067
Leu Thr Ser Lys	Ile Leu Val Thr	Asp Thr Ile Leu	Phe Ser Thr	
2610		2615	2620	
gtg tcc acg cca	cct tct aaa ttt	cca agt acg ggg	act ctg tct	8112
Val Ser Thr Pro	Pro Ser Lys Phe	Pro Ser Thr Gly	Thr Leu Ser	
2625		2630	2635	
gga gct tcc ttc	cct act tta ctc	ccg gac act cca	gcc atc cct	8157
Gly Ala Ser Phe	Pro Thr Leu Leu	Pro Asp Thr Pro	Ala Ile Pro	
2640		2645	2650	
ctc act gcc act	gag cca aca agt	tca tta gct aca	tcc ttt gat	8202
Leu Thr Ala Thr	Glu Pro Thr Ser	Ser Leu Ala Thr	Ser Phe Asp	
2655		2660	2665	
tcc acc cca ctg	gtg act ata gct	tcg gat agt ctt	ggc aca gtc	8247
Ser Thr Pro Leu	Val Thr Ile Ala	Ser Asp Ser Leu	Gly Thr Val	
2670		2675	2680	

395

cca gag act acc	ctg acc atg tca gag	acc tca aat ggt gat	gca	8292
Pro Glu Thr Thr	Leu Thr Met Ser Glu	Thr Ser Asn Gly Asp	Ala	
2685	2690	2695		
ctg gtt ctt aag	aca gta agt aac cca	gat agg agc atc cct	gga	8337
Leu Val Leu Lys	Thr Val Ser Asn Pro	Asp Arg Ser Ile Pro	Gly	
2700	2705	2710		
atc act atc caa	gga gta aca gaa agt	cca ctc cat cct tct	tcc	8382
Ile Thr Ile Gln	Gly Val Thr Glu Ser	Pro Leu His Pro Ser	Ser	
2715	2720	2725		
act tcc ccc tct	aag att gtt gct cca	cgg aat aca acc tat	gaa	8427
Thr Ser Pro Ser	Lys Ile Val Ala Pro	Arg Asn Thr Thr Tyr	Glu	
2730	2735	2740		
ggt tcg atc aca	gtg gca ctt tct act	ttg cct gcg gga act	act	8472
Gly Ser Ile Thr	Val Ala Leu Ser Thr	Leu Pro Ala Gly Thr	Thr	
2745	2750	2755		
ggt tcc ctt gta	ttc agt cag agt tct	gaa aac tca gag aca	acg	8517
Gly Ser Leu Val	Phe Ser Gln Ser Ser	Glu Asn Ser Glu Thr	Thr	
2760	2765	2770		
gct ttg gta gac	tca tca gct ggg ctt	gag agg gca tct gtg	atg	8562
Ala Leu Val Asp	Ser Ser Ala Gly Leu	Glu Arg Ala Ser Val	Met	
2775	2780	2785		
cca cta acc aca	gga agc cag ggt atg	gct agc tct gga gga	atc	8607
Pro Leu Thr Thr	Gly Ser Gln Gly Met	Ala Ser Ser Gly Gly	Ile	
2790	2795	2800		
aga agt ggg tcc	act cac tca act gga	acc aaa aca ttt tct	tct	8652
Arg Ser Gly Ser	Thr His Ser Thr Gly	Thr Lys Thr Phe Ser	Ser	
2805	2810	2815		
ctc cct ctg acc	atg aac cca ggt gag	gtt aca gcc atg tct	gaa	8697
Leu Pro Leu Thr	Met Asn Pro Gly Glu	Val Thr Ala Met Ser	Glu	
2820	2825	2830		
atc acc acg aac	aga ctg aca gct act	caa tca aca gca ccc	aaa	8742
Ile Thr Thr Asn	Arg Leu Thr Ala Thr	Gln Ser Thr Ala Pro	Lys	
2835	2840	2845		
ggg ata cct gtg	aag ccc acc agt gct	gag tca ggc ctc cta	aca	8787
Gly Ile Pro Val	Lys Pro Thr Ser Ala	Glu Ser Gly Leu Leu	Thr	
2850	2855	2860		
cct gtc tct gcc	tcc tca agc cca tca	aag gcc ttt gcc tca	ctg	8832
Pro Val Ser Ala	Ser Ser Ser Pro Ser	Lys Ala Phe Ala Ser	Leu	
2865	2870	2875		
act aca gct ccc	cca act tgg ggg atc	cca cag tct acc ttg	aca	8877

396

Thr Thr Ala Pro	Pro Thr Trp Gly Ile	Pro Gln Ser Thr Leu Thr	
2880	2885	2890	
ttt gag ttt tct	gag gtc cca agt ttg	gat act aag tcc gct tct	8922
Phe Glu Phe Ser	Glu Val Pro Ser Leu	Asp Thr Lys Ser Ala Ser	
2895	2900	2905	
tta cca act cct	gga cag tcc ctg aac	acc att cca gac tca gat	8967
Leu Pro Thr Pro	Gly Gln Ser Leu Asn	Thr Ile Pro Asp Ser Asp	
2910	2915	2920	
gca agc aca gca	tct tcc tca ctg tcc	aag tct cca gaa aaa aac	9012
Ala Ser Thr Ala	Ser Ser Ser Leu Ser	Lys Ser Pro Glu Lys Asn	
2925	2930	2935	
cca agg gca agg	atg atg act tcc aca	aag gcc ata agt gca agc	9057
Pro Arg Ala Arg	Met Met Thr Ser Thr	Lys Ala Ile Ser Ala Ser	
2940	2945	2950	
tca ttt caa tca	aca ggt ttt act gaa	acc cct gag gga tct gcc	9102
Ser Phe Gln Ser	Thr Gly Phe Thr Glu	Thr Pro Glu Gly Ser Ala	
2955	2960	2965	
tcc cct tct atg	gca ggg cat gaa ccc	aga gtc ccc act tca gga	9147
Ser Pro Ser Met	Ala Gly His Glu Pro	Arg Val Pro Thr Ser Gly	
2970	2975	2980	
aca ggg gac cct	aga tat gcc tca gag	agc atg tct tat cca gac	9192
Thr Gly Asp Pro	Arg Tyr Ala Ser Glu	Ser Met Ser Tyr Pro Asp	
2985	2990	2995	
cca agc aag gca	tca tca gct atg aca	tcg acc tct ctt gca tca	9237
Pro Ser Lys Ala	Ser Ser Ala Met Thr	Ser Thr Ser Leu Ala Ser	
3000	3005	3010	
aaa ctc aca act	ctc ttc agc aca ggt	caa gca gca agg tct ggt	9282
Lys Leu Thr Thr	Leu Phe Ser Thr Gly	Gln Ala Ala Arg Ser Gly	
3015	3020	3025	
tct agt tcc tct	ccc ata agc cta tcc	act gag aaa gaa aca agc	9327
Ser Ser Ser Ser	Pro Ile Ser Leu Ser	Thr Glu Lys Glu Thr Ser	
3030	3035	3040	
ttc ctt tcc ccc	act gca tcc acc tcc	aga aag act tca cta ttt	9372
Phe Leu Ser Pro	Thr Ala Ser Thr Ser	Arg Lys Thr Ser Leu Phe	
3045	3050	3055	
ctt ggg cct tcc	atg gca agg cag ccc	aac ata ttg gtg cat ctt	9417
Leu Gly Pro Ser	Met Ala Arg Gln Pro	Asn Ile Leu Val His Leu	
3060	3065	3070	
cag act tca gct	ctg aca ctt tct cca	aca tcc act cta aat atg	9462
Gln Thr Ser Ala	Leu Thr Leu Ser Pro	Thr Ser Thr Leu Asn Met	
3075	3080	3085	

397

tcc cag gag gag Ser Gln Glu Glu 3090	cct cct gag tta acc Pro Pro Glu Leu Thr 3095	tca agc cag acc att gca Ser Ser Gln Thr Ile Ala 3100	9507
gaa gaa gag gga Glu Glu Glu Gly 3105	aca aca gct gaa aca Thr Thr Ala Glu Thr 3110	cag acg tta acc ttc aca Gln Thr Leu Thr Phe Thr 3115	9552
cca tct gag acc Pro Ser Glu Thr 3120	cca aca tcc ttg tta Pro Thr Ser Leu Leu 3125	cct gtc tct tct ccc aca Pro Val Ser Ser Pro Thr 3130	9597
gaa ccc aca gcc Glu Pro Thr Ala 3135	aga aga aag agt tct Arg Arg Lys Ser Ser 3140	cca gaa aca tgg gca agc Pro Glu Thr Trp Ala Ser 3145	9642
tct att tca gtt Ser Ile Ser Val 3150	cct gcc aag acc tcc Pro Ala Lys Thr Ser 3155	ttg gtt gaa aca act gat Leu Val Glu Thr Thr Asp 3160	9687
gga acg cta gtg Gly Thr Leu Val 3165	acc acc ata aag atg Thr Thr Ile Lys Met 3170	tca agc cag gca gca caa Ser Ser Gln Ala Ala Gln 3175	9732
gga aat tcc acg Gly Asn Ser Thr 3180	tgg cct gcc cca gca Trp Pro Ala Pro Ala 3185	gag gag acg ggg acc agt Glu Glu Thr Gly Thr Ser 3190	9777
cca gca ggc aca Pro Ala Gly Thr 3195	tcc cca gga agc cca Ser Pro Gly Ser Pro 3200	gaa atg tct acc act ctc Glu Met Ser Thr Thr Leu 3205	9822
aaa atc atg agc Lys Ile Met Ser 3210	tcc aag gaa ccc agc Ser Lys Glu Pro Ser 3215	atc agc cca gag atc agg Ile Ser Pro Glu Ile Arg 3220	9867
tcc act gtg cga Ser Thr Val Arg 3225	aat tct cct tgg aag Asn Ser Pro Trp Lys 3230	act cca gaa aca act gtt Thr Pro Glu Thr Thr Val 3235	9912
ccc atg gag acc Pro Met Glu Thr 3240	aca gtg gaa cca gtc Thr Val Glu Pro Val 3245	acc ctt cag tcc aca gcc Thr Leu Gln Ser Thr Ala 3250	9957
cta gga agt ggc Leu Gly Ser Gly 3255	agc acc agc atc tct Ser Thr Ser Ile Ser 3260	cac ctg ccc aca gga acc His Leu Pro Thr Gly Thr 3265	10002
aca tca cca acc Thr Ser Pro Thr 3270	aag tca cca aca gaa Lys Ser Pro Thr Glu 3275	aat atg ttg gct aca gaa Asn Met Leu Ala Thr Glu 3280	10047
agg gtc tcc ctc	tcc cca tcc cca cct	gag gct tgg acc aac ctt	10092

398

Arg	Val	Ser	Leu	Ser	Pro	Ser	Pro	Pro	Glu	Ala	Trp	Thr	Asn	Leu	
			3285					3290					3295		
tat	tct	gga	act	cca	gga	ggg	acc	agg	cag	tca	ctg	gcc	aca	atg	10137
Tyr	Ser	Gly	Thr	Pro	Gly	Gly	Thr	Arg	Gln	Ser	Leu	Ala	Thr	Met	
			3300					3305					3310		
tcc	tct	gtc	tcc	cta	gag	tca	cca	act	gct	aga	agc	atc	aca	ggg	10182
Ser	Ser	Val	Ser	Leu	Glu	Ser	Pro	Thr	Ala	Arg	Ser	Ile	Thr	Gly	
			3315					3320					3325		
act	ggt	cag	caa	agc	agt	cca	gaa	ctg	gtt	tca	aag	aca	act	gga	10227
Thr	Gly	Gln	Gln	Ser	Ser	Pro	Glu	Leu	Val	Ser	Lys	Thr	Thr	Gly	
			3330					3335					3340		
atg	gaa	ttc	tct	atg	tgg	cat	ggc	tct	act	gga	ggg	acc	aca	ggg	10272
Met	Glu	Phe	Ser	Met	Trp	His	Gly	Ser	Thr	Gly	Gly	Thr	Thr	Gly	
			3345					3350					3355		
gac	aca	cat	gtc	tct	ctg	agc	aca	tct	tcc	aat	atc	ctt	gaa	gac	10317
Asp	Thr	His	Val	Ser	Leu	Ser	Thr	Ser	Ser	Asn	Ile	Leu	Glu	Asp	
			3360					3365					3370		
cct	gta	acc	agc	cca	aac	tct	gtg	agc	tca	ttg	aca	gat	aaa	tcc	10362
Pro	Val	Thr	Ser	Pro	Asn	Ser	Val	Ser	Ser	Leu	Thr	Asp	Lys	Ser	
			3375					3380					3385		
aaa	cat	aaa	acc	gag	aca	tgg	gta	agc	acc	aca	gcc	att	ccc	tcc	10407
Lys	His	Lys	Thr	Glu	Thr	Trp	Val	Ser	Thr	Thr	Ala	Ile	Pro	Ser	
			3390					3395					3400		
act	gtc	ctg	aat	aat	aag	ata	atg	gca	gct	gaa	caa	cag	aca	agt	10452
Thr	Val	Leu	Asn	Asn	Lys	Ile	Met	Ala	Ala	Glu	Gln	Gln	Thr	Ser	
			3405					3410					3415		
cga	tct	gtg	gat	gag	gct	tat	tca	tca	act	agt	tct	tgg	tca	gat	10497
Arg	Ser	Val	Asp	Glu	Ala	Tyr	Ser	Ser	Thr	Ser	Ser	Trp	Ser	Asp	
			3420					3425					3430		
cag	aca	tct	ggg	agt	gac	atc	acc	ctt	ggt	gca	tct	cct	gat	gtc	10542
Gln	Thr	Ser	Gly	Ser	Asp	Ile	Thr	Leu	Gly	Ala	Ser	Pro	Asp	Val	
			3435					3440					3445		
aca	aac	aca	tta	tac	atc	acc	tcc	aca	gca	caa	acc	acc	tca	cta	10587
Thr	Asn	Thr	Leu	Tyr	Ile	Thr	Ser	Thr	Ala	Gln	Thr	Thr	Ser	Leu	
			3450					3455					3460		
gtg	tct	ctg	ccc	tct	gga	gac	caa	ggc	att	aca	agc	ctc	acc	aat	10632
Val	Ser	Leu	Pro	Ser	Gly	Asp	Gln	Gly	Ile	Thr	Ser	Leu	Thr	Asn	
			3465					3470					3475		
ccc	tca	gga	gga	aaa	aca	agc	tct	gcg	tca	tct	gtc	aca	tct	cct	10677
Pro	Ser	Gly	Gly	Lys	Thr	Ser	Ser	Ala	Ser	Ser	Val	Thr	Ser	Pro	
			3480					3485					3490		

399

tca ata ggg ctt	gag act ctg agg gcc	aat gta agt gca gtg aaa	10722
Ser Ile Gly Leu	Glu Thr Leu Arg Ala	Asn Val Ser Ala Val Lys	
3495	3500	3505	
agt gac att gcc	cct act gct ggg cat	cta tct cag act tca tct	10767
Ser Asp Ile Ala	Pro Thr Ala Gly His	Leu Ser Gln Thr Ser Ser	
3510	3515	3520	
cct gcg gaa gtg	agc atc ctg gac gta	acc aca gct cct act cca	10812
Pro Ala Glu Val	Ser Ile Leu Asp Val	Thr Thr Ala Pro Thr Pro	
3525	3530	3535	
ggg atc tcc acc	acc atc acc acc atg	gga acc aac tca atc tca	10857
Gly Ile Ser Thr	Thr Ile Thr Thr Met	Gly Thr Asn Ser Ile Ser	
3540	3545	3550	
act acc aca ccc	aac cca gaa gtg ggt	atg agt acc atg gac agc	10902
Thr Thr Thr Pro	Asn Pro Glu Val Gly	Met Ser Thr Met Asp Ser	
3555	3560	3565	
acc ccg gcc aca	gag agg cgc aca act	tct aca gaa cac cct tcc	10947
Thr Pro Ala Thr	Glu Arg Arg Thr Thr	Ser Thr Glu His Pro Ser	
3570	3575	3580	
acc tgg tct tcc	aca gct gca tca gat	tcc tgg act gtc aca gac	10992
Thr Trp Ser Ser	Thr Ala Ala Ser Asp	Ser Trp Thr Val Thr Asp	
3585	3590	3595	
atg act tca aac	ttg aaa gtt gca aga	tct cct gga aca att tcc	11037
Met Thr Ser Asn	Leu Lys Val Ala Arg	Ser Pro Gly Thr Ile Ser	
3600	3605	3610	
aca atg cat aca	act tca ttc tta gcc	tca agc act gaa tta gac	11082
Thr Met His Thr	Thr Ser Phe Leu Ala	Ser Ser Thr Glu Leu Asp	
3615	3620	3625	
tcc atg tct act	ccc cat ggc cgt ata	act gtc att gga acc agc	11127
Ser Met Ser Thr	Pro His Gly Arg Ile	Thr Val Ile Gly Thr Ser	
3630	3635	3640	
ctg gtc act cca	tcc tct gat gct tca	gct gta aag aca gag acc	11172
Leu Val Thr Pro	Ser Ser Asp Ala Ser	Ala Val Lys Thr Glu Thr	
3645	3650	3655	
agt aca agt gaa	aga aca ttg agt cct	tca gac aca act gca tct	11217
Ser Thr Ser Glu	Arg Thr Leu Ser Pro	Ser Asp Thr Thr Ala Ser	
3660	3665	3670	
act ccc atc tca	act ttt tct cgt gtc	cag agg atg agc atc tca	11262
Thr Pro Ile Ser	Thr Phe Ser Arg Val	Gln Arg Met Ser Ile Ser	
3675	3680	3685	
gtt cct gac att	tta agt aca agt tgg	act ccc agt agt aca gaa	11307

400

Val Pro Asp Ile 3690	Leu Ser Thr Ser 3695	Thr Pro Ser Ser 3700	Glu	
gca gaa gat gtg Ala Glu Asp Val 3705	cct gtt tca atg gtt Pro Val Ser Met Val 3710	tct aca gat cat gct Ser Thr Asp His Ala 3715	agt Ser	11352
aca aag act gac Thr Lys Thr Asp 3720	cca aat acg ccc ctg Pro Asn Thr Pro Leu 3725	tcc act ttt ctg ttt Ser Thr Phe Leu Phe 3730	gat Asp	11397
tct ctg tcc act Ser Leu Ser Thr 3735	ctt gac tgg gac act Leu Asp Trp Asp Thr 3740	ggg aga tct ctg tca Gly Arg Ser Leu Ser 3745	tca Ser	11442
gcc aca gcc act Ala Thr Ala Thr 3750	acc tca gct cct cag Thr Ser Ala Pro Gln 3755	ggg gcc aca act ccc Gly Ala Thr Thr Pro 3760	cag Gln	11487
gaa ctc act ttg Glu Leu Thr Leu 3765	gaa acc atg atc agc Glu Thr Met Ile Ser 3770	cca gct acc tca cag Pro Ala Thr Ser Gln 3775	ttg Leu	11532
ccc ttc tct ata Pro Phe Ser Ile 3780	ggg cac att aca agt Gly His Ile Thr Ser 3785	gca gtc aca cca gct Ala Val Thr Pro Ala 3790	gca Ala	11577
atg gca agg agc Met Ala Arg Ser 3795	tct gga gtt act ttt Ser Gly Val Thr Phe 3800	tca aga cca gat ccc Ser Arg Pro Asp Pro 3805	aca Thr	11622
agc aaa aag gca Ser Lys Lys Ala 3810	gag cag act tcc act Glu Gln Thr Ser Thr 3815	cag ctt ccc acc acc Gln Leu Pro Thr Thr 3820	act Thr	11667
tct gca cat cca Ser Ala His Pro 3825	ggg cag gtg ccc aga Gly Gln Val Pro Arg 3830	tca gca gca aca act Ser Ala Ala Thr Thr 3835	ctg Leu	11712
gat gtg atc cca Asp Val Ile Pro 3840	cac aca gca aaa act His Thr Ala Lys Thr 3845	cca gat gca act ttt Pro Asp Ala Thr Phe 3850	cag Gln	11757
aga caa ggg cag Arg Gln Gly Gln 3855	aca gct ctt aca aca Thr Ala Leu Thr Thr 3860	gag gca aga gct aca Glu Ala Arg Ala Thr 3865	tct Ser	11802
gac tcc tgg aat Asp Ser Trp Asn 3870	gag aaa gaa aaa tca Glu Lys Glu Lys Ser 3875	acc cca agt gca cct Thr Pro Ser Ala Pro 3880	tgg Trp	11847
atc act gag atg Ile Thr Glu Met 3885	atg aat tct gtc tca Met Asn Ser Val Ser 3890	gaa gat acc atc aag Glu Asp Thr Ile Lys 3895	gag Glu	11892

401

gtt acc agc tcc tcc agt gta tta aag gac cct gaa tac gct gga Val Thr Ser Ser Ser Ser Val Leu Lys Asp Pro Glu Tyr Ala Gly 3900 3905 3910	11937
cat aaa ctt gga atc tgg gac gac ttc atc ccc aag ttt gga aaa His Lys Leu Gly Ile Trp Asp Asp Phe Ile Pro Lys Phe Gly Lys 3915 3920 3925	11982
gca gcc cat atg aga gag ttg ccc ctt ctg agt cca cca cag gac Ala Ala His Met Arg Glu Leu Pro Leu Leu Ser Pro Pro Gln Asp 3930 3935 3940	12027
aaa gag gca att cac cct tct aca aac aca gta gag acc aca ggc Lys Glu Ala Ile His Pro Ser Thr Asn Thr Val Glu Thr Thr Gly 3945 3950 3955	12072
tgg gtc aca agt tcc gaa cat gct tct cat tcc act atc cca gcc Trp Val Thr Ser Ser Glu His Ala Ser His Ser Thr Ile Pro Ala 3960 3965 3970	12117
cac tca gcg tca tcc aaa ctc aca tct cca gtg gtt aca acc tcc His Ser Ala Ser Ser Lys Leu Thr Ser Pro Val Val Thr Thr Ser 3975 3980 3985	12162
acc agg gaa caa gca ata gtt tct atg tca aca acc aca tgg cca Thr Arg Glu Gln Ala Ile Val Ser Met Ser Thr Thr Thr Trp Pro 3990 3995 4000	12207
gag tct aca agg gct aga aca gag cct aat tcc ttc ttg act att Glu Ser Thr Arg Ala Arg Thr Glu Pro Asn Ser Phe Leu Thr Ile 4005 4010 4015	12252
gaa ctg agg gac gtc agc cct tac atg gac acc agc tca acc aca Glu Leu Arg Asp Val Ser Pro Tyr Met Asp Thr Ser Ser Thr Thr 4020 4025 4030	12297
caa aca agt att atc tct tcc cca ggt tcc act gcg atc acc aag Gln Thr Ser Ile Ile Ser Ser Pro Gly Ser Thr Ala Ile Thr Lys 4035 4040 4045	12342
ggg cct aga aca gaa att acc tcc tct aag aga ata tcc agc tca Gly Pro Arg Thr Glu Ile Thr Ser Ser Lys Arg Ile Ser Ser Ser 4050 4055 4060	12387
ttc ctt gcc cag tct atg agg tcg tca gac agc ccc tca gaa gcc Phe Leu Ala Gln Ser Met Arg Ser Ser Asp Ser Pro Ser Glu Ala 4065 4070 4075	12432
atc acc agg ctg tct aac ttt cct gcc atg aca gaa tct gga gga Ile Thr Arg Leu Ser Asn Phe Pro Ala Met Thr Glu Ser Gly Gly 4080 4085 4090	12477
atg atc ctt gct atg caa aca agt cca cct ggc gct aca tca cta	12522

402

Met Ile Leu Ala	Met Gln Thr Ser Pro	Pro Gly Ala Thr Ser Leu	
4095	4100	4105	
agt gca cct act	ttg gat aca tca gcc	aca gcc tcc tgg aca ggg	12567
Ser Ala Pro Thr	Leu Asp Thr Ser Ala	Thr Ala Ser Trp Thr Gly	
4110	4115	4120	
act cca ctg gct	acg act cag aga ttt	aca tac tca gag aag acc	12612
Thr Pro Leu Ala	Thr Thr Gln Arg Phe	Thr Tyr Ser Glu Lys Thr	
4125	4130	4135	
act ctc ttt agc	aaa ggt cct gag gat	aca tca cag cca agc cct	12657
Thr Leu Phe Ser	Lys Gly Pro Glu Asp	Thr Ser Gln Pro Ser Pro	
4140	4145	4150	
ccc tct gtg gaa	gaa acc agc tct tcc	tct tcc ctg gta cct atc	12702
Pro Ser Val Glu	Glu Thr Ser Ser Ser	Ser Ser Leu Val Pro Ile	
4155	4160	4165	
cat gct aca acc	tcg cct tcc aat att	ttg ttg aca tca caa ggg	12747
His Ala Thr Thr	Ser Pro Ser Asn Ile	Leu Leu Thr Ser Gln Gly	
4170	4175	4180	
cac agt ccc tcc	tct act cca cct gtg	acc tca gtt ttc ttg tct	12792
His Ser Pro Ser	Ser Thr Pro Pro Val	Thr Ser Val Phe Leu Ser	
4185	4190	4195	
gag acc tct ggc	ctg ggg aag acc aca	gac atg tcg agg ata agc	12837
Glu Thr Ser Gly	Leu Gly Lys Thr Thr	Asp Met Ser Arg Ile Ser	
4200	4205	4210	
ttg gaa cct ggc	aca agt tta cct ccc	aat ttg agc agt aca gca	12882
Leu Glu Pro Gly	Thr Ser Leu Pro Pro	Asn Leu Ser Ser Thr Ala	
4215	4220	4225	
ggt gag gcg tta	tcc act tat gaa gcc	tcc aga gat aca aag gca	12927
Gly Glu Ala Leu	Ser Thr Tyr Glu Ala	Ser Arg Asp Thr Lys Ala	
4230	4235	4240	
att cat cat tct	gca gac aca gca gtg	acg aat atg gag gca acc	12972
Ile His His Ser	Ala Asp Thr Ala Val	Thr Asn Met Glu Ala Thr	
4245	4250	4255	
agt tct gaa tat	tct cct atc cca ggc	cat aca aag cca tcc aaa	13017
Ser Ser Glu Tyr	Ser Pro Ile Pro Gly	His Thr Lys Pro Ser Lys	
4260	4265	4270	
gcc aca tct cca	ttg gtt acc tcc cac	atc atg ggg gac atc act	13062
Ala Thr Ser Pro	Leu Val Thr Ser His	Ile Met Gly Asp Ile Thr	
4275	4280	4285	
tct tcc aca tca	gta ttt ggc tcc tcc	gag acc aca gag att gag	13107
Ser Ser Thr Ser	Val Phe Gly Ser Ser	Glu Thr Thr Glu Ile Glu	
4290	4295	4300	

403

aca gtg tcc tct	gtg aac cag gga ctt	cag gag aga agc aca tcc	13152
Thr Val Ser Ser	Val Asn Gln Gly Leu	Gln Glu Arg Ser Thr Ser	
4305	4310	4315	
cag gtg gcc agc	tct gct aca gag aca	agc act gtc att acc cat	13197
Gln Val Ala Ser	Ser Ala Thr Glu Thr	Ser Thr Val Ile Thr His	
4320	4325	4330	
gtg tct agt ggt	gat gct act act cat	gtc acc aag aca caa gcc	13242
Val Ser Ser Gly	Asp Ala Thr Thr His	Val Thr Lys Thr Gln Ala	
4335	4340	4345	
act ttc tct agc	gga aca tcc atc tca	agc cct cat cag ttt ata	13287
Thr Phe Ser Ser	Gly Thr Ser Ile Ser	Ser Pro His Gln Phe Ile	
4350	4355	4360	
act tct acc aac	aca ttt aca gat gtg	agc acc aac ccc tcc acc	13332
Thr Ser Thr Asn	Thr Phe Thr Asp Val	Ser Thr Asn Pro Ser Thr	
4365	4370	4375	
tct ctg ata atg	aca gaa tct tca gga	gtg acc atc acc acc caa	13377
Ser Leu Ile Met	Thr Glu Ser Ser Gly	Val Thr Ile Thr Thr Gln	
4380	4385	4390	
aca ggt cct act	gga gct gca aca cag	ggc cca tat ctc ttg gac	13422
Thr Gly Pro Thr	Gly Ala Ala Thr Gln	Gly Pro Tyr Leu Leu Asp	
4395	4400	4405	
aca tca acc atg	cct tac ttg aca gag	act cca tta gct gtg act	13467
Thr Ser Thr Met	Pro Tyr Leu Thr Glu	Thr Pro Leu Ala Val Thr	
4410	4415	4420	
cca gat ttt atg	caa tca gag aag acc	act ctc ata agc aaa ggt	13512
Pro Asp Phe Met	Gln Ser Glu Lys Thr	Thr Leu Ile Ser Lys Gly	
4425	4430	4435	
ccc aag gat gtg	acc tgg aca agc cct	ccc tct gtg gca gaa acc	13557
Pro Lys Asp Val	Thr Trp Thr Ser Pro	Pro Ser Val Ala Glu Thr	
4440	4445	4450	
agc tat ccc tct	tcc ctg aca cct ttc	ttg gtc aca acc ata cct	13602
Ser Tyr Pro Ser	Ser Leu Thr Pro Phe	Leu Val Thr Thr Ile Pro	
4455	4460	4465	
cct gcc act tcc	acg tta caa ggg caa	cat aca tcc tct cct gtt	13647
Pro Ala Thr Ser	Thr Leu Gln Gly Gln	His Thr Ser Ser Pro Val	
4470	4475	4480	
tct gcg act tca	gtt ctt acc tct gga	ctg gtg aag acc aca gat	13692
Ser Ala Thr Ser	Val Leu Thr Ser Gly	Leu Val Lys Thr Thr Asp	
4485	4490	4495	
atg ttg aac aca	agc atg gaa cct gtg	acc aat tca cct caa aat	13737

404

Met Leu Asn Thr	Ser Met Glu Pro Val	Thr Asn Ser Pro Gln Asn	
4500	4505	4510	
ttg aac aat cca	tca aat gag ata ctg	gcc act ttg gca gcc acc	13782
Leu Asn Asn Pro	Ser Asn Glu Ile Leu	Ala Thr Leu Ala Ala Thr	
4515	4520	4525	
aca gat ata gag	act att cat cct tcc	ata aac aaa gca gtg acc	13827
Thr Asp Ile Glu	Thr Ile His Pro Ser	Ile Asn Lys Ala Val Thr	
4530	4535	4540	
aat atg ggg act	gcc agt tca gca cat	gta ctg cat tcc act ctc	13872
Asn Met Gly Thr	Ala Ser Ser Ala His	Val Leu His Ser Thr Leu	
4545	4550	4555	
cca gtc agc tca	gaa cca tct aca gcc	aca tct cca atg gtt cct	13917
Pro Val Ser Ser	Glu Pro Ser Thr Ala	Thr Ser Pro Met Val Pro	
4560	4565	4570	
gcc tcc agc atg	ggg gac gct ctt gct	tct ata tca ata cct ggt	13962
Ala Ser Ser Met	Gly Asp Ala Leu Ala	Ser Ile Ser Ile Pro Gly	
4575	4580	4585	
tct gag acc aca	gac att gag gga gag	cca aca tcc tcc ctg act	14007
Ser Glu Thr Thr	Asp Ile Glu Gly Glu	Pro Thr Ser Ser Leu Thr	
4590	4595	4600	
gct gga cga aaa	gag aac agc acc ctc	cag gag atg aac tca act	14052
Ala Gly Arg Lys	Glu Asn Ser Thr Leu	Gln Glu Met Asn Ser Thr	
4605	4610	4615	
aca gag tca aac	atc atc ctc tcc aat	gtg tct gtg ggg gct att	14097
Thr Glu Ser Asn	Ile Ile Leu Ser Asn	Val Ser Val Gly Ala Ile	
4620	4625	4630	
act gaa gcc aca	aaa atg gaa gtc ccc	tct ttt gat gca aca ttc	14142
Thr Glu Ala Thr	Lys Met Glu Val Pro	Ser Phe Asp Ala Thr Phe	
4635	4640	4645	
ata cca act cct	gct cag tca aca aag	ttc cca gat att ttc tca	14187
Ile Pro Thr Pro	Ala Gln Ser Thr Lys	Phe Pro Asp Ile Phe Ser	
4650	4655	4660	
gta gcc agc agt	aga ctt tca aac tct	cct ccc atg aca ata tct	14232
Val Ala Ser Ser	Arg Leu Ser Asn Ser	Pro Pro Met Thr Ile Ser	
4665	4670	4675	
acc cac atg acc	acc acc cag aca ggg	tct tct gga gct aca tca	14277
Thr His Met Thr	Thr Thr Gln Thr Gly	Ser Ser Gly Ala Thr Ser	
4680	4685	4690	
aag att cca ctt	gcc tta gac aca tca	acc ttg gaa acc tca gca	14322
Lys Ile Pro Leu	Ala Leu Asp Thr Ser	Thr Leu Glu Thr Ser Ala	
4695	4700	4705	

405

ggg act cca tca	gtg gtg act gag	ggg ttt gcc cac tca	aaa ata	14367
Gly Thr Pro Ser	Val Val Thr Glu	Gly Phe Ala His Ser	Lys Ile	
4710	4715	4720		
acc act gca atg	aac aat gat gtc	aag gac gtg tca cag	aca aac	14412
Thr Thr Ala Met	Asn Asn Asp Val	Lys Asp Val Ser Gln	Thr Asn	
4725	4730	4735		
cct ccc ttt cag	gat gaa gcc agc	tct ccc tct tct caa	gca cct	14457
Pro Pro Phe Gln	Asp Glu Ala Ser	Ser Pro Ser Ser Gln	Ala Pro	
4740	4745	4750		
gtc ctt gtc aca	acc tta cct tct	tct gtt gct ttc aca	ccg caa	14502
Val Leu Val Thr	Thr Leu Pro Ser	Ser Val Ala Phe Thr	Pro Gln	
4755	4760	4765		
tgg cac agt acc	tcc tct cct gtt	tct atg tcc tca gtt	ctt act	14547
Trp His Ser Thr	Ser Ser Pro Val	Ser Met Ser Ser Val	Leu Thr	
4770	4775	4780		
tct tca ctg gta	aag acc gca gcc	aag gtg gat aca agc	tta gaa	14592
Ser Ser Leu Val	Lys Thr Ala Gly	Lys Val Asp Thr Ser	Leu Glu	
4785	4790	4795		
aca gtg acc agt	tca cct caa agt	atg agc aac act ttg	gat gac	14637
Thr Val Thr Ser	Ser Pro Gln Ser	Met Ser Asn Thr Leu	Asp Asp	
4800	4805	4810		
ata tcg gtc act	tca gca gcc acc	aca gat ata gag aca	acg cat	14682
Ile Ser Val Thr	Ser Ala Ala Thr	Thr Asp Ile Glu Thr	Thr His	
4815	4820	4825		
cct tcc ata aac	aca gta gtt acc	aat gtg ggg acc acc	ggt tca	14727
Pro Ser Ile Asn	Thr Val Val Thr	Asn Val Gly Thr Thr	Gly Ser	
4830	4835	4840		
gca ttt gaa tca	cat tct act gtc	tca gct tac cca gag	cca tct	14772
Ala Phe Glu Ser	His Ser Thr Val	Ser Ala Tyr Pro Glu	Pro Ser	
4845	4850	4855		
aaa agt cac att	ctc cca atg tta	cca cct cca cca tgg	aag aca	14817
Lys Ser His Ile	Leu Pro Met Leu	Pro Pro Pro Trp	Lys Thr	
4860	4865	4870		
cca caa ttt cca	cga tca ata cct	aaa tcc tct aag act	aca aga	14862
Pro Gln Phe Pro	Arg Ser Ile Pro	Lys Ser Ser Lys Thr	Thr Arg	
4875	4880	4885		
act gag act gag	aca act tcc tcc	ctg act cct aaa ctg	agg gag	14907
Thr Glu Thr Glu	Thr Thr Ser Ser	Leu Thr Pro Lys Leu	Arg Glu	
4890	4895	4900		
acc agc atc tcc	cag gag atc acc	tcg tcc aca gag aca	agc act	14952

406

Thr Ser Ile Ser	Gln Glu Ile Thr Ser	Ser Thr Glu Thr Ser Thr	
4905	4910	4915	
gtt cct tac aaa gag ctc act ggt gcc act acc gag gta tcc agg			14997
Val Pro Tyr Lys Glu Leu Thr Gly Ala Thr Thr Glu Val Ser Arg			
4920	4925	4930	
aca gat gtc act tcc tct agc agt aca tcc ttc cct ggc cct gat			15042
Thr Asp Val Thr Ser Ser Ser Ser Thr Ser Phe Pro Gly Pro Asp			
4935	4940	4945	
cag tcc aca gtg tca cta gac atc tcc aca gaa acc aac acc agg			15087
Gln Ser Thr Val Ser Leu Asp Ile Ser Thr Glu Thr Asn Thr Arg			
4950	4955	4960	
ctg tct acc tcc cca ata atg aca gaa tct gca gaa ata acc atc			15132
Leu Ser Thr Ser Pro Ile Met Thr Glu Ser Ala Glu Ile Thr Ile			
4965	4970	4975	
acc acc caa aca ggt cct cat ggg gct aca tca cag gat act ttt			15177
Thr Thr Gln Thr Gly Pro His Gly Ala Thr Ser Gln Asp Thr Phe			
4980	4985	4990	
acc atg gac cca tca aat aca acc ccc cag gca ggg atc cac tca			15222
Thr Met Asp Pro Ser Asn Thr Thr Pro Gln Ala Gly Ile His Ser			
4995	5000	5005	
gct atg act cat gga ttt tca caa ttg gat gtg acc act ctt atg			15267
Ala Met Thr His Gly Phe Ser Gln Leu Asp Val Thr Thr Leu Met			
5010	5015	5020	
agc aga att cca cag gat gta tca tgg aca agt cct ccc tct gtg			15312
Ser Arg Ile Pro Gln Asp Val Ser Trp Thr Ser Pro Pro Ser Val			
5025	5030	5035	
gat aaa acc agc tcc ccc tct tcc ttt ctg tcc tca cct gca atg			15357
Asp Lys Thr Ser Ser Pro Ser Ser Phe Leu Ser Ser Pro Ala Met			
5040	5045	5050	
acc aca cct tcc ctg att tct tct acc tta cca gag gat aag ctc			15402
Thr Thr Pro Ser Leu Ile Ser Ser Thr Leu Pro Glu Asp Lys Leu			
5055	5060	5065	
tcc tct cct atg act tca ctt ctc acc tct ggc cta gtg aag att			15447
Ser Ser Pro Met Thr Ser Leu Leu Thr Ser Gly Leu Val Lys Ile			
5070	5075	5080	
aca gac ata tta cgt aca cgc ttg gaa cct gtg acc agc tca ctt			15492
Thr Asp Ile Leu Arg Thr Arg Leu Glu Pro Val Thr Ser Ser Leu			
5085	5090	5095	
cca aat ttc agc agc acc tca gat aag ata ctg gcc act tct aaa			15537
Pro Asn Phe Ser Ser Thr Ser Asp Lys Ile Leu Ala Thr Ser Lys			
5100	5105	5110	

407

gac agt aaa gac	aca aag gaa att ttt	cct tct ata aac aca gaa	15582
Asp Ser Lys Asp	Thr Lys Glu Ile Phe	Pro Ser Ile Asn Thr Glu	
5115	5120	5125	
gag acc aat gtg	aaa gcc aac aac tct	gga cat gaa tcc cat tcc	15627
Glu Thr Asn Val	Lys Ala Asn Asn Ser	Gly His Glu Ser His Ser	
5130	5135	5140	
cct gca ctg gct	gac tca gag aca ccc	aaa gcc aca act caa atg	15672
Pro Ala Leu Ala	Asp Ser Glu Thr Pro	Lys Ala Thr Thr Gln Met	
5145	5150	5155	
gtt atc acc acc	act gtg gga gat cca	gct cct tcc aca tca atg	15717
Val Ile Thr Thr	Thr Val Gly Asp Pro	Ala Pro Ser Thr Ser Met	
5160	5165	5170	
cca gtg cat ggt	tcc tct gag act aca	aac att aag aga gag cca	15762
Pro Val His Gly	Ser Ser Glu Thr Thr	Asn Ile Lys Arg Glu Pro	
5175	5180	5185	
aca tat ttc ttg	act cct aga ctg aga	gag acc agt acc tct cag	15807
Thr Tyr Phe Leu	Thr Pro Arg Leu Arg	Glu Thr Ser Thr Ser Gln	
5190	5195	5200	
gag tcc agc ttt	ccc acg gac aca agt	ttt cta ctt tcc aaa gtc	15852
Glu Ser Ser Phe	Pro Thr Asp Thr Ser	Phe Leu Leu Ser Lys Val	
5205	5210	5215	
ccc act ggt act	att act gag gtc tcc	agt aca ggg gtc aac tct	15897
Pro Thr Gly Thr	Ile Thr Glu Val Ser	Ser Thr Gly Val Asn Ser	
5220	5225	5230	
tct agc aaa att	tcc acc cca gac cat	gat aag tcc aca gtg cca	15942
Ser Ser Lys Ile	Ser Thr Pro Asp His	Asp Lys Ser Thr Val Pro	
5235	5240	5245	
cct gac acc ttc	aca gga gag atc ccc	agg gtc ttc acc tcc tct	15987
Pro Asp Thr Phe	Thr Gly Glu Ile Pro	Arg Val Phe Thr Ser Ser	
5250	5255	5260	
att aag aca aaa	tct gca gaa atg acg	atc acc acc caa gca agt	16032
Ile Lys Thr Lys	Ser Ala Glu Met Thr	Ile Thr Thr Gln Ala Ser	
5265	5270	5275	
cct cct gag tct	gca tcg cac agt acc	ctt ccc ttg gac aca tca	16077
Pro Pro Glu Ser	Ala Ser His Ser Thr	Leu Pro Leu Asp Thr Ser	
5280	5285	5290	
acc aca ctt tcc	cag gga ggg act cat	tca act gtg act cag gga	16122
Thr Thr Leu Ser	Gln Gly Gly Thr His	Ser Thr Val Thr Gln Gly	
5295	5300	5305	
ttc cca tac tca	gag gtg acc act ctc	atg ggc atg ggt cct ggg	16167

408

Phe	Pro	Tyr	Ser	Glu	Val	Thr	Thr	Leu	Met	Gly	Met	Gly	Pro	Gly		
			5310					5315					5320			
aat	gtg	tca	tgg	atg	aca	act	ccc	cct	gtg	gaa	gaa	acc	agc	tct	16212	
Asn	Val	Ser	Trp	Met	Thr	Thr	Pro	Pro	Val	Glu	Glu	Thr	Ser	Ser		
			5325					5330					5335			
gtg	tct	tcc	ctg	atg	tct	tca	cct	gcc	atg	aca	tcc	cct	tct	cct	16257	
Val	Ser	Ser	Leu	Met	Ser	Ser	Pro	Ala	Met	Thr	Ser	Pro	Ser	Pro		
			5340					5345					5350			
gtt	tcc	tcc	aca	tca	cca	cag	agc	atc	ccc	tcc	tct	cct	ctt	cct	16302	
Val	Ser	Ser	Thr	Ser	Pro	Gln	Ser	Ile	Pro	Ser	Ser	Pro	Leu	Pro		
			5355					5360					5365			
gtg	act	gca	ctt	cct	act	tct	gtt	ctg	gtg	aca	acc	aca	gat	gtg	16347	
Val	Thr	Ala	Leu	Pro	Thr	Ser	Val	Leu	Val	Thr	Thr	Thr	Asp	Val		
			5370					5375					5380			
ttg	ggc	aca	aca	agc	cca	gag	tct	gta	acc	agt	tca	cct	cca	aat	16392	
Leu	Gly	Thr	Thr	Ser	Pro	Glu	Ser	Val	Thr	Ser	Ser	Pro	Pro	Asn		
			5385					5390					5395			
ttg	agc	agc	atc	act	cat	gag	aga	ccg	gcc	act	tac	aaa	gac	act	16437	
Leu	Ser	Ser	Ile	Thr	His	Glu	Arg	Pro	Ala	Thr	Tyr	Lys	Asp	Thr		
			5400					5405					5410			
gca	cac	aca	gaa	gcc	gcc	atg	cat	cat	tcc	aca	aac	acc	gca	gtg	16482	
Ala	His	Thr	Glu	Ala	Ala	Met	His	His	Ser	Thr	Asn	Thr	Ala	Val		
			5415					5420					5425			
acc	aat	gta	ggg	act	tcc	ggg	tct	gga	cat	aaa	tca	caa	tcc	tct	16527	
Thr	Asn	Val	Gly	Thr	Ser	Gly	Ser	Gly	His	Lys	Ser	Gln	Ser	Ser		
			5430					5435					5440			
gtc	cta	gct	gac	tca	gag	aca	tcg	aaa	gcc	aca	cct	ctg	atg	agt	16572	
Val	Leu	Ala	Asp	Ser	Glu	Thr	Ser	Lys	Ala	Thr	Pro	Leu	Met	Ser		
			5445					5450					5455			
acc	acc	tcc	acc	ctg	ggg	gac	aca	agt	gtt	tcc	aca	tca	act	cct	16617	
Thr	Thr	Ser	Thr	Leu	Gly	Asp	Thr	Ser	Val	Ser	Thr	Ser	Thr	Pro		
			5460					5465					5470			
aat	atc	tct	cag	act	aac	caa	att	caa	aca	gag	cca	aca	gca	tcc	16662	
Asn	Ile	Ser	Gln	Thr	Asn	Gln	Ile	Gln	Thr	Glu	Pro	Thr	Ala	Ser		
			5475					5480					5485			
ctg	agc	cct	aga	ctg	agg	gag	agc	agc	acg	tct	gag	aag	acc	agc	16707	
Leu	Ser	Pro	Arg	Leu	Arg	Glu	Ser	Ser	Thr	Ser	Glu	Lys	Thr	Ser		
			5490					5495					5500			
tca	aca	aca	gag	aca	aat	act	gcc	ttt	tct	tat	gtg	ccc	aca	ggg	16752	
Ser	Thr	Thr	Glu	Thr	Asn	Thr	Ala	Phe	Ser	Tyr	Val	Pro	Thr	Gly		
			5505					5510					5515			

409

gct att act cag gcc tcc aga aca gaa atc tcc tct agc aga aca	16797
Ala Ile Thr Gln Ala Ser Arg Thr Glu Ile Ser Ser Ser Arg Thr	
5520 5525 5530	
tcc atc tca gac ctt gat cgg ccc aca ata gca ccc gac atc tcc	16842
Ser Ile Ser Asp Leu Asp Arg Pro Thr Ile Ala Pro Asp Ile Ser	
5535 5540 5545	
aca gga atg atc acc agg ctc ttc acc tcc ccc atc atg aca aaa	16887
Thr Gly Met Ile Thr Arg Leu Phe Thr Ser Pro Ile Met Thr Lys	
5550 5555 5560	
tct gca gaa atg acc gtc acc act caa aca act act cct ggg gct	16932
Ser Ala Glu Met Thr Val Thr Thr Gln Thr Thr Thr Pro Gly Ala	
5565 5570 5575	
aca tca cag ggt atc ctt cct tgg gac aca tca acc aca ctt ttc	16977
Thr Ser Gln Gly Ile Leu Pro Trp Asp Thr Ser Thr Thr Leu Phe	
5580 5585 5590	
cag gga ggg act cat tca acc gtg tct cag gga ttc cca cac tca	17022
Gln Gly Gly Thr His Ser Thr Val Ser Gln Gly Phe Pro His Ser	
5595 5600 5605	
gag ata acc act ctt cgg agc aga acc cct gga gat gtg tca tgg	17067
Glu Ile Thr Thr Leu Arg Ser Arg Thr Pro Gly Asp Val Ser Trp	
5610 5615 5620	
atg aca act ccc cct gtg gaa gaa acc agc tct ggg ttt tcc ctg	17112
Met Thr Thr Pro Pro Val Glu Glu Thr Ser Ser Gly Phe Ser Leu	
5625 5630 5635	
atg tca cct tcc atg aca tcc cct tct cct gtt tcc tcc aca tca	17157
Met Ser Pro Ser Met Thr Ser Pro Ser Pro Val Ser Ser Thr Ser	
5640 5645 5650	
cca gag agc atc ccc tcc tct cct ctc cct gtg act gca ctt ctt	17202
Pro Glu Ser Ile Pro Ser Ser Pro Leu Pro Val Thr Ala Leu Leu	
5655 5660 5665	
act tct gtt ctg gtg aca acc acc aat gta ttg ggc aca aca agc	17247
Thr Ser Val Leu Val Thr Thr Thr Asn Val Leu Gly Thr Thr Ser	
5670 5675 5680	
cca gag acc gta acg agt tca cct cca aat tta agc agc ccc aca	17292
Pro Glu Thr Val Thr Ser Ser Pro Pro Asn Leu Ser Ser Pro Thr	
5685 5690 5695	
cag gag aga ctg acc act tac aaa gac act gcg cac aca gaa gcc	17337
Gln Glu Arg Leu Thr Thr Tyr Lys Asp Thr Ala His Thr Glu Ala	
5700 5705 5710	
atg cat gct tcc atg cat aca aac act gca gtg gcc aac gtc ggg	17382

410

Met His Ala Ser	Met His Thr Asn Thr	Ala Val Ala Asn Val Gly	
5715	5720	5725	
acc tcc att tct	gga cat gaa tca caa	tct tct gtc cca gct gat	17427
Thr Ser Ile Ser	Gly His Glu Ser Gln	Ser Ser Val Pro Ala Asp	
5730	5735	5740	
tca cac aca tcc	aaa gcc aca tct cca	atg ggt atc acc ttc gcc	17472
Ser His Thr Ser	Lys Ala Thr Ser Pro	Met Gly Ile Thr Phe Ala	
5745	5750	5755	
atg ggg gat aca	agt gtt tct aca tca	act cct gcc ttc ttt gag	17517
Met Gly Asp Thr	Ser Val Ser Thr Ser	Thr Pro Ala Phe Phe Glu	
5760	5765	5770	
act aga att cag	act gaa tca aca tcc	tct ttg att cct gga tta	17562
Thr Arg Ile Gln	Thr Glu Ser Thr Ser	Ser Leu Ile Pro Gly Leu	
5775	5780	5785	
agg gac acc agg	acg tct gag gag atc	aac act gtg aca gag acc	17607
Arg Asp Thr Arg	Thr Ser Glu Glu Ile	Asn Thr Val Thr Glu Thr	
5790	5795	5800	
agc act gtc ctt	tca gaa gtg ccc act	act act act act gag gtc	17652
Ser Thr Val Leu	Ser Glu Val Pro Thr	Thr Thr Thr Thr Glu Val	
5805	5810	5815	
tcc agg aca gaa	gtt atc act tcc agc	aga aca acc atc tca ggg	17697
Ser Arg Thr Glu	Val Ile Thr Ser Ser	Arg Thr Thr Ile Ser Gly	
5820	5825	5830	
cct gat cat tcc	aaa atg tca ccc tac	atc tcc aca gaa acc atc	17742
Pro Asp His Ser	Lys Met Ser Pro Tyr	Ile Ser Thr Glu Thr Ile	
5835	5840	5845	
acc agg ctc tcc	act ttt cct ttt gta	aca gga tcc aca gaa atg	17787
Thr Arg Leu Ser	Thr Phe Pro Phe Val	Thr Gly Ser Thr Glu Met	
5850	5855	5860	
gcc atc acc aac	caa aca ggt cct ata	ggg act atc tca cag gct	17832
Ala Ile Thr Asn	Gln Thr Gly Pro Ile	Gly Thr Ile Ser Gln Ala	
5865	5870	5875	
acc ctt acc ctg	gac aca tca agc aca	gct tcc tgg gaa ggg act	17877
Thr Leu Thr Leu	Asp Thr Ser Ser Thr	Ala Ser Trp Glu Gly Thr	
5880	5885	5890	
cac tca cct gtg	act cag aga ttt cca	cac tca gag gag acc act	17922
His Ser Pro Val	Thr Gln Arg Phe Pro	His Ser Glu Glu Thr Thr	
5895	5900	5905	
act atg agc aga	agt act aag ggc gtg	tca tgg caa agc cct ccc	17967
Thr Met Ser Arg	Ser Thr Lys Gly Val	Ser Trp Gln Ser Pro Pro	
5910	5915	5920	

411

tct gtg gaa gaa acc agt tct cct tct tcc cca gtg cct tta cct	18012
Ser Val Glu Glu Thr Ser Ser Pro Ser Ser Pro Val Pro Leu Pro	
5925 5930 5935	
gca ata acc tca cat tca tct ctt tat tcc gca gta tca gga agt	18057
Ala Ile Thr Ser His Ser Ser Leu Tyr Ser Ala Val Ser Gly Ser	
5940 5945 5950	
agc ccc act tct gct ctc cct gtg act tcc ctt ctc acc tct ggc	18102
Ser Pro Thr Ser Ala Leu Pro Val Thr Ser Leu Leu Thr Ser Gly	
5955 5960 5965	
agg agg aag acc ata gac atg ttg gac aca cac tca gaa ctt gtg	18147
Arg Arg Lys Thr Ile Asp Met Leu Asp Thr His Ser Glu Leu Val	
5970 5975 5980	
acc agc tcc tta cca agt gca agt agc ttc tca ggt gag ata ctc	18192
Thr Ser Ser Leu Pro Ser Ala Ser Ser Phe Ser Gly Glu Ile Leu	
5985 5990 5995	
act tct gaa gcc tcc aca aat aca gag aca att cac ttt tca gag	18237
Thr Ser Glu Ala Ser Thr Asn Thr Glu Thr Ile His Phe Ser Glu	
6000 6005 6010	
aac aca gca gaa acc aat atg ggg acc acc aat tct atg cat aaa	18282
Asn Thr Ala Glu Thr Asn Met Gly Thr Thr Asn Ser Met His Lys	
6015 6020 6025	
cta cat tcc tct gtc tca atc cac tcc cag cca tcc gga cac aca	18327
Leu His Ser Ser Val Ser Ile His Ser Gln Pro Ser Gly His Thr	
6030 6035 6040	
cct cca aag gtt act gga tct atg atg gag gac gct att gtt tcc	18372
Pro Pro Lys Val Thr Gly Ser Met Met Glu Asp Ala Ile Val Ser	
6045 6050 6055	
aca tca aca cct ggt tct cct gag act aaa aat gtt gac aga gac	18417
Thr Ser Thr Pro Gly Ser Pro Glu Thr Lys Asn Val Asp Arg Asp	
6060 6065 6070	
tca aca tcc cct ctg act cct gaa ctg aaa gag gac agc acc gcc	18462
Ser Thr Ser Pro Leu Thr Pro Glu Leu Lys Glu Asp Ser Thr Ala	
6075 6080 6085	
ctg gtg atg aac tca act aca gag tca aac act gtt ttc tcc agt	18507
Leu Val Met Asn Ser Thr Thr Glu Ser Asn Thr Val Phe Ser Ser	
6090 6095 6100	
gtg tcc ctg gat gct gct act gag gtc tcc agg gca gaa gtc acc	18552
Val Ser Leu Asp Ala Ala Thr Glu Val Ser Arg Ala Glu Val Thr	
6105 6110 6115	
tac tat gat cct aca ttc atg cca gct tct gct cag tca aca aag	18597

412

Tyr Tyr Asp Pro	Thr Phe Met Pro	Ala	Ser Ala Gln Ser Thr Lys	
6120		6125	6130	
tcc cca gac att	tca cct gaa gcc agc	agc agt cat tct aac tct	18642	
Ser Pro Asp Ile	Ser Pro Glu Ala Ser	Ser Ser His Ser Asn Ser		
6135	6140	6145		
cct ccc ttg aca	ata tct aca cac aag	acc atc gcc aca caa aca	18687	
Pro Pro Leu Thr	Ile Ser Thr His Lys	Thr Ile Ala Thr Gln Thr		
6150	6155	6160		
ggg cct tct ggg	gtg aca tct ctt ggc	caa ctg acc ctg gac aca	18732	
Gly Pro Ser Gly	Val Thr Ser Leu Gly	Gln Leu Thr Leu Asp Thr		
6165	6170	6175		
tca acc ata gcc	acc tca gca gga act	cca tca gcc aga act cag	18777	
Ser Thr Ile Ala	Thr Ser Ala Gly Thr	Pro Ser Ala Arg Thr Gln		
6180	6185	6190		
gat ttt gta gat	tca gaa aca acc agt	gtc atg aac aat gat ctc	18822	
Asp Phe Val Asp	Ser Glu Thr Thr Ser	Val Met Asn Asn Asp Leu		
6195	6200	6205		
aat gat gtg ttg	aag aca agc cct ttc	tct gca gaa gaa gcc aac	18867	
Asn Asp Val Leu	Lys Thr Ser Pro Phe	Ser Ala Glu Glu Ala Asn		
6210	6215	6220		
tct ctc tct tct	cag gca cct ctc ctt	gtg aca acc tca cct tct	18912	
Ser Leu Ser Ser	Gln Ala Pro Leu Leu	Val Thr Thr Ser Pro Ser		
6225	6230	6235		
cct gta act tcc	aca ttg caa gag cac	agt acc tcc tct ctt gtt	18957	
Pro Val Thr Ser	Thr Leu Gln Glu His	Ser Thr Ser Ser Leu Val		
6240	6245	6250		
tct gtg acc tca	gta ccc acc cct aca	ctg gcg aag atc aca gac	19002	
Ser Val Thr Ser	Val Pro Thr Pro Thr	Leu Ala Lys Ile Thr Asp		
6255	6260	6265		
atg gac aca aac	tta gaa cct gtg act	cgt tca cct caa aat tta	19047	
Met Asp Thr Asn	Leu Glu Pro Val Thr	Arg Ser Pro Gln Asn Leu		
6270	6275	6280		
agg aac acc ttg	gcc act tca gaa gcc	acc aca gat aca cac aca	19092	
Arg Asn Thr Leu	Ala Thr Ser Glu Ala	Thr Thr Asp Thr His Thr		
6285	6290	6295		
atg cat cct tct	ata aac aca gca atg	gcc aat gtg ggg acc acc	19137	
Met His Pro Ser	Ile Asn Thr Ala Met	Ala Asn Val Gly Thr Thr		
6300	6305	6310		
agt tca cca aat	gaa ttc tat ttt act	gtc tca cct gac tca gac	19182	
Ser Ser Pro Asn	Glu Phe Tyr Phe Thr	Val Ser Pro Asp Ser Asp		
6315	6320	6325		

413

cca tat aaa gcc	aca tcc gca gta gtt	atc act tcc acc tcg ggg	19227
Pro Tyr Lys Ala	Thr Ser Ala Val Val	Ile Thr Ser Thr Ser Gly	
6330	6335	6340	
gac tca ata gtt	tcc aca tca atg cct	aga tcc tct gcg atg aaa	19272
Asp Ser Ile Val	Ser Thr Ser Met Pro	Arg Ser Ser Ala Met Lys	
6345	6350	6355	
aag att gag tct	gag aca act ttc tcc	ctg ata ttt aga ctg agg	19317
Lys Ile Glu Ser	Glu Thr Thr Phe Ser	Leu Ile Phe Arg Leu Arg	
6360	6365	6370	
gag act agc acc	tcc cag aaa att ggc	tca tcc tca gac aca agc	19362
Glu Thr Ser Thr	Ser Gln Lys Ile Gly	Ser Ser Ser Asp Thr Ser	
6375	6380	6385	
acg gtc ttt gac	aaa gca ttc act gct	gct act act gag gtc tcc	19407
Thr Val Phe Asp	Lys Ala Phe Thr Ala	Ala Thr Thr Glu Val Ser	
6390	6395	6400	
aga aca gaa ctc	acc tcc tct agc aga	aca tcc atc caa ggc act	19452
Arg Thr Glu Leu	Thr Ser Ser Ser Arg	Thr Ser Ile Gln Gly Thr	
6405	6410	6415	
gaa aag ccc aca	atg tca ccg gac acc	tcc aca aga tct gtc acc	19497
Glu Lys Pro Thr	Met Ser Pro Asp Thr	Ser Thr Arg Ser Val Thr	
6420	6425	6430	
atg ctt tct act	ttt gct ggc ctg aca	aaa tcc gaa gaa agg acc	19542
Met Leu Ser Thr	Phe Ala Gly Leu Thr	Lys Ser Glu Glu Arg Thr	
6435	6440	6445	
att gcc acc caa	aca ggt cct cat agg	gcg aca tca cag ggt acc	19587
Ile Ala Thr Gln	Thr Gly Pro His Arg	Ala Thr Ser Gln Gly Thr	
6450	6455	6460	
ctt acc tgg gac	aca tca atc aca acc	tca cag gca ggg acc cac	19632
Leu Thr Trp Asp	Thr Ser Ile Thr Thr	Ser Gln Ala Gly Thr His	
6465	6470	6475	
tca gct atg act	cat gga ttt tca caa	tta gat ttg tcc act ctt	19677
Ser Ala Met Thr	His Gly Phe Ser Gln	Leu Asp Leu Ser Thr Leu	
6480	6485	6490	
acg agt aga gtt	cct gag tac ata tca	ggg aca agc cca ccc tct	19722
Thr Ser Arg Val	Pro Glu Tyr Ile Ser	Gly Thr Ser Pro Pro Ser	
6495	6500	6505	
gtg gaa aaa acc	agc tct tcc tct tcc	ctt ctg tct tta cca gca	19767
Val Glu Lys Thr	Ser Ser Ser Ser Ser	Leu Leu Ser Leu Pro Ala	
6510	6515	6520	
ata acc tca ccg	tcc cct gta cct act	aca tta cca gaa agt agg	19812

414

Ile Thr Ser Pro	Ser Pro Val Pro	Thr	Thr Leu Pro Glu	Ser Arg	
6525		6530		6535	
ccg tct tct cct	gtt cat ctg act	tca	ctc ccc acc tct	ggc cta	19857
Pro Ser Ser Pro	Val His Leu Thr	Ser	Leu Pro Thr Ser	Gly Leu	
6540		6545		6550	
gtg aag acc aca	gat atg ctg gca	tct	gtg gcc agt tta	cct cca	19902
Val Lys Thr Thr	Asp Met Leu Ala	Ser	Val Ala Ser Leu	Pro Pro	
6555		6560		6565	
aac ttg ggc agc	acc tca cat aag	ata	ccg act act tca	gaa gac	19947
Asn Leu Gly Ser	Thr Ser His Lys	Ile	Pro Thr Thr Ser	Glu Asp	
6570		6575		6580	
att aaa gat aca	gag aaa atg tat	cct	tcc aca aac ata	gca gta	19992
Ile Lys Asp Thr	Glu Lys Met Tyr	Pro	Ser Thr Asn Ile	Ala Val	
6585		6590		6595	
acc aat gtg ggg	acc acc act tct	gaa	aag gaa tct tat	tcg tct	20037
Thr Asn Val Gly	Thr Thr Thr Ser	Glu	Lys Glu Ser Tyr	Ser Ser	
6600		6605		6610	
gtc cca gcc tac	tca gaa cca ccc	aaa	gtc acc tct cca	atg gtt	20082
Val Pro Ala Tyr	Ser Glu Pro Pro	Lys	Val Thr Ser Pro	Met Val	
6615		6620		6625	
acc tct ttc aac	ata agg gac acc	att	gtt tcc aca tcc	atg cct	20127
Thr Ser Phe Asn	Ile Arg Asp Thr	Ile	Val Ser Thr Ser	Met Pro	
6630		6635		6640	
ggc tcc tct gag	att aca agg att	gag	atg gag tca aca	ttc tcc	20172
Gly Ser Ser Glu	Ile Thr Arg Ile	Glu	Met Glu Ser Thr	Phe Ser	
6645		6650		6655	
gtg gct cat ggg	ctg aag gga acc	agc	acc tcc cag gac	ccc atc	20217
Val Ala His Gly	Leu Lys Gly Thr	Ser	Thr Ser Gln Asp	Pro Ile	
6660		6665		6670	
gta tcc aca gag	aaa agt gct gtc	ctt	cac aag ttg acc	act ggt	20262
Val Ser Thr Glu	Lys Ser Ala Val	Leu	His Lys Leu Thr	Thr Gly	
6675		6680		6685	
gct act gag acc	tct agg aca gaa	gtt	gcc tct tct aga	aga aca	20307
Ala Thr Glu Thr	Ser Arg Thr Glu	Val	Ala Ser Ser Arg	Arg Thr	
6690		6695		6700	
tcc att cca ggc	cct gat cat tcc	aca	gag tca cca gac	atc tcc	20352
Ser Ile Pro Gly	Pro Asp His Ser	Thr	Glu Ser Pro Asp	Ile Ser	
6705		6710		6715	
act gaa gtg atc	ccc agc ctg cct	atc	tcc ctt ggc att	aca gaa	20397
Thr Glu Val Ile	Pro Ser Leu Pro	Ile	Ser Leu Gly Ile	Thr Glu	
6720		6725		6730	

415

tct tca aat atg acc atc atc act cga aca ggt cct cct ctt ggc	20442
Ser Ser Asn Met Thr Ile Ile Thr Arg Thr Gly Pro Pro Leu Gly	
6735 6740 6745	
tct aca tca cag ggc aca ttt acc ttg gac aca cca act aca tcc	20487
Ser Thr Ser Gln Gly Thr Phe Thr Leu Asp Thr Pro Thr Thr Ser	
6750 6755 6760	
tcc agg gca gga aca cac tcg atg gcg act cag gaa ttt cca cac	20532
Ser Arg Ala Gly Thr His Ser Met Ala Thr Gln Glu Phe Pro His	
6765 6770 6775	
tca gaa atg acc act gtc atg aac aag gac cct gag att cta tca	20577
Ser Glu Met Thr Thr Val Met Asn Lys Asp Pro Glu Ile Leu Ser	
6780 6785 6790	
tgg aca atc cct cct tct ata gag aaa acc agc ttc tcc tct tcc	20622
Trp Thr Ile Pro Pro Ser Ile Glu Lys Thr Ser Phe Ser Ser Ser	
6795 6800 6805	
ctg atg cct tca cca gcc atg act tca cct cct gtt tcc tca aca	20667
Leu Met Pro Ser Pro Ala Met Thr Ser Pro Pro Val Ser Ser Thr	
6810 6815 6820	
tta cca aag acc att cac acc act cct tct cct atg acc tca ctg	20712
Leu Pro Lys Thr Ile His Thr Thr Pro Ser Pro Met Thr Ser Leu	
6825 6830 6835	
ctc acc cct agc cta gtg atg acc aca gac aca ttg ggc aca agc	20757
Leu Thr Pro Ser Leu Val Met Thr Thr Asp Thr Leu Gly Thr Ser	
6840 6845 6850	
cca gaa cct aca acc agt tca cct cca aat ttg agc agt acc tca	20802
Pro Glu Pro Thr Thr Ser Ser Pro Pro Asn Leu Ser Ser Thr Ser	
6855 6860 6865	
cat gag ata ctg aca aca gat gaa gac acc aca gct ata gaa gcc	20847
His Glu Ile Leu Thr Thr Asp Glu Asp Thr Thr Ala Ile Glu Ala	
6870 6875 6880	
atg cat cct tcc aca agc aca gca gcg act aat gtg gaa acc acc	20892
Met His Pro Ser Thr Ser Thr Ala Ala Thr Asn Val Glu Thr Thr	
6885 6890 6895	
agt tct gga cat ggg tca caa tcc tct gtc cta gct gac tca gaa	20937
Ser Ser Gly His Gly Ser Gln Ser Ser Val Leu Ala Asp Ser Glu	
6900 6905 6910	
aaa acc aag gcc aca gct cca atg gat acc acc tcc acc atg ggg	20982
Lys Thr Lys Ala Thr Ala Pro Met Asp Thr Thr Ser Thr Met Gly	
6915 6920 6925	
cat aca act gtt tcc aca tca atg tct gtt tcc tct gag act aca	21027

416

His Thr Thr Val 6930	Ser Thr Ser Met 6935	Val Ser Ser Glu Thr Thr 6940	
aaa att aag aga Lys Ile Lys Arg 6945	gag tca aca tat tcc Glu Ser Thr Tyr Ser 6950	ttg act cct gga ctg aga Leu Thr Pro Gly Leu Arg 6955	21072
gag acc agc att Glu Thr Ser Ile 6960	tcc caa aat gcc agc Ser Gln Asn Ala Ser 6965	ttt tcc act gac aca agt Phe Ser Thr Asp Thr Ser 6970	21117
att gtt ctt tca Ile Val Leu Ser 6975	gaa gtc ccc act ggt Glu Val Pro Thr Gly 6980	act act gct gag gtc tcc Thr Thr Ala Glu Val Ser 6985	21162
agg aca gaa gtc Arg Thr Glu Val 6990	acc tcc tct ggt aga Thr Ser Ser Gly Arg 6995	aca tcc atc cct ggc cct Thr Ser Ile Pro Gly Pro 7000	21207
tct cag tcc aca Ser Gln Ser Thr 7005	gtt ttg cca gaa ata Val Leu Pro Glu Ile 7010	tcc aca aga aca atg aca Ser Thr Arg Thr Met Thr 7015	21252
agg ctc ttt gcc Arg Leu Phe Ala 7020	tcg ccc acc atg aca Ser Pro Thr Met Thr 7025	gaa tca gca gaa atg acc Glu Ser Ala Glu Met Thr 7030	21297
atc ccc act caa Ile Pro Thr Gln 7035	aca ggt cct tct ggg Thr Gly Pro Ser Gly 7040	tct acc tca cag gat acc Ser Thr Ser Gln Asp Thr 7045	21342
ctt acc ttg gac Leu Thr Leu Asp 7050	aca tcc acc aca aag Thr Ser Thr Thr Lys 7055	tcc cag gca aag act cat Ser Gln Ala Lys Thr His 7060	21387
tca act ttg act Ser Thr Leu Thr 7065	cag aga ttt cca cac Gln Arg Phe Pro His 7070	tca gag atg acc act ctc Ser Glu Met Thr Thr Leu 7075	21432
atg agc aga ggt Met Ser Arg Gly 7080	cct gga gat atg tca Pro Gly Asp Met Ser 7085	tgg caa agc tct ccc tct Trp Gln Ser Ser Pro Ser 7090	21477
ctg gaa aat ccc Leu Glu Asn Pro 7095	agc tct ctc cct tcc Ser Ser Leu Pro Ser 7100	ctg ctg tct tta cct gcc Leu Leu Ser Leu Pro Ala 7105	21522
aca acc tca cct Thr Thr Ser Pro 7110	cct ccc att tcc tcc Pro Pro Ile Ser Ser 7115	aca tta cca gtg act atc Thr Leu Pro Val Thr Ile 7120	21567
tcc tcc tct cct Ser Ser Ser Pro 7125	ctt cct gtg act tca Leu Pro Val Thr Ser 7130	ctt ctc acc tct agc ccg Leu Leu Thr Ser Ser Pro 7135	21612

417

gta acg acc aca gac atg tta cac aca agc cca gaa ctt gta acc	21657
Val Thr Thr Thr Asp Met Leu His Thr Ser Pro Glu Leu Val Thr	
7140 7145 7150	
agt tca cct cca aag ctg agc cac act tca gat gag aga ctg acc	21702
Ser Ser Pro Pro Lys Leu Ser His Thr Ser Asp Glu Arg Leu Thr	
7155 7160 7165	
act ggc aag gac acc aca aat aca gaa gct gtg cat cct tcc aca	21747
Thr Gly Lys Asp Thr Thr Asn Thr Glu Ala Val His Pro Ser Thr	
7170 7175 7180	
aac aca gca gcg tcc aat gtg gag att ccc agc tct gga cat gaa	21792
Asn Thr Ala Ala Ser Asn Val Glu Ile Pro Ser Ser Gly His Glu	
7185 7190 7195	
tcc cct tcc tct gcc tta gct gac tca gag aca tcc aaa gcc aca	21837
Ser Pro Ser Ser Ala Leu Ala Asp Ser Glu Thr Ser Lys Ala Thr	
7200 7205 7210	
tca cca atg ttt att acc tcc acc cag gag gat aca act gtt gcc	21882
Ser Pro Met Phe Ile Thr Ser Thr Gln Glu Asp Thr Thr Val Ala	
7215 7220 7225	
ata tca acc cct cac ttc ttg gag act agc aga att cag aaa gag	21927
Ile Ser Thr Pro His Phe Leu Glu Thr Ser Arg Ile Gln Lys Glu	
7230 7235 7240	
tca att tcc tcc ctg agc cct aaa ttg agg gag aca ggc agt tct	21972
Ser Ile Ser Ser Leu Ser Pro Lys Leu Arg Glu Thr Gly Ser Ser	
7245 7250 7255	
gtg gag aca agc tca gcc ata gag aca agt gct gtc ctt tct gaa	22017
Val Glu Thr Ser Ser Ala Ile Glu Thr Ser Ala Val Leu Ser Glu	
7260 7265 7270	
gtg tcc gtt ggt gct act act gag atc tcc agg aca gaa gtc acc	22062
Val Ser Val Gly Ala Thr Thr Glu Ile Ser Arg Thr Glu Val Thr	
7275 7280 7285	
tcc tct agc aga aca tcc atc tct ggt tct gct gag tcc aca atg	22107
Ser Ser Ser Arg Thr Ser Ile Ser Gly Ser Ala Glu Ser Thr Met	
7290 7295 7300	
ttg cca gaa ata tcc acc aca aga aaa atc att aag ttc cct act	22152
Leu Pro Glu Ile Ser Thr Thr Arg Lys Ile Ile Lys Phe Pro Thr	
7305 7310 7315	
tcc ccc atc ctg gca gaa tca tca gaa atg acc atc aag acc caa	22197
Ser Pro Ile Leu Ala Glu Ser Ser Glu Met Thr Ile Lys Thr Gln	
7320 7325 7330	
aca agt cct cct ggg tct aca tca gag agt acc ttt aca tta gac	22242

418

Thr Ser Pro Pro	Gly Ser Thr Ser	Glu Ser Thr Phe Thr	Leu Asp	
7335		7340	7345	
aca tca acc act	ccc tcc ttg gta	ata acc cat tcg act	atg act	22287
Thr Ser Thr Thr	Pro Ser Leu Val	Ile Thr His Ser Thr	Met Thr	
7350		7355	7360	
cag aga ttg cca	cac tca gag ata	acc act ctt gtg agt	aga ggt	22332
Gln Arg Leu Pro	His Ser Glu Ile	Thr Thr Leu Val Ser	Arg Gly	
7365		7370	7375	
gct ggg gat gtg	cca cgg ccc agc	tct ctc cct gtg gaa	gaa aca	22377
Ala Gly Asp Val	Pro Arg Pro Ser	Ser Leu Pro Val Glu	Glu Thr	
7380		7385	7390	
agc cct cca tct	tcc cag ctg tct	tta tct gcc atg atc	tca cct	22422
Ser Pro Pro Ser	Ser Ser Gln Leu Ser	Leu Ser Ala Met Ile	Ser Pro	
7395		7400	7405	
tct cct gtt tct	tcc aca tta cca	gca agt agc cac tcc	tct tct	22467
Ser Pro Val Ser	Ser Thr Leu Pro	Ala Ser Ser His Ser	Ser Ser	
7410		7415	7420	
gct tct gtg act	tca ctt ctg aca	cca ggc caa gtg aag	act act	22512
Ala Ser Val Thr	Ser Leu Leu Thr	Pro Gly Gln Val Lys	Thr Thr	
7425		7430	7435	
gag gtg ttg gac	gca agt gca gaa	cct gaa acc agt tca	cct cca	22557
Glu Val Leu Asp	Ala Ser Ala Glu	Pro Glu Thr Ser Ser	Pro Pro	
7440		7445	7450	
agt ttg agc agc	acc tca gtt gaa	ata ctg gcc acc tct	gaa gtc	22602
Ser Leu Ser Ser	Thr Ser Val Glu	Ile Leu Ala Thr Ser	Glu Val	
7455		7460	7465	
acc aca gat acg	gag aaa att cat	cct ttc tca aac acg	gca gta	22647
Thr Thr Asp Thr	Glu Lys Ile His	Pro Phe Ser Asn Thr	Ala Val	
7470		7475	7480	
acc aaa gtt gga	act tcc agt tct	gga cat gaa tcc cct	tcc tct	22692
Thr Lys Val Gly	Thr Ser Ser Ser	Gly His Glu Ser Pro	Ser Ser	
7485		7490	7495	
gtc cta cct gac	tca gag aca acc	aaa gcc aca tcg gca	atg ggt	22737
Val Leu Pro Asp	Ser Glu Thr Thr	Lys Ala Thr Ser Ala	Met Gly	
7500		7505	7510	
acc atc tcc att	atg ggg gat aca	agt gtt tct aca tta	act cct	22782
Thr Ile Ser Ile	Met Gly Asp Thr	Ser Val Ser Thr Leu	Thr Pro	
7515		7520	7525	
gcc tta tct aac	act agg aaa att	cag tca gag cca gct	tcc tca	22827
Ala Leu Ser Asn	Thr Arg Lys Ile	Gln Ser Glu Pro Ala	Ser Ser	
7530		7535	7540	

419

ctg acc acc aga	ttg agg gag acc agc	acc tct gaa gag acc agc	22872
Leu Thr Thr Arg	Leu Arg Glu Thr Ser	Thr Ser Glu Glu Thr Ser	
7545	7550	7555	
tta gcc aca gaa	gca aac act gtt ctt	tct aaa gtg tcc act ggt	22917
Leu Ala Thr Glu	Ala Asn Thr Val Leu	Ser Lys Val Ser Thr Gly	
7560	7565	7570	
gct act act gag	gtc tcc agg aca gaa	gcc atc tcc ttt agc aga	22962
Ala Thr Thr Glu	Val Ser Arg Thr Glu	Ala Ile Ser Phe Ser Arg	
7575	7580	7585	
aca tcc atg tca	ggc cct gag cag tcc	aca atg tca caa gac atc	23007
Thr Ser Met Ser	Gly Pro Glu Gln Ser	Thr Met Ser Gln Asp Ile	
7590	7595	7600	
tcc ata gga acc	atc ccc agg att tct	gcc tcc tct gtc ctg aca	23052
Ser Ile Gly Thr	Ile Pro Arg Ile Ser	Ala Ser Ser Val Leu Thr	
7605	7610	7615	
gaa tct gca aaa	atg acc atc aca acc	caa aca ggt cct tcg gag	23097
Glu Ser Ala Lys	Met Thr Ile Thr Thr	Gln Thr Gly Pro Ser Glu	
7620	7625	7630	
tct aca cta gaa	agt acc ctt aat ttg	aac aca gca acc aca ccc	23142
Ser Thr Leu Glu	Ser Thr Leu Asn Leu	Asn Thr Ala Thr Thr Pro	
7635	7640	7645	
tct tgg gtg gaa	acc cac tct ata gta	att cag gga ttt cca cac	23187
Ser Trp Val Glu	Thr His Ser Ile Val	Ile Gln Gly Phe Pro His	
7650	7655	7660	
cca gag atg acc	act tcc atg ggc aga	ggt cct gga ggt gtg tca	23232
Pro Glu Met Thr	Thr Ser Met Gly Arg	Gly Pro Gly Gly Val Ser	
7665	7670	7675	
tgg cct agc cct	ccc ttt gtg aaa gaa	acc agc cct cca tcc tcc	23277
Trp Pro Ser Pro	Pro Phe Val Lys Glu	Thr Ser Pro Pro Ser Ser	
7680	7685	7690	
ccg ctg tct tta	cct gcc gtg acc tca	cct cat cct gtt tcc acc	23322
Pro Leu Ser Leu	Pro Ala Val Thr Ser	Pro His Pro Val Ser Thr	
7695	7700	7705	
aca ttc cta gca	cat atc ccc ccc tct	ccc ctt cct gtg act tca	23367
Thr Phe Leu Ala	His Ile Pro Pro Ser	Pro Leu Pro Val Thr Ser	
7710	7715	7720	
ctt ctc acc tct	ggc ccg gcg aca acc	aca gat atc ttg ggt aca	23412
Leu Leu Thr Ser	Gly Pro Ala Thr Thr	Thr Asp Ile Leu Gly Thr	
7725	7730	7735	
agc aca gaa cct	gga acc agt tca tct	tca agt ttg agc acc acc	23457

420

Ser Thr Glu Pro	Gly Thr Ser Ser Ser	Ser Ser Leu Ser Thr Thr	
7740	7745	7750	
tcc cat gag aga	ctg acc act tac aaa	gac act gca cat aca gaa	23502
Ser His Glu Arg	Leu Thr Thr Tyr Lys	Asp Thr Ala His Thr Glu	
7755	7760	7765	
gcc gtg cat cct	tcc aca aac aca gga	ggg acc aat gtg gca acc	23547
Ala Val His Pro	Ser Thr Asn Thr Gly	Gly Thr Asn Val Ala Thr	
7770	7775	7780	
acc agc tct gga	tat aaa tca cag tcc	tct gtc cta gct gac tca	23592
Thr Ser Ser Gly	Tyr Lys Ser Gln Ser	Ser Val Leu Ala Asp Ser	
7785	7790	7795	
tct cca atg tgt	acc acc tcc acc atg	ggg gat aca agt gtt ctc	23637
Ser Pro Met Cys	Thr Thr Ser Thr Met	Gly Asp Thr Ser Val Leu	
7800	7805	7810	
aca tca act cct	gcc ttc ctt gag act	agg agg att cag aca gag	23682
Thr Ser Thr Pro	Ala Phe Leu Glu Thr	Arg Arg Ile Gln Thr Glu	
7815	7820	7825	
cta gct tcc tcc	ctg acc cct gga ttg	agg gag tcc agt ggc tct	23727
Leu Ala Ser Ser	Leu Thr Pro Gly Leu	Arg Glu Ser Ser Gly Ser	
7830	7835	7840	
gaa ggg acc agc	tca ggc acc aag atg	agc act gtc ctc tct aaa	23772
Glu Gly Thr Ser	Ser Gly Thr Lys Met	Ser Thr Val Leu Ser Lys	
7845	7850	7855	
gtg ccc act ggt	gct act act gag atc	tcc aag gaa gac gtc acc	23817
Val Pro Thr Gly	Ala Thr Thr Glu Ile	Ser Lys Glu Asp Val Thr	
7860	7865	7870	
tcc atc cca ggt	ccc gct caa tcc aca	ata tca cca gac atc tcc	23862
Ser Ile Pro Gly	Pro Ala Gln Ser Thr	Ile Ser Pro Asp Ile Ser	
7875	7880	7885	
aca aga acc gtc	agc tgg ttc tct aca	tcc cct gtc atg aca gaa	23907
Thr Arg Thr Val	Ser Trp Phe Ser Thr	Ser Pro Val Met Thr Glu	
7890	7895	7900	
tca gca gaa ata	acc atg aac acc cat	aca agt cct tta ggg gcc	23952
Ser Ala Glu Ile	Thr Met Asn Thr His	Thr Ser Pro Leu Gly Ala	
7905	7910	7915	
aca aca caa ggc	acc agt act ttg gcc	acg tca agc aca acc tct	23997
Thr Thr Gln Gly	Thr Ser Thr Leu Ala	Thr Ser Ser Thr Thr Ser	
7920	7925	7930	
ttg aca atg aca	cac tca act ata tct	caa gga ttt tca cac tca	24042
Leu Thr Met Thr	His Ser Thr Ile Ser	Gln Gly Phe Ser His Ser	
7935	7940	7945	

421

cag atg agc act	ctt atg agg agg ggt	cct gag gat gta tca tgg	24087
Gln Met Ser Thr	Leu Met Arg Arg Gly	Pro Glu Asp Val Ser Trp	
7950	7955	7960	
atg agc cct ccc	ctt ctg gaa aaa act	aga cct tcc ttt tct ctg	24132
Met Ser Pro Pro	Leu Leu Glu Lys Thr	Arg Pro Ser Phe Ser Leu	
7965	7970	7975	
atg tct tca cca	gcc aca act tca cct	tct cct gtt tcc tcc aca	24177
Met Ser Ser Pro	Ala Thr Thr Ser Pro	Ser Pro Val Ser Ser Thr	
7980	7985	7990	
tta cca gag agc	atc tct tcc tct cct	ctt cct gtg act tca ctc	24222
Leu Pro Glu Ser	Ile Ser Ser Ser Pro	Leu Pro Val Thr Ser Leu	
7995	8000	8005	
ctc acg tct ggc	ttg gca aaa act aca	gat atg ttg cac aaa agc	24267
Leu Thr Ser Gly	Leu Ala Lys Thr Thr	Asp Met Leu His Lys Ser	
8010	8015	8020	
tca gaa cct gta	acc aac tca cct gca	aat ttg agc agc acc tca	24312
Ser Glu Pro Val	Thr Asn Ser Pro Ala	Asn Leu Ser Ser Thr Ser	
8025	8030	8035	
gtt gaa ata ctg	gcc acc tct gaa gtc	acc aca gat aca gag aaa	24357
Val Glu Ile Leu	Ala Thr Ser Glu Val	Thr Thr Asp Thr Glu Lys	
8040	8045	8050	
act cat cct tct	tca aac aga aca gtg	acc gat gtg ggg acc tcc	24402
Thr His Pro Ser	Ser Asn Arg Thr Val	Thr Asp Val Gly Thr Ser	
8055	8060	8065	
agt tct gga cat	gaa tcc act tcc ttt	gtc cta gct gac tca cag	24447
Ser Ser Gly His	Glu Ser Thr Ser Phe	Val Leu Ala Asp Ser Gln	
8070	8075	8080	
aca tcc aaa gtc	aca tct cca atg gtt	att acc tcc acc atg gag	24492
Thr Ser Lys Val	Thr Ser Pro Met Val	Ile Thr Ser Thr Met Glu	
8085	8090	8095	
gat acg agt gtc	tcc aca tca act cct	ggc ttt ttt gag act agc	24537
Asp Thr Ser Val	Ser Thr Ser Thr Pro	Gly Phe Phe Glu Thr Ser	
8100	8105	8110	
aga att cag aca	gaa cca aca tcc tcc	ctg acc ctt gga ctg aga	24582
Arg Ile Gln Thr	Glu Pro Thr Ser Ser	Leu Thr Leu Gly Leu Arg	
8115	8120	8125	
aag acc agc agc	tct gag ggg acc agc	tta gcc aca gag atg agc	24627
Lys Thr Ser Ser	Ser Glu Gly Thr Ser	Leu Ala Thr Glu Met Ser	
8130	8135	8140	
act gtc ctt tct	gga gtg ccc act ggt	gcc act gct gaa gtc tcc	24672

422

Thr Val Leu Ser	Gly Val Pro Thr	Gly Ala Thr Ala Glu Val Ser	
8145		8150 8155	
agg aca gaa gtc	acc tcc tct agc aga	aca tcc atc tca ggc ttt	24717
Arg Thr Glu Val	Thr Ser Ser Ser Arg	Thr Ser Ile Ser Gly Phe	
8160	8165	8170	
gct cag ctc aca	gtg tca cca gag act	tcc aca gaa acc atc acc	24762
Ala Gln Leu Thr	Val Ser Pro Glu Thr	Ser Thr Glu Thr Ile Thr	
8175	8180	8185	
aga ctc cct acc	tcc agc ata atg aca	gaa tca gca gaa atg atg	24807
Arg Leu Pro Thr	Ser Ser Ile Met Thr	Glu Ser Ala Glu Met Met	
8190	8195	8200	
atc aag aca caa	aca gat cct cct ggg	tct aca cca gag agt act	24852
Ile Lys Thr Gln	Thr Asp Pro Pro Gly	Ser Thr Pro Glu Ser Thr	
8205	8210	8215	
cat act gtg gac	ata tca aca aca ccc	aac tgg gta gaa acc cac	24897
His Thr Val Asp	Ile Ser Thr Thr Pro	Asn Trp Val Glu Thr His	
8220	8225	8230	
tcg act gtg act	cag aga ttt tca cac	tca gag atg acc act ctt	24942
Ser Thr Val Thr	Gln Arg Phe Ser His	Ser Glu Met Thr Thr Leu	
8235	8240	8245	
gtg agc aga agc	cct ggt gat atg tta	tgg cct agt caa tcc tct	24987
Val Ser Arg Ser	Pro Gly Asp Met Leu	Trp Pro Ser Gln Ser Ser	
8250	8255	8260	
gtg gaa gaa acc	agc tct gcc tct tcc	ctg ctg tct ctg cct gcc	25032
Val Glu Glu Thr	Ser Ser Ala Ser Ser	Leu Leu Ser Leu Pro Ala	
8265	8270	8275	
acg acc tca cct	tct cct gtt tcc tct	aca tta gta gag gat ttc	25077
Thr Thr Ser Pro	Ser Pro Val Ser Ser	Thr Leu Val Glu Asp Phe	
8280	8285	8290	
cct tcc gct tct	ctt cct gtg act tct	ctt ctc acc cct ggc ctg	25122
Pro Ser Ala Ser	Leu Pro Val Thr Ser	Leu Leu Thr Pro Gly Leu	
8295	8300	8305	
gtg ata acc aca	gac agg atg ggc ata	agc aga gaa cct gga acc	25167
Val Ile Thr Thr	Asp Arg Met Gly Ile	Ser Arg Glu Pro Gly Thr	
8310	8315	8320	
agt tcc act tca	aat ttg agc agc acc	tcc cat gag aga ctg acc	25212
Ser Ser Thr Ser	Asn Leu Ser Ser Thr	Ser His Glu Arg Leu Thr	
8325	8330	8335	
act ttg gaa gac	act gta gat aca gaa	gac atg cag cct tcc aca	25257
Thr Leu Glu Asp	Thr Val Asp Thr Glu	Asp Met Gln Pro Ser Thr	
8340	8345	8350	

423

cac aca gca gtg	acc aac gtg agg acc	tcc att tct gga cat gaa	25302
His Thr Ala Val	Thr Asn Val Arg Thr	Ser Ile Ser Gly His Glu	
8355	8360	8365	
tca caa tct tct	gtc cta tct gac tca	gag aca ccc aaa gcc aca	25347
Ser Gln Ser Ser	Val Leu Ser Asp Ser	Glu Thr Pro Lys Ala Thr	
8370	8375	8380	
tct cca atg ggt	acc acc tac acc atg	ggg gaa acg agt gtt tcc	25392
Ser Pro Met Gly	Thr Thr Tyr Thr Met	Gly Glu Thr Ser Val Ser	
8385	8390	8395	
ata tcc act tct	gac ttc ttt gag acc	agc aga att cag ata gaa	25437
Ile Ser Thr Ser	Asp Phe Phe Glu Thr	Ser Arg Ile Gln Ile Glu	
8400	8405	8410	
cca aca tcc tcc	ctg act tct gga ttg	agg gag acc agc agc tct	25482
Pro Thr Ser Ser	Leu Thr Ser Gly Leu	Arg Glu Thr Ser Ser Ser	
8415	8420	8425	
gag agg atc agc	tca gcc aca gag gga	agc act gtc ctt tct gaa	25527
Glu Arg Ile Ser	Ser Ala Thr Glu Gly	Ser Thr Val Leu Ser Glu	
8430	8435	8440	
gtg ccc agt ggt	gct acc act gag gtc	tcc agg aca gaa gtg ata	25572
Val Pro Ser Gly	Ala Thr Thr Glu Val	Ser Arg Thr Glu Val Ile	
8445	8450	8455	
tcc tct agg gga	aca tcc atg tca ggg	cct gat cag ttc acc ata	25617
Ser Ser Arg Gly	Thr Ser Met Ser Gly	Pro Asp Gln Phe Thr Ile	
8460	8465	8470	
tca cca gac atc	tct act gaa gcg atc	acc agg ctt tct act tcc	25662
Ser Pro Asp Ile	Ser Thr Glu Ala Ile	Thr Arg Leu Ser Thr Ser	
8475	8480	8485	
ccc att atg aca	gaa tca gca gaa agt	gcc atc act att gag aca	25707
Pro Ile Met Thr	Glu Ser Ala Glu Ser	Ala Ile Thr Ile Glu Thr	
8490	8495	8500	
ggt tct cct ggg	gct aca tca gag ggt	acc ctc acc ttg gac acc	25752
Gly Ser Pro Gly	Ala Thr Ser Glu Gly	Thr Leu Thr Leu Asp Thr	
8505	8510	8515	
tca aca aca acc	ttt tgg tca ggg acc	cac tca act gca tct cca	25797
Ser Thr Thr Thr	Phe Trp Ser Gly Thr	His Ser Thr Ala Ser Pro	
8520	8525	8530	
gga ttt tca cac	tca gag atg acc act	ctt atg agt aga act cct	25842
Gly Phe Ser His	Ser Glu Met Thr Thr	Leu Met Ser Arg Thr Pro	
8535	8540	8545	
gga gat gtg cca	tgg ccg agc ctt ccc	tct gtg gaa gaa gcc agc	25887

424

Gly Asp Val Pro	Trp Pro Ser Leu Pro	Ser Val Glu Glu Ala Ser	
8550	8555	8560	
tct gtc tct tcc	tca ctg tct tca cct	gcc atg acc tca act tct	25932
Ser Val Ser Ser	Ser Leu Ser Ser Pro	Ala Met Thr Ser Thr Ser	
8565	8570	8575	
ttt ttc tcc aca	tta cca gag agc atc	tcc tcc tct cct cat cct	25977
Phe Phe Ser Thr	Leu Pro Glu Ser Ile	Ser Ser Ser Pro His Pro	
8580	8585	8590	
gtg act gca ctt	ctc acc ctt ggc cca	gtg aag acc aca gac atg	26022
Val Thr Ala Leu	Leu Thr Leu Gly Pro	Val Lys Thr Thr Asp Met	
8595	8600	8605	
ttg cgc aca agc	tca gaa cct gaa acc	agt tca cct cca aat ttg	26067
Leu Arg Thr Ser	Ser Glu Pro Glu Thr	Ser Ser Pro Pro Asn Leu	
8610	8615	8620	
agc agc acc tca	gct gaa ata tta gcc	acg tct gaa gtc acc aaa	26112
Ser Ser Thr Ser	Ala Glu Ile Leu Ala	Thr Ser Glu Val Thr Lys	
8625	8630	8635	
gat aga gag aaa	att cat ccc tcc tca	aac aca cct gta gtc aat	26157
Asp Arg Glu Lys	Ile His Pro Ser Ser	Asn Thr Pro Val Val Asn	
8640	8645	8650	
gta ggg act gtg	att tat aaa cat cta	tcc cct tcc tct gtt ttg	26202
Val Gly Thr Val	Ile Tyr Lys His Leu	Ser Pro Ser Ser Val Leu	
8655	8660	8665	
gct gac tta gtg	aca aca aaa ccc aca	tct cca atg gct acc acc	26247
Ala Asp Leu Val	Thr Thr Lys Pro Thr	Ser Pro Met Ala Thr Thr	
8670	8675	8680	
tcc act ctg ggg	aat aca agt gtt tcc	aca tca act cct gcc ttc	26292
Ser Thr Leu Gly	Asn Thr Ser Val Ser	Thr Ser Thr Pro Ala Phe	
8685	8690	8695	
cca gaa act atg	atg aca cag cca act	tcc tcc ctg act tct gga	26337
Pro Glu Thr Met	Met Thr Gln Pro Thr	Ser Ser Leu Thr Ser Gly	
8700	8705	8710	
tta agg gag atc	agt acc tct caa gag	acc agc tca gca aca gag	26382
Leu Arg Glu Ile	Ser Thr Ser Gln Glu	Thr Ser Ser Ala Thr Glu	
8715	8720	8725	
aga agt gct tct	ctt tct gga atg ccc	act ggt gct act act aag	26427
Arg Ser Ala Ser	Leu Ser Gly Met Pro	Thr Gly Ala Thr Thr Lys	
8730	8735	8740	
gtc tcc aga aca	gaa gcc ctc tcc tta	ggc aga aca tcc acc cca	26472
Val Ser Arg Thr	Glu Ala Leu Ser Leu	Gly Arg Thr Ser Thr Pro	
8745	8750	8755	

425

ggt cct gct caa tcc aca ata tca cca gaa atc tcc acg gaa acc	26517
Gly Pro Ala Gln Ser Thr Ile Ser Pro Glu Ile Ser Thr Glu Thr	
8760 8765 8770	
atc act aga att tct act ccc ctc acc acg aca gga tca gca gaa	26562
Ile Thr Arg Ile Ser Thr Pro Leu Thr Thr Thr Gly Ser Ala Glu	
8775 8780 8785	
atg acc atc acc ccc aaa aca ggt cat tct ggg gca tcc tca caa	26607
Met Thr Ile Thr Pro Lys Thr Gly His Ser Gly Ala Ser Ser Gln	
8790 8795 8800	
ggt acc ttt acc ttg gac aca tca agc aga gcc tcc tgg cca gga	26652
Gly Thr Phe Thr Leu Asp Thr Ser Ser Arg Ala Ser Trp Pro Gly	
8805 8810 8815	
act cac tca gct gca act cac aga tct cca cac tca ggg atg acc	26697
Thr His Ser Ala Ala Thr His Arg Ser Pro His Ser Gly Met Thr	
8820 8825 8830	
act cct atg agc aga ggt cct gag gat gtg tca tgg cca agc cgc	26742
Thr Pro Met Ser Arg Gly Pro Glu Asp Val Ser Trp Pro Ser Arg	
8835 8840 8845	
cca tca gtg gaa aaa act agc cct cca tct tcc ctg gtg tct tta	26787
Pro Ser Val Glu Lys Thr Ser Pro Pro Ser Ser Leu Val Ser Leu	
8850 8855 8860	
tct gca gta acc tca cct tcg cca ctt tat tcc aca cca tct gag	26832
Ser Ala Val Thr Ser Pro Ser Pro Leu Tyr Ser Thr Pro Ser Glu	
8865 8870 8875	
agt agc cac tca tct cct ctc cgg gtg act tct ctt ttc acc cct	26877
Ser Ser His Ser Ser Pro Leu Arg Val Thr Ser Leu Phe Thr Pro	
8880 8885 8890	
gtc atg atg aag acc aca gac atg ttg gac aca agc ttg gaa cct	26922
Val Met Met Lys Thr Thr Asp Met Leu Asp Thr Ser Leu Glu Pro	
8895 8900 8905	
gtg acc act tca cct ccc agt atg aat atc acc tca gat gag agt	26967
Val Thr Thr Ser Pro Pro Ser Met Asn Ile Thr Ser Asp Glu Ser	
8910 8915 8920	
ctg gcc act tct aaa gcc acc atg gag aca gag gca att cag ctt	27012
Leu Ala Thr Ser Lys Ala Thr Met Glu Thr Glu Ala Ile Gln Leu	
8925 8930 8935	
tca gaa aac aca gct gtg act cag atg ggc acc atc agc gct aga	27057
Ser Glu Asn Thr Ala Val Thr Gln Met Gly Thr Ile Ser Ala Arg	
8940 8945 8950	
caa gaa ttc tat tcc tct tat cca ggc ctc cca gag cca tcc aaa	27102

426

Gln	Glu	Phe	Tyr	Ser	Ser	Tyr	Pro	Gly	Leu	Pro	Glu	Pro	Ser	Lys	
			8955					8960					8965		
gtg	aca	tct	cca	gtg	gtc	acc	tct	tcc	acc	ata	aaa	gac	att	gtt	27147
Val	Thr	Ser	Pro	Val	Val	Thr	Ser	Ser	Thr	Ile	Lys	Asp	Ile	Val	
			8970					8975					8980		
tct	aca	acc	ata	cct	gct	tcc	tct	gag	ata	aca	aga	att	gag	atg	27192
Ser	Thr	Thr	Ile	Pro	Ala	Ser	Ser	Glu	Ile	Thr	Arg	Ile	Glu	Met	
			8985					8990					8995		
gag	tca	aca	tcc	acc	ctg	acc	ccc	aca	cca	agg	gag	acc	agc	acc	27237
Glu	Ser	Thr	Ser	Thr	Leu	Thr	Pro	Thr	Pro	Arg	Glu	Thr	Ser	Thr	
			9000					9005					9010		
tcc	cag	gag	atc	cac	tca	gcc	aca	aag	cca	agc	act	gtt	cct	tac	27282
Ser	Gln	Glu	Ile	His	Ser	Ala	Thr	Lys	Pro	Ser	Thr	Val	Pro	Tyr	
			9015					9020					9025		
aag	gca	ctc	act	agt	gcc	acg	att	gag	gac	tcc	atg	aca	caa	gtc	27327
Lys	Ala	Leu	Thr	Ser	Ala	Thr	Ile	Glu	Asp	Ser	Met	Thr	Gln	Val	
			9030					9035					9040		
atg	tcc	tct	agc	aga	gga	cct	agc	cct	gat	cag	tcc	aca	atg	tca	27372
Met	Ser	Ser	Ser	Arg	Gly	Pro	Ser	Pro	Asp	Gln	Ser	Thr	Met	Ser	
			9045					9050					9055		
caa	gac	ata	tcc	agt	gaa	gtg	atc	acc	agg	ctc	tct	acc	tcc	ccc	27417
Gln	Asp	Ile	Ser	Ser	Glu	Val	Ile	Thr	Arg	Leu	Ser	Thr	Ser	Pro	
			9060					9065					9070		
atc	aag	gca	gaa	tct	aca	gaa	atg	acc	att	acc	acc	caa	aca	ggc	27462
Ile	Lys	Ala	Glu	Ser	Thr	Glu	Met	Thr	Ile	Thr	Thr	Gln	Thr	Gly	
			9075					9080					9085		
tct	cct	ggg	gct	aca	tca	agg	ggc	acc	ctt	acc	ttg	gac	act	tca	27507
Ser	Pro	Gly	Ala	Thr	Ser	Arg	Gly	Thr	Leu	Thr	Leu	Asp	Thr	Ser	
			9090					9095					9100		
aca	act	ttt	atg	tca	ggg	acc	cac	tca	act	gca	tct	caa	gga	ttt	27552
Thr	Thr	Phe	Met	Ser	Gly	Thr	His	Ser	Thr	Ala	Ser	Gln	Gly	Phe	
			9105					9110					9115		
tca	cac	tca	cag	atg	acc	gct	ctt	atg	agt	aga	act	cct	gga	gat	27597
Ser	His	Ser	Gln	Met	Thr	Ala	Leu	Met	Ser	Arg	Thr	Pro	Gly	Asp	
			9120					9125					9130		
gtg	cca	tgg	cta	agc	cat	ccc	tct	gtg	gaa	gaa	gcc	agc	tct	gcc	27642
Val	Pro	Trp	Leu	Ser	His	Pro	Ser	Val	Glu	Glu	Ala	Ser	Ser	Ala	
			9135					9140					9145		
tct	ttc	tca	ctg	tct	tca	cct	gtc	atg	acc	tca	tct	tct	ccc	gtt	27687
Ser	Phe	Ser	Leu	Ser	Ser	Pro	Val	Met	Thr	Ser	Ser	Ser	Pro	Val	
			9150					9155					9160		

427

tct tcc aca tta	cca gac agc atc cac	tct tct tcg ctt cct	gtg	27732
Ser Ser Thr Leu	Pro Asp Ser Ile His	Ser Ser Ser Leu Pro	Val	
9165	9170	9175		
aca tca ctt ctc	acc tca ggg ctg gtg	aag acc aca gag ctg	ttg	27777
Thr Ser Leu Leu	Thr Ser Gly Leu Val	Lys Thr Thr Glu Leu	Leu	
9180	9185	9190		
ggc aca agc tca	gaa cct gaa acc agt	tca ccc cca aat ttg	agc	27822
Gly Thr Ser Ser	Glu Pro Glu Thr Ser	Ser Pro Pro Asn Leu	Ser	
9195	9200	9205		
agc acc tca gct	gaa ata ctg gcc acc	act gaa gtc act aca	gat	27867
Ser Thr Ser Ala	Glu Ile Leu Ala Thr	Thr Glu Val Thr Thr	Asp	
9210	9215	9220		
aca gag aaa ctg	gag atg acc aat gtg	gta acc tca ggt tat	aca	27912
Thr Glu Lys Leu	Glu Met Thr Asn Val	Val Thr Ser Gly Tyr	Thr	
9225	9230	9235		
cat gaa tct cct	tcc tct gtc cta gct	gac tca gtg aca aca	aag	27957
His Glu Ser Pro	Ser Ser Val Leu Ala	Asp Ser Val Thr Thr	Lys	
9240	9245	9250		
gcc aca tct tca	atg ggt atc acc tac	ccc aca gga gat aca	aat	28002
Ala Thr Ser Ser	Met Gly Ile Thr Tyr	Pro Thr Gly Asp Thr	Asn	
9255	9260	9265		
gtt ctc aca tca	acc cct gcc ttc tct	gac acc agt agg att	caa	28047
Val Leu Thr Ser	Thr Pro Ala Phe Ser	Asp Thr Ser Arg Ile	Gln	
9270	9275	9280		
aca aag tca aag	ctc tca ctg act cct	ggg ttg atg gag acc	agc	28092
Thr Lys Ser Lys	Leu Ser Leu Thr Pro	Gly Leu Met Glu Thr	Ser	
9285	9290	9295		
atc tct gaa gag	acc agc tct gcc aca	gaa aaa agc act gtc	ctt	28137
Ile Ser Glu Glu	Thr Ser Ser Ala Thr	Glu Lys Ser Thr Val	Leu	
9300	9305	9310		
tct agt gtg ccc	act ggt gct act act	gag gtc tcc agg aca	gaa	28182
Ser Ser Val Pro	Thr Gly Ala Thr Thr	Glu Val Ser Arg Thr	Glu	
9315	9320	9325		
gcc atc tct tct	agc aga aca tcc atc	cca ggc cct gct caa	tcc	28227
Ala Ile Ser Ser	Ser Arg Thr Ser Ile	Pro Gly Pro Ala Gln	Ser	
9330	9335	9340		
aca atg tca tca	gac acc tcc atg gaa	acc atc act aga att	tct	28272
Thr Met Ser Ser	Asp Thr Ser Met Glu	Thr Ile Thr Arg Ile	Ser	
9345	9350	9355		
acc ccc ctc aca	agg aaa gaa tca aca	gac atg gcc atc acc	ccc	28317

428

Thr Pro Leu Thr	Arg Lys Glu Ser Thr	Asp Met Ala Ile Thr	Pro	
9360	9365	9370		
aaa aca ggt cct	tct ggg gct acc tcg	cag ggt acc ttt acc	ttg	28362
Lys Thr Gly Pro	Ser Gly Ala Thr Ser	Gln Gly Thr Phe Thr	Leu	
9375	9380	9385		
gac tca tca agc	aca gcc tcc tgg cca	gga act cac tca gct	aca	28407
Asp Ser Ser Ser	Thr Ala Ser Trp Pro	Gly Thr His Ser Ala	Thr	
9390	9395	9400		
act cag aga ttt	cca cag tca gtg gtg	aca act cct atg agc	aga	28452
Thr Gln Arg Phe	Pro Gln Ser Val Val	Thr Thr Pro Met Ser	Arg	
9405	9410	9415		
ggt cct gag gat	gtg tca tgg cca agc	ccg ctg tct gtg gaa	aaa	28497
Gly Pro Glu Asp	Val Ser Trp Pro Ser	Pro Leu Ser Val Glu	Lys	
9420	9425	9430		
aac agc cct cca	tct tcc ctg gta tct	tca tct tca gta acc	tca	28542
Asn Ser Pro Pro	Ser Ser Leu Val Ser	Ser Ser Ser Val Thr	Ser	
9435	9440	9445		
cct tcg cca ctt	tat tcc aca cca tct	ggg agt agc cac tcc	tct	28587
Pro Ser Pro Leu	Tyr Ser Thr Pro Ser	Gly Ser Ser His Ser	Ser	
9450	9455	9460		
cct gtc cct gtc	act tct ctt ttc acc	tct atc atg atg aag	gcc	28632
Pro Val Pro Val	Thr Ser Leu Phe Thr	Ser Ile Met Met Lys	Ala	
9465	9470	9475		
aca gac atg ttg	gat gca agt ttg gaa	cct gag acc act tca	gct	28677
Thr Asp Met Leu	Asp Ala Ser Leu Glu	Pro Glu Thr Thr Ser	Ala	
9480	9485	9490		
ccc aat atg aat	atc acc tca gat gag	agt ctg gcc gct tct	aaa	28722
Pro Asn Met Asn	Ile Thr Ser Asp Glu	Ser Leu Ala Ala Ser	Lys	
9495	9500	9505		
gcc acc acg gag	aca gag gca att cac	gtt ttt gaa aat aca	gca	28767
Ala Thr Thr Glu	Thr Glu Ala Ile His	Val Phe Glu Asn Thr	Ala	
9510	9515	9520		
gcg tcc cat gtg	gaa acc acc agt gct	aca gag gaa ctg tat	tcc	28812
Ala Ser His Val	Glu Thr Thr Ser Ala	Thr Glu Glu Leu Tyr	Ser	
9525	9530	9535		
tct tcc cca ggc	ttc tca gag cca aca	aaa gtg ata tct cca	gtg	28857
Ser Ser Pro Gly	Phe Ser Glu Pro Thr	Lys Val Ile Ser Pro	Val	
9540	9545	9550		
gtc acc tct tcc	tct ata aga gac aac	atg gtt tcc aca aca	atg	28902
Val Thr Ser Ser	Ser Ile Arg Asp Asn	Met Val Ser Thr Thr	Met	
9555	9560	9565		

429

cct ggc tcc tct	ggc att aca agg att	gag ata gag tca atg tca	28947
Pro Gly Ser Ser	Gly Ile Thr Arg Ile	Glu Ile Glu Ser Met Ser	
9570	9575	9580	
tct ctg acc cct	gga ctg agg gag acc	aga acc tcc cag gac atc	28992
Ser Leu Thr Pro	Gly Leu Arg Glu Thr	Arg Thr Ser Gln Asp Ile	
9585	9590	9595	
acc tca tcc aca	gag aca agc act gtc	ctt tac aag atg ccc tct	29037
Thr Ser Ser Thr	Glu Thr Ser Thr Val	Leu Tyr Lys Met Pro Ser	
9600	9605	9610	
ggt gcc act cct	gag gtc tcc agg aca	gaa gtt atg ccc tct agc	29082
Gly Ala Thr Pro	Glu Val Ser Arg Thr	Glu Val Met Pro Ser Ser	
9615	9620	9625	
aga aca tcc att	cct ggc cct gct cag	tcc aca atg tca cta gac	29127
Arg Thr Ser Ile	Pro Gly Pro Ala Gln	Ser Thr Met Ser Leu Asp	
9630	9635	9640	
atc tcc gat gaa	gtt gtc acc agg ctg	tct acc tct ccc atc atg	29172
Ile Ser Asp Glu	Val Val Thr Arg Leu	Ser Thr Ser Pro Ile Met	
9645	9650	9655	
aca gaa tct gca	gaa ata acc atc acc	acc caa aca ggt tat tct	29217
Thr Glu Ser Ala	Glu Ile Thr Ile Thr	Thr Gln Thr Gly Tyr Ser	
9660	9665	9670	
ctg gct aca tcc	cag gtt acc ctt ccc	ttg ggc acc tca atg acc	29262
Leu Ala Thr Ser	Gln Val Thr Leu Pro	Leu Gly Thr Ser Met Thr	
9675	9680	9685	
ttt ttg tca ggg	acc cac tca act atg	tct caa gga ctt tca cac	29307
Phe Leu Ser Gly	Thr His Ser Thr Met	Ser Gln Gly Leu Ser His	
9690	9695	9700	
tca gag atg acc	aat ctt atg agc agg	ggt cct gaa agt ctg tca	29352
Ser Glu Met Thr	Asn Leu Met Ser Arg	Gly Pro Glu Ser Leu Ser	
9705	9710	9715	
tgg acg agc cct	cgc ttt gtg gaa aca	act aga tct tcc tct tct	29397
Trp Thr Ser Pro	Arg Phe Val Glu Thr	Thr Arg Ser Ser Ser Ser	
9720	9725	9730	
ctg aca tca tta	cct ctc acg acc tca	ctt tct cct gtg tcc tcc	29442
Leu Thr Ser Leu	Pro Leu Thr Thr Ser	Leu Ser Pro Val Ser Ser	
9735	9740	9745	
aca tta cta gac	agt agc ccc tcc tct	cct ctt cct gtg act tca	29487
Thr Leu Leu Asp	Ser Ser Pro Ser Ser	Pro Leu Pro Val Thr Ser	
9750	9755	9760	
ctt atc ctc cca	ggc ctg gtg aag act	aca gaa gtg ttg gat aca	29532

430

Leu	Ile	Leu	Pro	Gly	Leu	Val	Lys	Thr	Thr	Glu	Val	Leu	Asp	Thr	
			9765					9770					9775		
agc	tca	gag	cct	aaa	acc	agt	tca	tct	cca	aat	ttg	agc	agc	acc	29577
Ser	Ser	Glu	Pro	Lys	Thr	Ser	Ser	Ser	Pro	Asn	Leu	Ser	Ser	Thr	
			9780					9785					9790		
tca	gtt	gaa	ata	ccg	gcc	acc	tct	gaa	atc	atg	aca	gat	aca	gag	29622
Ser	Val	Glu	Ile	Pro	Ala	Thr	Ser	Glu	Ile	Met	Thr	Asp	Thr	Glu	
			9795					9800					9805		
aaa	att	cat	cct	tcc	tca	aac	aca	gcg	gtg	gcc	aaa	gtg	agg	acc	29667
Lys	Ile	His	Pro	Ser	Ser	Asn	Thr	Ala	Val	Ala	Lys	Val	Arg	Thr	
			9810					9815					9820		
tcc	agt	tct	gtt	cat	gaa	tct	cat	tcc	tct	gtc	cta	gct	gac	tca	29712
Ser	Ser	Ser	Val	His	Glu	Ser	His	Ser	Ser	Val	Leu	Ala	Asp	Ser	
			9825					9830					9835		
gaa	aca	acc	ata	acc	ata	cct	tca	atg	ggg	atc	acc	tcc	gct	gtg	29757
Glu	Thr	Thr	Ile	Thr	Ile	Pro	Ser	Met	Gly	Ile	Thr	Ser	Ala	Val	
			9840					9845					9850		
gac	gat	acc	act	gtt	ttc	aca	tca	aat	cct	gcc	ttc	tct	gag	act	29802
Asp	Asp	Thr	Thr	Val	Phe	Thr	Ser	Asn	Pro	Ala	Phe	Ser	Glu	Thr	
			9855					9860					9865		
agg	agg	att	ccg	aca	gag	cca	aca	ttc	tca	ttg	act	cct	gga	ttc	29847
Arg	Arg	Ile	Pro	Thr	Glu	Pro	Thr	Phe	Ser	Leu	Thr	Pro	Gly	Phe	
			9870					9875					9880		
agg	gag	act	agc	acc	tct	gaa	gag	acc	acc	tca	atc	aca	gaa	aca	29892
Arg	Glu	Thr	Ser	Thr	Ser	Glu	Glu	Thr	Thr	Ser	Ile	Thr	Glu	Thr	
			9885					9890					9895		
agt	gca	gtc	ctt	tat	gga	gtg	ccc	act	agt	gct	act	act	gaa	gtc	29937
Ser	Ala	Val	Leu	Tyr	Gly	Val	Pro	Thr	Ser	Ala	Thr	Thr	Glu	Val	
			9900					9905					9910		
tcc	atg	aca	gaa	atc	atg	tcc	tct	aat	aga	aca	cac	atc	cct	gac	29982
Ser	Met	Thr	Glu	Ile	Met	Ser	Ser	Asn	Arg	Thr	His	Ile	Pro	Asp	
			9915					9920					9925		
tct	gat	cag	tcc	acg	atg	tct	cca	gac	atc	atc	act	gaa	gtg	atc	30027
Ser	Asp	Gln	Ser	Thr	Met	Ser	Pro	Asp	Ile	Ile	Thr	Glu	Val	Ile	
			9930					9935					9940		
acc	agg	ctc	tct	tcc	tca	tcc	atg	atg	tca	gaa	tca	aca	caa	atg	30072
Thr	Arg	Leu	Ser	Ser	Ser	Ser	Met	Met	Ser	Glu	Ser	Thr	Gln	Met	
			9945					9950					9955		
acc	atc	acc	acc	caa	aaa	agt	tct	cct	ggg	gct	aca	gca	cag	agt	30117
Thr	Ile	Thr	Thr	Gln	Lys	Ser	Ser	Pro	Gly	Ala	Thr	Ala	Gln	Ser	
			9960					9965					9970		

431

act ctt acc ttg gcc aca aca aca gcc ccc ttg gca agg acc cac	30162
Thr Leu Thr Leu Ala Thr Thr Thr Ala Pro Leu Ala Arg Thr His	
9975 9980 9985	
tca act gtt cct cct aga ttt tta cac tca gag atg aca act ctt	30207
Ser Thr Val Pro Pro Arg Phe Leu His Ser Glu Met Thr Thr Leu	
9990 9995 10000	
atg agt agg agt cct gaa aat cca tca tgg aag agc tct ccc ttt	30252
Met Ser Arg Ser Pro Glu Asn Pro Ser Trp Lys Ser Ser Pro Phe	
10005 10010 10015	
gtg gaa aaa act agc tct tca tct tct ctg ttg tcc tta cct gtc	30297
Val Glu Lys Thr Ser Ser Ser Ser Ser Leu Leu Ser Leu Pro Val	
10020 10025 10030	
acg acc tca cct tct gtt tct tcc aca tta ccg cag agt atc cct	30342
Thr Thr Ser Pro Ser Val Ser Ser Thr Leu Pro Gln Ser Ile Pro	
10035 10040 10045	
tcc tcc tct ttt tct gtg act tca ctc ctc acc cca ggc atg gtg	30387
Ser Ser Ser Phe Ser Val Thr Ser Leu Leu Thr Pro Gly Met Val	
10050 10055 10060	
aag act aca gac aca agc aca gaa cct gga acc agt tta tct cca	30432
Lys Thr Thr Asp Thr Ser Thr Glu Pro Gly Thr Ser Leu Ser Pro	
10065 10070 10075	
aat ctg agt ggc acc tca gtt gaa ata ctg gct gcc tct gaa gtc	30477
Asn Leu Ser Gly Thr Ser Val Glu Ile Leu Ala Ala Ser Glu Val	
10080 10085 10090	
acc aca gat aca gag aaa att cat cct tct tca agc atg gca gtg	30522
Thr Thr Asp Thr Glu Lys Ile His Pro Ser Ser Ser Met Ala Val	
10095 10100 10105	
acc aat gtg gga acc acc agt tct gga cat gaa cta tat tcc tct	30567
Thr Asn Val Gly Thr Thr Ser Ser Gly His Glu Leu Tyr Ser Ser	
10110 10115 10120	
gtt tca atc cac tcg gag cca tcc aag gct aca tac cca gtg ggt	30612
Val Ser Ile His Ser Glu Pro Ser Lys Ala Thr Tyr Pro Val Gly	
10125 10130 10135	
act ccc tct tcc atg gct gaa acc tct att tcc aca tca atg cct	30657
Thr Pro Ser Ser Met Ala Glu Thr Ser Ile Ser Thr Ser Met Pro	
10140 10145 10150	
gct aat ttt gag acc aca gga ttt gag gct gag cca ttt tct cat	30702
Ala Asn Phe Glu Thr Thr Gly Phe Glu Ala Glu Pro Phe Ser His	
10155 10160 10165	
ttg act tct gga ttt agg aag aca aac atg tcc ctg gac acc agc	30747

432

Leu Thr Ser Gly	Phe Arg Lys Thr Asn	Met Ser Leu Asp Thr	Ser	
10170	10175	10180		
tca gtc aca cca	aca aat aca cct tct	tct cct ggg tcc act	cac	30792
Ser Val Thr Pro	Thr Asn Thr Pro Ser	Ser Pro Gly Ser Thr	His	
10185	10190	10195		
ctt tta cag agt	tcc aag act gat ttc	acc tct tct gca aaa	aca	30837
Leu Leu Gln Ser	Ser Lys Thr Asp Phe	Thr Ser Ser Ala Lys	Thr	
10200	10205	10210		
tca tcc cca gac	tgg cct cca gcc tca	cag tat act gaa att	cca	30882
Ser Ser Pro Asp	Trp Pro Pro Ala Ser	Gln Tyr Thr Glu Ile	Pro	
10215	10220	10225		
gtg gac ata atc	acc ccc ttt aat gct	tct cca tct att acg	gag	30927
Val Asp Ile Ile	Thr Pro Phe Asn Ala	Ser Pro Ser Ile Thr	Glu	
10230	10235	10240		
tcc act ggg ata	acc tcc ttc cca gaa	tcc agg ttt act atg	tct	30972
Ser Thr Gly Ile	Thr Ser Phe Pro Glu	Ser Arg Phe Thr Met	Ser	
10245	10250	10255		
gta aca gaa agt	act cat cat ctg agt	aca gat ttg ctg cct	tca	31017
Val Thr Glu Ser	Thr His His Leu Ser	Thr Asp Leu Leu Pro	Ser	
10260	10265	10270		
gct gag act att	tcc act ggc aca gtg	atg cct tct cta tca	gag	31062
Ala Glu Thr Ile	Ser Thr Gly Thr Val	Met Pro Ser Leu Ser	Glu	
10275	10280	10285		
gcc atg act tca	ttt gcc acc act gga	gtt cca cga gcc atc	tca	31107
Ala Met Thr Ser	Phe Ala Thr Thr Gly	Val Pro Arg Ala Ile	Ser	
10290	10295	10300		
ggt tca ggt agt	cca ttc tct agg aca	gag tca ggc cct ggg	gat	31152
Gly Ser Gly Ser	Pro Phe Ser Arg Thr	Glu Ser Gly Pro Gly	Asp	
10305	10310	10315		
gct act ctg tcc	acc att gca gag agc	ctg cct tca tcc act	cct	31197
Ala Thr Leu Ser	Thr Ile Ala Glu Ser	Leu Pro Ser Ser Thr	Pro	
10320	10325	10330		
gtg cca ttc tcc	tct tca acc ttc act	acc act gat tct tca	acc	31242
Val Pro Phe Ser	Ser Ser Thr Phe Thr	Thr Thr Asp Ser Ser	Thr	
10335	10340	10345		
atc cca gcc ctc	cat gag ata act tcc	tct tca gct acc cca	tat	31287
Ile Pro Ala Leu	His Glu Ile Thr Ser	Ser Ser Ala Thr Pro	Tyr	
10350	10355	10360		
aga gtg gac acc	agt ctt ggg aca gag	agc agc act act gaa	gga	31332
Arg Val Asp Thr	Ser Leu Gly Thr Glu	Ser Ser Thr Thr Glu	Gly	
10365	10370	10375		

433

cgc ttg gtt atg gtc agt act ttg gac act tca agc caa cca ggc 31377
 Arg Leu Val Met Val Ser Thr Leu Asp Thr Ser Ser Gln Pro Gly
 10380 10385 10390

agg aca tct tca aca ccc att ttg gat acc aga atg aca gag agc 31422
 Arg Thr Ser Ser Thr Pro Ile Leu Asp Thr Arg Met Thr Glu Ser
 10395 10400 10405

gtt gag ctg gga aca gtg aca agt gct tat caa gtt cct tca ctc 31467
 Val Glu Leu Gly Thr Val Thr Ser Ala Tyr Gln Val Pro Ser Leu
 10410 10415 10420

tca aca cgg ttg aca aga act gat ggc att 31497
 Ser Thr Arg Leu Thr Arg Thr Asp Gly Ile
 10425 10430

<210> 310

<211> 10431

<212> PRT

<213> Homo sapiens

<400> 310

Met Leu Lys Pro Ser Gly Leu Pro Gly Ser Ser Ser Pro Thr Arg Ser
 1 5 10 15

Leu Met Thr Gly Ser Arg Ser Thr Lys Ala Thr Pro Glu Met Asp Ser
 20 25 30

Gly Leu Thr Gly Ala Thr Leu Ser Pro Lys Thr Ser Thr Gly Ala Ile
 35 40 45

Val Val Thr Glu His Thr Leu Pro Phe Thr Ser Pro Asp Lys Thr Leu
 50 55 60

Ala Ser Pro Thr Ser Ser Val Val Gly Arg Thr Thr Gln Ser Leu Gly
 65 70 75 80

Val Met Ser Ser Ala Leu Pro Glu Ser Thr Ser Arg Gly Met Thr His
 85 90 95

434

Ser Glu Gln Arg Thr Ser Pro Ser Leu Ser Pro Gln Val Asn Gly Thr
 100 105 110

Pro Ser Arg Asn Tyr Pro Ala Thr Ser Met Val Ser Gly Leu Ser Ser
 115 120 125

Pro Arg Thr Arg Thr Ser Ser Thr Glu Gly Asn Phe Thr Lys Glu Ala
 130 135 140

Ser Thr Tyr Thr Leu Thr Val Glu Thr Thr Ser Gly Pro Val Thr Glu
 145 150 155 160

Lys Tyr Thr Val Pro Thr Glu Thr Ser Thr Thr Glu Gly Asp Ser Thr
 165 170 175

Glu Thr Pro Trp Asp Thr Arg Tyr Ile Pro Val Lys Ile Thr Ser Pro
 180 185 190

Met. Lys Thr Phe Ala Asp Ser Thr Ala Ser Lys Glu Asn Ala Pro Val
 195 200 205

Ser Met Thr Pro Ala Glu Thr Thr Val Thr Asp Ser His Thr Pro Gly
 210 215 220

Arg Thr Asn Pro Ser Phe Gly Thr Leu Tyr Ser Ser Phe Leu Asp Leu
 225 230 235 240

Ser Pro Lys Gly Thr Pro Asn Ser Arg Gly Glu Thr Ser Leu Glu Leu
 245 250 255

Ile Leu Ser Thr Thr Gly Tyr Pro Phe Ser Ser Pro Glu Pro Gly Ser
 260 265 270

Ala Gly His Ser Arg Ile Ser Thr Ser Ala Pro Leu Ser Ser Ser Ala
 275 280 285

Ser Val Leu Asp Asn Lys Ile Ser Glu Thr Ser Ile Phe Ser Gly Gln
 290 295 300

Ser Leu Thr Ser Pro Leu Ser Pro Gly Val Pro Glu Ala Arg Ala Ser
 305 310 315 320

[illegible]

436

Ser Glu Pro Gln His Thr Gln Trp Val Glu Thr Ser Pro Ser Met Lys
 530 535 540

Thr Glu Arg Pro Pro Ala Ser Thr Ser Val Ala Ala Pro Ile Thr Thr
 545 550 555 560

Ser Val Pro Ser Val Val Ser Gly Phe Thr Thr Leu Lys Thr Ser Ser
 565 570 575

Thr Lys Gly Ile Trp Leu Glu Glu Thr Ser Ala Asp Thr Leu Ile Gly
 580 585 590

Glu Ser Thr Ala Gly Pro Thr Thr His Gln Phe Ala Val Pro Thr Gly
 595 600 605

Ile Ser Met Thr Gly Gly Ser Ser Thr Arg Gly Ser Gln Gly Thr Thr
 610 615 620

His Leu Leu Thr Arg Ala Thr Ala Ser Ser Glu Thr Ser Ala Asp Leu
 625 630 635 640

Thr Leu Ala Thr Asn Gly Val Pro Val Ser Val Ser Pro Ala Val Ser
 645 650 655

Lys Thr Ala Ala Gly Ser Ser Pro Pro Gly Gly Thr Lys Pro Ser Tyr
 660 665 670

Thr Met Val Ser Ser Val Ile Pro Glu Thr Ser Ser Leu Gln Ser Ser
 675 680 685

Ala Phe Arg Glu Gly Thr Ser Leu Gly Leu Thr Pro Leu Asn Thr Arg
 690 695 700

His Pro Phe Ser Ser Pro Glu Pro Asp Ser Ala Gly His Thr Lys Ile
 705 710 715 720

Ser Thr Ser Ile Pro Leu Leu Ser Ser Ala Ser Val Leu Glu Asp Lys
 725 730 735

Val Ser Ala Thr Ser Thr Phe Ser His His Lys Ala Thr Ser Ser Ile
 740 745 750

437

Thr Thr Gly Thr Pro Glu Ile Ser Thr Lys Thr Lys Pro Ser Ser Ala
755 760 765

Val Leu Ser Ser Met Thr Leu Ser Asn Ala Ala Thr Ser Pro Glu Arg
770 775 780

Val Arg Asn Ala Thr Ser Pro Leu Thr His Pro Ser Pro Ser Gly Glu
785 790 795 800

Glu Thr Ala Gly Ser Val Leu Thr Leu Ser Thr Ser Ala Glu Thr Thr
805 810 815

Asp Ser Pro Asn Ile His Pro Thr Gly Thr Leu Thr Ser Glu Ser Ser
820 825 830

Glu Ser Pro Ser Thr Leu Ser Leu Pro Ser Val Ser Gly Val Lys Thr
835 840 845

Thr Phe Ser Ser Ser Thr Pro Ser Thr His Leu Phe Thr Ser Gly Glu
850 855 860

Glu Thr Glu Glu Thr Ser Asn Pro Ser Val Ser Gln Pro Glu Thr Ser
865 870 875 880

Val Ser Arg Val Arg Thr Thr Leu Ala Ser Thr Ser Val Pro Thr Pro
885 890 895

Val Phe Pro Thr Met Asp Thr Trp Pro Thr Arg Ser Ala Gln Phe Ser
900 905 910

Ser Ser His Leu Val Ser Glu Leu Arg Ala Thr Ser Ser Thr Ser Val
915 920 925

Thr Asn Ser Thr Gly Ser Ala Leu Pro Lys Ile Ser His Leu Thr Gly
930 935 940

Thr Ala Thr Met Ser Gln Thr Asn Arg Asp Thr Phe Asn Asp Ser Ala
945 950 955 960

438

Ala Pro Gln Ser Thr Thr Trp Pro Glu Thr Ser Pro Arg Phe Lys Thr
 965 970 975

Gly Leu Pro Ser Ala Thr Thr Thr Val Ser Thr Ser Ala Thr Ser Leu
 980 985 990

Ser Ala Thr Val Met Val Ser Lys Phe Thr Ser Pro Ala Thr Ser Ser
 995 1000 1005

Met Glu Ala Thr Ser Ile Arg Glu Pro Ser Thr Thr Ile Leu Thr
 1010 1015 1020

Thr Glu Thr Thr Asn Gly Pro Gly Ser Met Ala Val Ala Ser Thr
 1025 1030 1035

Asn Ile Pro Ile Gly Lys Gly Tyr Ile Thr Glu Gly Arg Leu Asp
 1040 1045 1050

Thr Ser His Leu Pro Ile Gly Thr Thr Ala Ser Ser Glu Thr Ser
 1055 1060 1065

Met Asp Phe Thr Met Ala Lys Glu Ser Val Ser Met Ser Val Ser
 1070 1075 1080

Pro Ser Gln Ser Met Asp Ala Ala Gly Ser Ser Thr Pro Gly Arg
 1085 1090 1095

Thr Ser Gln Phe Val Asp Thr Phe Ser Asp Asp Val Tyr His Leu
 1100 1105 1110

Thr Ser Arg Glu Ile Thr Ile Pro Arg Asp Gly Thr Ser Ser Ala
 1115 1120 1125

Leu Thr Pro Gln Met Thr Ala Thr His Pro Pro Ser Pro Asp Pro
 1130 1135 1140

Gly Ser Ala Arg Ser Thr Trp Leu Gly Ile Leu Ser Ser Ser Pro
 1145 1150 1155

Ser Ser Pro Thr Pro Lys Val Thr Met Ser Ser Thr Phe Ser Thr
 1160 1165 1170

439

Gln	Arg	Val	Thr	Thr	Ser	Met	Ile	Met	Asp	Thr	Val	Glu	Thr	Ser
1175						1180					1185			
Arg	Trp	Asn	Met	Pro	Asn	Leu	Pro	Ser	Thr	Thr	Ser	Leu	Thr	Pro
1190						1195					1200			
Ser	Asn	Ile	Pro	Thr	Ser	Gly	Ala	Ile	Gly	Lys	Ser	Thr	Leu	Val
1205						1210					1215			
Pro	Leu	Asp	Thr	Pro	Ser	Pro	Ala	Thr	Ser	Leu	Glu	Ala	Ser	Glu
1220						1225					1230			
Gly	Gly	Leu	Pro	Thr	Leu	Ser	Thr	Tyr	Pro	Glu	Ser	Thr	Asn	Thr
1235						1240					1245			
Pro	Ser	Ile	His	Leu	Gly	Ala	His	Ala	Ser	Ser	Glu	Ser	Pro	Ser
1250						1255					1260			
Thr	Ile	Lys	Leu	Thr	Met	Ala	Ser	Val	Val	Lys	Pro	Gly	Ser	Tyr
1265						1270					1275			
Thr	Pro	Leu	Thr	Phe	Pro	Ser	Ile	Glu	Thr	His	Ile	His	Val	Ser
1280						1285					1290			
Thr	Ala	Arg	Met	Ala	Tyr	Ser	Ser	Gly	Ser	Ser	Pro	Glu	Met	Thr
1295						1300					1305			
Ala	Pro	Gly	Glu	Thr	Asn	Thr	Gly	Ser	Thr	Trp	Asp	Pro	Thr	Thr
1310						1315					1320			
Tyr	Ile	Thr	Thr	Thr	Asp	Pro	Lys	Asp	Thr	Ser	Ser	Ala	Gln	Val
1325						1330					1335			
Ser	Thr	Pro	His	Ser	Val	Arg	Thr	Leu	Arg	Thr	Thr	Glu	Asn	His
1340						1345					1350			
Pro	Lys	Thr	Glu	Ser	Ala	Thr	Pro	Ala	Ala	Tyr	Ser	Gly	Ser	Pro
1355						1360					1365			

440

Lys Ile Ser Ser Ser Pro Asn Leu Thr Ser Pro Ala Thr Lys Ala
 1370 1375 1380

Trp Thr Ile Thr Asp Thr Thr Glu His Ser Thr Gln Leu His Tyr
 1385 1390 1395

Thr Lys Leu Ala Glu Lys Ser Ser Gly Phe Glu Thr Gln Ser Ala
 1400 1405 1410

Pro Gly Pro Val Ser Val Val Ile Pro Thr Ser Pro Thr Ile Gly
 1415 1420 1425

Ser Ser Thr Leu Glu Leu Thr Ser Asp Val Pro Gly Glu Pro Leu
 1430 1435 1440

Val Leu Ala Pro Ser Glu Gln Thr Thr Ile Thr Leu Pro Met Ala
 1445 1450 1455

Thr Trp Leu Ser Thr Ser Leu Thr Glu Glu Met Ala Ser Thr Asp
 1460 1465 1470

Leu Asp Ile Ser Ser Pro Ser Ser Pro Met Ser Thr Phe Ala Ile
 1475 1480 1485

Phe Pro Pro Met Ser Thr Pro Ser His Glu Leu Ser Lys Ser Glu
 1490 1495 1500

Ala Asp Thr Ser Ala Ile Arg Asn Thr Asp Ser Thr Thr Leu Asp
 1505 1510 1515

Gln His Leu Gly Ile Arg Ser Leu Gly Arg Thr Gly Asp Leu Thr
 1520 1525 1530

Thr Val Pro Ile Thr Pro Leu Thr Thr Thr Trp Thr Ser Val Ile
 1535 1540 1545

Glu His Ser Thr Gln Ala Gln Asp Thr Leu Ser Ala Thr Met Ser
 1550 1555 1560

Pro Thr His Val Thr Gln Ser Leu Lys Asp Gln Thr Ser Ile Pro
 1565 1570 1575

441

Ala Ser	Ala Ser Pro Ser	His	Leu Thr Glu Val	Tyr	Pro Glu Leu
1580		1585		1590	
Gly Thr	Gln Gly Arg Ser	Ser	Ser Glu Ala Thr	Thr	Phe Trp Lys
1595		1600		1605	
Pro Ser	Thr Asp Thr Leu	Ser	Arg Glu Ile Glu	Thr	Gly Pro Thr
1610		1615		1620	
Asn Ile	Gln Ser Thr Pro	Pro	Met Asp Asn Thr	Thr	Thr Gly Ser
1625		1630		1635	
Ser Ser	Ser Gly Val Thr	Leu	Gly Ile Ala His	Leu	Pro Ile Gly
1640		1645		1650	
Thr Ser	Ser Pro Ala Glu	Thr	Ser Thr Asn Met	Ala	Leu Glu Arg
1655		1660		1665	
Arg Ser	Ser Thr Ala Thr	Val	Ser Met Ala Gly	Thr	Met Gly Leu
1670		1675		1680	
Leu Val	Thr Ser Ala Pro	Gly	Arg Ser Ile Ser	Gln	Ser Leu Gly
1685		1690		1695	
Arg Val	Ser Ser Val Leu	Ser	Glu Ser Thr Thr	Glu	Gly Val Thr
1700		1705		1710	
Asp Ser	Ser Lys Gly Ser	Ser	Pro Arg Leu Asn	Thr	Gln Gly Asn
1715		1720		1725	
Thr Ala	Leu Ser Ser Ser	Leu	Glu Pro Ser Tyr	Ala	Glu Gly Ser
1730		1735		1740	
Gln Met	Ser Thr Ser Ile	Pro	Leu Thr Ser Ser	Pro	Thr Thr Pro
1745		1750		1755	
Asp Val	Glu Phe Ile Gly	Gly	Ser Thr Phe Trp	Thr	Lys Glu Val
1760		1765		1770	

442

Thr Thr Val Met Thr Ser Asp Ile Ser Lys Ser Ser Ala Arg Thr
 1775 1780 1785

Glu Ser Ser Ser Ala Thr Leu Met Ser Thr Ala Leu Gly Ser Thr
 1790 1795 1800

Glu Asn Thr Gly Lys Glu Lys Leu Arg Thr Ala Ser Met Asp Leu
 1805 1810 1815

Pro Ser Pro Thr Pro Ser Met Glu Val Thr Pro Trp Ile Ser Leu
 1820 1825 1830

Thr Leu Ser Asn Ala Pro Asn Thr Thr Asp Ser Leu Asp Leu Ser
 1835 1840 1845

His Gly Val His Thr Ser Ser Ala Gly Thr Leu Ala Thr Asp Arg
 1850 1855 1860

Ser Leu Asn Thr Gly Val Thr Arg Ala Ser Arg Leu Glu Asn Gly
 1865 1870 1875

Ser Asp Thr Ser Ser Lys Ser Leu Ser Met Gly Asn Ser Thr His
 1880 1885 1890

Thr Ser Met Thr Asp Thr Glu Lys Ser Glu Val Ser Ser Ser Ile
 1895 1900 1905

His Pro Arg Pro Glu Thr Ser Ala Pro Gly Ala Glu Thr Thr Leu
 1910 1915 1920

Thr Ser Thr Pro Gly Asn Arg Ala Ile Ser Leu Thr Leu Pro Phe
 1925 1930 1935

Ser Ser Ile Pro Val Glu Glu Val Ile Ser Thr Gly Ile Thr Ser
 1940 1945 1950

Gly Pro Asp Ile Asn Ser Ala Pro Met Thr His Ser Pro Ile Thr
 1955 1960 1965

Pro Pro Thr Ile Val Trp Thr Ser Thr Gly Thr Ile Glu Gln Ser
 1970 1975 1980

443

Thr	Gln	Pro	Leu	His	Ala	Val	Ser	Ser	Glu	Lys	Val	Ser	Val	Gln
1985						1990					1995			
Thr	Gln	Ser	Thr	Pro	Tyr	Val	Asn	Ser	Val	Ala	Val	Ser	Ala	Ser
2000						2005					2010			
Pro	Thr	His	Glu	Asn	Ser	Val	Ser	Ser	Gly	Ser	Ser	Thr	Ser	Ser
2015						2020					2025			
Pro	Tyr	Ser	Ser	Ala	Ser	Leu	Glu	Ser	Leu	Asp	Ser	Thr	Ile	Ser
2030						2035					2040			
Arg	Arg	Asn	Ala	Ile	Thr	Ser	Trp	Leu	Trp	Asp	Leu	Thr	Thr	Ser
2045						2050					2055			
Leu	Pro	Thr	Thr	Thr	Trp	Pro	Ser	Thr	Ser	Leu	Ser	Glu	Ala	Leu
2060						2065					2070			
Ser	Ser	Gly	His	Ser	Gly	Val	Ser	Asn	Pro	Ser	Ser	Thr	Thr	Thr
2075						2080					2085			
Glu	Phe	Pro	Leu	Phe	Ser	Ala	Ala	Ser	Thr	Ser	Ala	Ala	Lys	Gln
2090						2095					2100			
Arg	Asn	Pro	Glu	Thr	Glu	Thr	His	Gly	Pro	Gln	Asn	Thr	Ala	Ala
2105						2110					2115			
Ser	Thr	Leu	Asn	Thr	Asp	Ala	Ser	Ser	Val	Thr	Gly	Leu	Ser	Glu
2120						2125					2130			
Thr	Pro	Val	Gly	Ala	Ser	Ile	Ser	Ser	Glu	Val	Pro	Leu	Pro	Met
2135						2140					2145			
Ala	Ile	Thr	Ser	Arg	Ser	Asp	Val	Ser	Gly	Leu	Thr	Ser	Glu	Ser
2150						2155					2160			
Thr	Ala	Asn	Pro	Ser	Leu	Gly	Thr	Ala	Ser	Ser	Ala	Gly	Thr	Lys
2165						2170					2175			

444

Leu Thr 2180	Arg Thr Ile Ser 2185	Leu Pro Thr Ser Glu Ser 2190	Leu Val Ser
Phe Arg 2195	Met Asn Lys Asp 2200	Pro Trp Thr Val Ser Ile 2205	Pro Leu Gly
Ser His 2210	Pro Thr Thr Asn Thr 2215	Glu Thr Ser Ile Pro 2220	Val Asn Ser
Ala Gly 2225	Pro Pro Gly Leu Ser 2230	Thr Val Ala Ser Asp 2235	Val Ile Asp
Thr Pro 2240	Ser Asp Gly Ala Glu 2245	Ser Ile Pro Thr Val 2250	Ser Phe Ser
Pro Ser 2255	Pro Asp Thr Glu Val 2260	Thr Thr Ile Ser His 2265	Phe Pro Glu
Lys Thr 2270	Thr His Ser Phe Arg 2275	Thr Ile Ser Ser Leu 2280	Thr His Glu
Leu Thr 2285	Ser Arg Val Thr Pro 2290	Ile Pro Gly Asp Trp 2295	Met Ser Ser
Ala Met 2300	Ser Thr Lys Pro Thr 2305	Gly Ala Ser Pro Ser 2310	Ile Thr Leu
Gly Glu 2315	Arg Arg Thr Ile Thr 2320	Ser Ala Ala Pro Thr 2325	Thr Ser Pro
Ile Val 2330	Leu Thr Ala Ser Phe 2335	Thr Glu Thr Ser Thr 2340	Val Ser Leu
Asp Asn 2345	Glu Thr Thr Val Lys 2350	Thr Ser Asp Ile Leu 2355	Asp Ala Arg
Lys Thr 2360	Asn Glu Leu Pro Ser 2365	Asp Ser Ser Ser Ser 2370	Ser Asp Leu
Ile Asn 2375	Thr Ser Ile Ala Ser 2380	Ser Thr Met Asp Val 2385	Thr Lys Thr

445

Ala Ser	Ile Ser	Pro Thr	Ser	Ile Ser	Gly Met	Thr	Ala Ser	Ser
2390			2395			2400		
Ser Pro	Ser Leu	Phe Ser	Ser	Asp Arg	Pro Gln	Val	Pro Thr	Ser
2405			2410			2415		
Thr Thr	Glu Thr	Asn Thr	Ala	Thr Ser	Pro Ser	Val	Ser Ser	Asn
2420			2425			2430		
Thr Tyr	Ser Leu	Asp Gly	Gly	Ser Asn	Val Gly	Gly	Thr Pro	Ser
2435			2440			2445		
Thr Leu	Pro Pro	Phe Thr	Ile	Thr His	Pro Val	Glu	Thr Ser	Ser
2450			2455			2460		
Ala Leu	Leu Ala	Trp Ser	Arg	Pro Val	Arg Thr	Phe	Ser Thr	Met
2465			2470			2475		
Val Ser	Thr Asp	Thr Ala	Ser	Gly Glu	Asn Pro	Thr	Ser Ser	Asn
2480			2485			2490		
Ser Val	Val Thr	Ser Val	Pro	Ala Pro	Gly Thr	Trp	Thr Ser	Val
2495			2500			2505		
Gly Ser	Thr Thr	Asp Leu	Pro	Ala Met	Gly Phe	Leu	Lys Thr	Ser
2510			2515			2520		
Pro Ala	Gly Glu	Ala His	Ser	Leu Leu	Ala Ser	Thr	Ile Glu	Pro
2525			2530			2535		
Ala Thr	Ala Phe	Thr Pro	His	Leu Ser	Ala Ala	Val	Val Thr	Gly
2540			2545			2550		
Ser Ser	Ala Thr	Ser Glu	Ala	Ser Leu	Leu Thr	Thr	Ser Glu	Ser
2555			2560			2565		
Lys Ala	Ile His	Ser Ser	Pro	Gln Thr	Pro Thr	Thr	Pro Thr	Ser
2570			2575			2580		

446

Gly Ala Asn Trp Glu Thr Ser Ala Thr Pro Glu Ser Leu Leu Val
 2585 2590 2595

Val Thr Glu Thr Ser Asp Thr Thr Leu Thr Ser Lys Ile Leu Val
 2600 2605 2610

Thr Asp Thr Ile Leu Phe Ser Thr Val Ser Thr Pro Pro Ser Lys
 2615 2620 2625

Phe Pro Ser Thr Gly Thr Leu Ser Gly Ala Ser Phe Pro Thr Leu
 2630 2635 2640

Leu Pro Asp Thr Pro Ala Ile Pro Leu Thr Ala Thr Glu Pro Thr
 2645 2650 2655

Ser Ser Leu Ala Thr Ser Phe Asp Ser Thr Pro Leu Val Thr Ile
 2660 2665 2670

Ala Ser Asp Ser Leu Gly Thr Val Pro Glu Thr Thr Leu Thr Met
 2675 2680 2685

Ser Glu Thr Ser Asn Gly Asp Ala Leu Val Leu Lys Thr Val Ser
 2690 2695 2700

Asn Pro Asp Arg Ser Ile Pro Gly Ile Thr Ile Gln Gly Val Thr
 2705 2710 2715

Glu Ser Pro Leu His Pro Ser Ser Thr Ser Pro Ser Lys Ile Val
 2720 2725 2730

Ala Pro Arg Asn Thr Thr Tyr Glu Gly Ser Ile Thr Val Ala Leu
 2735 2740 2745

Ser Thr Leu Pro Ala Gly Thr Thr Gly Ser Leu Val Phe Ser Gln
 2750 2755 2760

Ser Ser Glu Asn Ser Glu Thr Thr Ala Leu Val Asp Ser Ser Ala
 2765 2770 2775

Gly Leu Glu Arg Ala Ser Val Met Pro Leu Thr Thr Gly Ser Gln
 2780 2785 2790

447

Gly	Met	Ala	Ser	Ser	Gly	Gly	Ile	Arg	Ser	Gly	Ser	Thr	His	Ser
2795						2800					2805			
Thr	Gly	Thr	Lys	Thr	Phe	Ser	Ser	Leu	Pro	Leu	Thr	Met	Asn	Pro
2810						2815					2820			
Gly	Glu	Val	Thr	Ala	Met	Ser	Glu	Ile	Thr	Thr	Asn	Arg	Leu	Thr
2825						2830					2835			
Ala	Thr	Gln	Ser	Thr	Ala	Pro	Lys	Gly	Ile	Pro	Val	Lys	Pro	Thr
2840						2845					2850			
Ser	Ala	Glu	Ser	Gly	Leu	Leu	Thr	Pro	Val	Ser	Ala	Ser	Ser	Ser
2855						2860					2865			
Pro	Ser	Lys	Ala	Phe	Ala	Ser	Leu	Thr	Thr	Ala	Pro	Pro	Thr	Trp
2870						2875					2880			
Gly	Ile	Pro	Gln	Ser	Thr	Leu	Thr	Phe	Glu	Phe	Ser	Glu	Val	Pro
2885						2890					2895			
Ser	Leu	Asp	Thr	Lys	Ser	Ala	Ser	Leu	Pro	Thr	Pro	Gly	Gln	Ser
2900						2905					2910			
Leu	Asn	Thr	Ile	Pro	Asp	Ser	Asp	Ala	Ser	Thr	Ala	Ser	Ser	Ser
2915						2920					2925			
Leu	Ser	Lys	Ser	Pro	Glu	Lys	Asn	Pro	Arg	Ala	Arg	Met	Met	Thr
2930						2935					2940			
Ser	Thr	Lys	Ala	Ile	Ser	Ala	Ser	Ser	Phe	Gln	Ser	Thr	Gly	Phe
2945						2950					2955			
Thr	Glu	Thr	Pro	Glu	Gly	Ser	Ala	Ser	Pro	Ser	Met	Ala	Gly	His
2960						2965					2970			
Glu	Pro	Arg	Val	Pro	Thr	Ser	Gly	Thr	Gly	Asp	Pro	Arg	Tyr	Ala
2975						2980					2985			

448

Ser Glu Ser Met Ser Tyr Pro Asp Pro Ser Lys Ala Ser Ser Ala
 2990 2995 3000

Met Thr Ser Thr Ser Leu Ala Ser Lys Leu Thr Thr Leu Phe Ser
 3005 3010 3015

Thr Gly Gln Ala Ala Arg Ser Gly Ser Ser Ser Ser Pro Ile Ser
 3020 3025 3030

Leu Ser Thr Glu Lys Glu Thr Ser Phe Leu Ser Pro Thr Ala Ser
 3035 3040 3045

Thr Ser Arg Lys Thr Ser Leu Phe Leu Gly Pro Ser Met Ala Arg
 3050 3055 3060

Gln Pro Asn Ile Leu Val His Leu Gln Thr Ser Ala Leu Thr Leu
 3065 3070 3075

Ser Pro Thr Ser Thr Leu Asn Met Ser Gln Glu Glu Pro Pro Glu
 3080 3085 3090

Leu Thr Ser Ser Gln Thr Ile Ala Glu Glu Glu Gly Thr Thr Ala
 3095 3100 3105

Glu Thr Gln Thr Leu Thr Phe Thr Pro Ser Glu Thr Pro Thr Ser
 3110 3115 3120

Leu Leu Pro Val Ser Ser Pro Thr Glu Pro Thr Ala Arg Arg Lys
 3125 3130 3135

Ser Ser Pro Glu Thr Trp Ala Ser Ser Ile Ser Val Pro Ala Lys
 3140 3145 3150

Thr Ser Leu Val Glu Thr Thr Asp Gly Thr Leu Val Thr Thr Ile
 3155 3160 3165

Lys Met Ser Ser Gln Ala Ala Gln Gly Asn Ser Thr Trp Pro Ala
 3170 3175 3180

Pro Ala Glu Glu Thr Gly Thr Ser Pro Ala Gly Thr Ser Pro Gly
 3185 3190 3195

449

Ser Pro Glu Met Ser Thr Thr Leu Lys Ile Met Ser Ser Lys Glu
 3200 3205 3210

Pro Ser Ile Ser Pro Glu Ile Arg Ser Thr Val Arg Asn Ser Pro
 3215 3220 3225

Trp Lys Thr Pro Glu Thr Thr Val Pro Met Glu Thr Thr Val Glu
 3230 3235 3240

Pro Val Thr Leu Gln Ser Thr Ala Leu Gly Ser Gly Ser Thr Ser
 3245 3250 3255

Ile Ser His Leu Pro Thr Gly Thr Thr Ser Pro Thr Lys Ser Pro
 3260 3265 3270

Thr Glu Asn Met Leu Ala Thr Glu Arg Val Ser Leu Ser Pro Ser
 3275 3280 3285

Pro Pro Glu Ala Trp Thr Asn Leu Tyr Ser Gly Thr Pro Gly Gly
 3290 3295 3300

Thr Arg Gln Ser Leu Ala Thr Met Ser Ser Val Ser Leu Glu Ser
 3305 3310 3315

Pro Thr Ala Arg Ser Ile Thr Gly Thr Gly Gln Gln Ser Ser Pro
 3320 3325 3330

Glu Leu Val Ser Lys Thr Thr Gly Met Glu Phe Ser Met Trp His
 3335 3340 3345

Gly Ser Thr Gly Gly Thr Thr Gly Asp Thr His Val Ser Leu Ser
 3350 3355 3360

Thr Ser Ser Asn Ile Leu Glu Asp Pro Val Thr Ser Pro Asn Ser
 3365 3370 3375

Val Ser Ser Leu Thr Asp Lys Ser Lys His Lys Thr Glu Thr Trp
 3380 3385 3390

450

Val Ser Thr Thr Ala Ile Pro Ser Thr Val Leu Asn Asn Lys Ile
 3395 3400 3405

Met Ala Ala Glu Gln Gln Thr Ser Arg Ser Val Asp Glu Ala Tyr
 3410 3415 3420

Ser Ser Thr Ser Ser Trp Ser Asp Gln Thr Ser Gly Ser Asp Ile
 3425 3430 3435

Thr Leu Gly Ala Ser Pro Asp Val Thr Asn Thr Leu Tyr Ile Thr
 3440 3445 3450

Ser Thr Ala Gln Thr Thr Ser Leu Val Ser Leu Pro Ser Gly Asp
 3455 3460 3465

Gln Gly Ile Thr Ser Leu Thr Asn Pro Ser Gly Gly Lys Thr Ser
 3470 3475 3480

Ser Ala Ser Ser Val Thr Ser Pro Ser Ile Gly Leu Glu Thr Leu
 3485 3490 3495

Arg Ala Asn Val Ser Ala Val Lys Ser Asp Ile Ala Pro Thr Ala
 3500 3505 3510

Gly His Leu Ser Gln Thr Ser Ser Pro Ala Glu Val Ser Ile Leu
 3515 3520 3525

Asp Val Thr Thr Ala Pro Thr Pro Gly Ile Ser Thr Thr Ile Thr
 3530 3535 3540

Thr Met Gly Thr Asn Ser Ile Ser Thr Thr Thr Pro Asn Pro Glu
 3545 3550 3555

Val Gly Met Ser Thr Met Asp Ser Thr Pro Ala Thr Glu Arg Arg
 3560 3565 3570

Thr Thr Ser Thr Glu His Pro Ser Thr Trp Ser Ser Thr Ala Ala
 3575 3580 3585

Ser Asp Ser Trp Thr Val Thr Asp Met Thr Ser Asn Leu Lys Val
 3590 3595 3600

451

Ala Arg Ser Pro Gly Thr Ile Ser Thr Met His Thr Thr Ser Phe
3605 3610 3615

Leu Ala Ser Ser Thr Glu Leu Asp Ser Met Ser Thr Pro His Gly
3620 3625 3630

Arg Ile Thr Val Ile Gly Thr Ser Leu Val Thr Pro Ser Ser Asp
3635 3640 3645

Ala Ser Ala Val Lys Thr Glu Thr Ser Thr Ser Glu Arg Thr Leu
3650 3655 3660

Ser Pro Ser Asp Thr Thr Ala Ser Thr Pro Ile Ser Thr Phe Ser
3665 3670 3675

Arg Val Gln Arg Met Ser Ile Ser Val Pro Asp Ile Leu Ser Thr
3680 3685 3690

Ser Trp Thr Pro Ser Ser Thr Glu Ala Glu Asp Val Pro Val Ser
3695 3700 3705

Met Val Ser Thr Asp His Ala Ser Thr Lys Thr Asp Pro Asn Thr
3710 3715 3720

Pro Leu Ser Thr Phe Leu Phe Asp Ser Leu Ser Thr Leu Asp Trp
3725 3730 3735

Asp Thr Gly Arg Ser Leu Ser Ser Ala Thr Ala Thr Thr Ser Ala
3740 3745 3750

Pro Gln Gly Ala Thr Thr Pro Gln Glu Leu Thr Leu Glu Thr Met
3755 3760 3765

Ile Ser Pro Ala Thr Ser Gln Leu Pro Phe Ser Ile Gly His Ile
3770 3775 3780

Thr Ser Ala Val Thr Pro Ala Ala Met Ala Arg Ser Ser Gly Val
3785 3790 3795

452

Thr Phe Ser Arg Pro Asp Pro Thr Ser Lys Lys Ala Glu Gln Thr
 3800 3805 3810

Ser Thr Gln Leu Pro Thr Thr Thr Ser Ala His Pro Gly Gln Val
 3815 3820 3825

Pro Arg Ser Ala Ala Thr Thr Leu Asp Val Ile Pro His Thr Ala
 3830 3835 3840

Lys Thr Pro Asp Ala Thr Phe Gln Arg Gln Gly Gln Thr Ala Leu
 3845 3850 3855

Thr Thr Glu Ala Arg Ala Thr Ser Asp Ser Trp Asn Glu Lys Glu
 3860 3865 3870

Lys Ser Thr Pro Ser Ala Pro Trp Ile Thr Glu Met Met Asn Ser
 3875 3880 3885

Val Ser Glu Asp Thr Ile Lys Glu Val Thr Ser Ser Ser Ser Val
 3890 3895 3900

Leu Lys Asp Pro Glu Tyr Ala Gly His Lys Leu Gly Ile Trp Asp
 3905 3910 3915

Asp Phe Ile Pro Lys Phe Gly Lys Ala Ala His Met Arg Glu Leu
 3920 3925 3930

Pro Leu Leu Ser Pro Pro Gln Asp Lys Glu Ala Ile His Pro Ser
 3935 3940 3945

Thr Asn Thr Val Glu Thr Thr Gly Trp Val Thr Ser Ser Glu His
 3950 3955 3960

Ala Ser His Ser Thr Ile Pro Ala His Ser Ala Ser Ser Lys Leu
 3965 3970 3975

Thr Ser Pro Val Val Thr Thr Ser Thr Arg Glu Gln Ala Ile Val
 3980 3985 3990

Ser Met Ser Thr Thr Thr Trp Pro Glu Ser Thr Arg Ala Arg Thr
 3995 4000 4005

453

Glu Pro Asn Ser Phe Leu Thr	Ile Glu Leu Arg Asp	Val Ser Pro
4010	4015	4020
Tyr Met Asp Thr Ser Ser Thr	Thr Gln Thr Ser Ile	Ile Ser Ser
4025	4030	4035
Pro Gly Ser Thr Ala Ile Thr	Lys Gly Pro Arg Thr	Glu Ile Thr
4040	4045	4050
Ser Ser Lys Arg Ile Ser Ser	Ser Phe Leu Ala Gln	Ser Met Arg
4055	4060	4065
Ser Ser Asp Ser Pro Ser Glu	Ala Ile Thr Arg Leu	Ser Asn Phe
4070	4075	4080
Pro Ala Met Thr Glu Ser Gly	Gly Met Ile Leu Ala	Met Gln Thr
4085	4090	4095
Ser Pro Pro Gly Ala Thr Ser	Leu Ser Ala Pro Thr	Leu Asp Thr
4100	4105	4110
Ser Ala Thr Ala Ser Trp Thr	Gly Thr Pro Leu Ala	Thr Thr Gln
4115	4120	4125
Arg Phe Thr Tyr Ser Glu Lys	Thr Thr Leu Phe Ser	Lys Gly Pro
4130	4135	4140
Glu Asp Thr Ser Gln Pro Ser	Pro Pro Ser Val Glu	Glu Thr Ser
4145	4150	4155
Ser Ser Ser Ser Leu Val Pro	Ile His Ala Thr Thr	Ser Pro Ser
4160	4165	4170
Asn Ile Leu Leu Thr Ser Gln	Gly His Ser Pro Ser	Ser Thr Pro
4175	4180	4185
Pro Val Thr Ser Val Phe Leu	Ser Glu Thr Ser Gly	Leu Gly Lys
4190	4195	4200

454

Thr Thr Asp Met Ser Arg Ile Ser Leu Glu Pro Gly Thr Ser Leu
 4205 4210 4215

Pro Pro Asn Leu Ser Ser Thr Ala Gly Glu Ala Leu Ser Thr Tyr
 4220 4225 4230

Glu Ala Ser Arg Asp Thr Lys Ala Ile His His Ser Ala Asp Thr
 4235 4240 4245

Ala Val Thr Asn Met Glu Ala Thr Ser Ser Glu Tyr Ser Pro Ile
 4250 4255 4260

Pro Gly His Thr Lys Pro Ser Lys Ala Thr Ser Pro Leu Val Thr
 4265 4270 4275

Ser His Ile Met Gly Asp Ile Thr Ser Ser Thr Ser Val Phe Gly
 4280 4285 4290

Ser Ser Glu Thr Thr Glu Ile Glu Thr Val Ser Ser Val Asn Gln
 4295 4300 4305

Gly Leu Gln Glu Arg Ser Thr Ser Gln Val Ala Ser Ser Ala Thr
 4310 4315 4320

Glu Thr Ser Thr Val Ile Thr His Val Ser Ser Gly Asp Ala Thr
 4325 4330 4335

Thr His Val Thr Lys Thr Gln Ala Thr Phe Ser Ser Gly Thr Ser
 4340 4345 4350

Ile Ser Ser Pro His Gln Phe Ile Thr Ser Thr Asn Thr Phe Thr
 4355 4360 4365

Asp Val Ser Thr Asn Pro Ser Thr Ser Leu Ile Met Thr Glu Ser
 4370 4375 4380

Ser Gly Val Thr Ile Thr Thr Gln Thr Gly Pro Thr Gly Ala Ala
 4385 4390 4395

Thr Gln Gly Pro Tyr Leu Leu Asp Thr Ser Thr Met Pro Tyr Leu
 4400 4405 4410

455

Thr Glu Thr Pro Leu Ala Val Thr Pro Asp Phe Met Gln Ser Glu
 4415 4420 4425

Lys Thr Thr Leu Ile Ser Lys Gly Pro Lys Asp Val Thr Trp Thr
 4430 4435 4440

Ser Pro Pro Ser Val Ala Glu Thr Ser Tyr Pro Ser Ser Leu Thr
 4445 4450 4455

Pro Phe Leu Val Thr Thr Ile Pro Pro Ala Thr Ser Thr Leu Gln
 4460 4465 4470

Gly Gln His Thr Ser Ser Pro Val Ser Ala Thr Ser Val Leu Thr
 4475 4480 4485

Ser Gly Leu Val Lys Thr Thr Asp Met Leu Asn Thr Ser Met Glu
 4490 4495 4500

Pro Val Thr Asn Ser Pro Gln Asn Leu Asn Asn Pro Ser Asn Glu
 4505 4510 4515

Ile Leu Ala Thr Leu Ala Ala Thr Thr Asp Ile Glu Thr Ile His
 4520 4525 4530

Pro Ser Ile Asn Lys Ala Val Thr Asn Met Gly Thr Ala Ser Ser
 4535 4540 4545

Ala His Val Leu His Ser Thr Leu Pro Val Ser Ser Glu Pro Ser
 4550 4555 4560

Thr Ala Thr Ser Pro Met Val Pro Ala Ser Ser Met Gly Asp Ala
 4565 4570 4575

Leu Ala Ser Ile Ser Ile Pro Gly Ser Glu Thr Thr Asp Ile Glu
 4580 4585 4590

Gly Glu Pro Thr Ser Ser Leu Thr Ala Gly Arg Lys Glu Asn Ser
 4595 4600 4605

456

Thr Leu Gln Glu Met Asn Ser Thr Thr Glu Ser Asn Ile Ile Leu
 4610 4615 4620
 Ser Asn Val Ser Val Gly Ala Ile Thr Glu Ala Thr Lys Met Glu
 4625 4630 4635
 Val Pro Ser Phe Asp Ala Thr Phe Ile Pro Thr Pro Ala Gln Ser
 4640 4645 4650
 Thr Lys Phe Pro Asp Ile Phe Ser Val Ala Ser Ser Arg Leu Ser
 4655 4660 4665
 Asn Ser Pro Pro Met Thr Ile Ser Thr His Met Thr Thr Thr Gln
 4670 4675 4680
 Thr Gly Ser Ser Gly Ala Thr Ser Lys Ile Pro Leu Ala Leu Asp
 4685 4690 4695
 Thr Ser Thr Leu Glu Thr Ser Ala Gly Thr Pro Ser Val Val Thr
 4700 4705 4710
 Glu Gly Phe Ala His Ser Lys Ile Thr Thr Ala Met Asn Asn Asp
 4715 4720 4725
 Val Lys Asp Val Ser Gln Thr Asn Pro Pro Phe Gln Asp Glu Ala
 4730 4735 4740
 Ser Ser Pro Ser Ser Gln Ala Pro Val Leu Val Thr Thr Leu Pro
 4745 4750 4755
 Ser Ser Val Ala Phe Thr Pro Gln Trp His Ser Thr Ser Ser Pro
 4760 4765 4770
 Val Ser Met Ser Ser Val Leu Thr Ser Ser Leu Val Lys Thr Ala
 4775 4780 4785
 Gly Lys Val Asp Thr Ser Leu Glu Thr Val Thr Ser Ser Pro Gln
 4790 4795 4800
 Ser Met Ser Asn Thr Leu Asp Asp Ile Ser Val Thr Ser Ala Ala
 4805 4810 4815

457

Thr	Thr	Asp	Ile	Glu	Thr	Thr	His	Pro	Ser	Ile	Asn	Thr	Val	Val
4820						4825					4830			
Thr	Asn	Val	Gly	Thr	Thr	Gly	Ser	Ala	Phe	Glu	Ser	His	Ser	Thr
4835						4840					4845			
Val	Ser	Ala	Tyr	Pro	Glu	Pro	Ser	Lys	Ser	His	Ile	Leu	Pro	Met
4850						4855					4860			
Leu	Pro	Pro	Pro	Pro	Trp	Lys	Thr	Pro	Gln	Phe	Pro	Arg	Ser	Ile
4865						4870					4875			
Pro	Lys	Ser	Ser	Lys	Thr	Thr	Arg	Thr	Glu	Thr	Glu	Thr	Thr	Ser
4880						4885					4890			
Ser	Leu	Thr	Pro	Lys	Leu	Arg	Glu	Thr	Ser	Ile	Ser	Gln	Glu	Ile
4895						4900					4905			
Thr	Ser	Ser	Thr	Glu	Thr	Ser	Thr	Val	Pro	Tyr	Lys	Glu	Leu	Thr
4910						4915					4920			
Gly	Ala	Thr	Thr	Glu	Val	Ser	Arg	Thr	Asp	Val	Thr	Ser	Ser	Ser
4925						4930					4935			
Ser	Thr	Ser	Phe	Pro	Gly	Pro	Asp	Gln	Ser	Thr	Val	Ser	Leu	Asp
4940						4945					4950			
Ile	Ser	Thr	Glu	Thr	Asn	Thr	Arg	Leu	Ser	Thr	Ser	Pro	Ile	Met
4955						4960					4965			
Thr	Glu	Ser	Ala	Glu	Ile	Thr	Ile	Thr	Thr	Gln	Thr	Gly	Pro	His
4970						4975					4980			
Gly	Ala	Thr	Ser	Gln	Asp	Thr	Phe	Thr	Met	Asp	Pro	Ser	Asn	Thr
4985						4990					4995			
Thr	Pro	Gln	Ala	Gly	Ile	His	Ser	Ala	Met	Thr	His	Gly	Phe	Ser
5000						5005					5010			

458

Gln Leu Asp Val Thr Thr Leu Met Ser Arg Ile Pro Gln Asp Val		
5015	5020	5025
Ser Trp Thr Ser Pro Pro Ser Val Asp Lys Thr Ser Ser Pro Ser		
5030	5035	5040
Ser Phe Leu Ser Ser Pro Ala Met Thr Thr Pro Ser Leu Ile Ser		
5045	5050	5055
Ser Thr Leu Pro Glu Asp Lys Leu Ser Ser Pro Met Thr Ser Leu		
5060	5065	5070
Leu Thr Ser Gly Leu Val Lys Ile Thr Asp Ile Leu Arg Thr Arg		
5075	5080	5085
Leu Glu Pro Val Thr Ser Ser Leu Pro Asn Phe Ser Ser Thr Ser		
5090	5095	5100
Asp Lys Ile Leu Ala Thr Ser Lys Asp Ser Lys Asp Thr Lys Glu		
5105	5110	5115
Ile Phe Pro Ser Ile Asn Thr Glu Glu Thr Asn Val Lys Ala Asn		
5120	5125	5130
Asn Ser Gly His Glu Ser His Ser Pro Ala Leu Ala Asp Ser Glu		
5135	5140	5145
Thr Pro Lys Ala Thr Thr Gln Met Val Ile Thr Thr Thr Val Gly		
5150	5155	5160
Asp Pro Ala Pro Ser Thr Ser Met Pro Val His Gly Ser Ser Glu		
5165	5170	5175
Thr Thr Asn Ile Lys Arg Glu Pro Thr Tyr Phe Leu Thr Pro Arg		
5180	5185	5190
Leu Arg Glu Thr Ser Thr Ser Gln Glu Ser Ser Phe Pro Thr Asp		
5195	5200	5205
Thr Ser Phe Leu Leu Ser Lys Val Pro Thr Gly Thr Ile Thr Glu		
5210	5215	5220

459

Val Ser	Ser Thr Gly Val	Asn	Ser Ser Ser Lys	Ile	Ser Thr Pro
5225		5230		5235	
Asp His	Asp Lys Ser Thr	Val	Pro Pro Asp Thr	Phe	Thr Gly Glu
5240		5245		5250	
Ile Pro	Arg Val Phe Thr	Ser	Ser Ile Lys Thr	Lys	Ser Ala Glu
5255		5260		5265	
Met Thr	Ile Thr Thr Gln	Ala	Ser Pro Pro Glu	Ser	Ala Ser His
5270		5275		5280	
Ser Thr	Leu Pro Leu Asp	Thr	Ser Thr Thr Leu	Ser	Gln Gly Gly
5285		5290		5295	
Thr His	Ser Thr Val Thr	Gln	Gly Phe Pro Tyr	Ser	Glu Val Thr
5300		5305		5310	
Thr Leu	Met Gly Met Gly	Pro	Gly Asn Val Ser	Trp	Met Thr Thr
5315		5320		5325	
Pro Pro	Val Glu Glu Thr	Ser	Ser Val Ser Ser	Leu	Met Ser Ser
5330		5335		5340	
Pro Ala	Met Thr Ser Pro	Ser	Pro Val Ser Ser	Thr	Ser Pro Gln
5345		5350		5355	
Ser Ile	Pro Ser Ser Pro	Leu	Pro Val Thr Ala	Leu	Pro Thr Ser
5360		5365		5370	
Val Leu	Val Thr Thr Thr	Asp	Val Leu Gly Thr	Thr	Ser Pro Glu
5375		5380		5385	
Ser Val	Thr Ser Ser Pro	Pro	Asn Leu Ser Ser	Ile	Thr His Glu
5390		5395		5400	
Arg Pro	Ala Thr Tyr Lys	Asp	Thr Ala His Thr	Glu	Ala Ala Met
5405		5410		5415	

460

His	His	Ser	Thr	Asn	Thr	Ala	Val	Thr	Asn	Val	Gly	Thr	Ser	Gly
5420						5425					5430			
Ser	Gly	His	Lys	Ser	Gln	Ser	Ser	Val	Leu	Ala	Asp	Ser	Glu	Thr
5435						5440					5445			
Ser	Lys	Ala	Thr	Pro	Leu	Met	Ser	Thr	Thr	Ser	Thr	Leu	Gly	Asp
5450						5455					5460			
Thr	Ser	Val	Ser	Thr	Ser	Thr	Pro	Asn	Ile	Ser	Gln	Thr	Asn	Gln
5465						5470					5475			
Ile	Gln	Thr	Glu	Pro	Thr	Ala	Ser	Leu	Ser	Pro	Arg	Leu	Arg	Glu
5480						5485					5490			
Ser	Ser	Thr	Ser	Glu	Lys	Thr	Ser	Ser	Thr	Thr	Glu	Thr	Asn	Thr
5495						5500					5505			
Ala	Phe	Ser	Tyr	Val	Pro	Thr	Gly	Ala	Ile	Thr	Gln	Ala	Ser	Arg
5510						5515					5520			
Thr	Glu	Ile	Ser	Ser	Ser	Arg	Thr	Ser	Ile	Ser	Asp	Leu	Asp	Arg
5525						5530					5535			
Pro	Thr	Ile	Ala	Pro	Asp	Ile	Ser	Thr	Gly	Met	Ile	Thr	Arg	Leu
5540						5545					5550			
Phe	Thr	Ser	Pro	Ile	Met	Thr	Lys	Ser	Ala	Glu	Met	Thr	Val	Thr
5555						5560					5565			
Thr	Gln	Thr	Thr	Thr	Pro	Gly	Ala	Thr	Ser	Gln	Gly	Ile	Leu	Pro
5570						5575					5580			
Trp	Asp	Thr	Ser	Thr	Thr	Leu	Phe	Gln	Gly	Gly	Thr	His	Ser	Thr
5585						5590					5595			
Val	Ser	Gln	Gly	Phe	Pro	His	Ser	Glu	Ile	Thr	Thr	Leu	Arg	Ser
5600						5605					5610			
Arg	Thr	Pro	Gly	Asp	Val	Ser	Trp	Met	Thr	Thr	Pro	Pro	Val	Glu
5615						5620					5625			

461

Glu Thr 5630	Ser Ser Gly Phe Ser 5635	Leu Met Ser Pro Ser 5640	Met Thr Ser
Pro Ser 5645	Pro Val Ser Ser Thr 5650	Ser Pro Glu Ser Ile 5655	Pro Ser Ser
Pro Leu 5660	Pro Val Thr Ala Leu 5665	Leu Thr Ser Val Leu 5670	Val Thr Thr
Thr Asn 5675	Val Leu Gly Thr Thr 5680	Ser Pro Glu Thr Val 5685	Thr Ser Ser
Pro Pro 5690	Asn Leu Ser Ser Pro 5695	Thr Gln Glu Arg Leu 5700	Thr Thr Tyr
Lys Asp 5705	Thr Ala His Thr Glu 5710	Ala Met His Ala Ser 5715	Met His Thr
Asn Thr 5720	Ala Val Ala Asn Val 5725	Gly Thr Ser Ile Ser 5730	Gly His Glu
Ser Gln 5735	Ser Ser Val Pro Ala 5740	Asp Ser His Thr Ser 5745	Lys Ala Thr
Ser Pro 5750	Met Gly Ile Thr Phe 5755	Ala Met Gly Asp Thr 5760	Ser Val Ser
Thr Ser 5765	Thr Pro Ala Phe Phe 5770	Glu Thr Arg Ile Gln 5775	Thr Glu Ser
Thr Ser 5780	Ser Leu Ile Pro Gly 5785	Leu Arg Asp Thr Arg 5790	Thr Ser Glu
Glu Ile 5795	Asn Thr Val Thr Glu 5800	Thr Ser Thr Val Leu 5805	Ser Glu Val
Pro Thr 5810	Thr Thr Thr Thr Glu 5815	Val Ser Arg Thr Glu 5820	Val Ile Thr

462

Ser 5825	Ser	Arg	Thr	Thr	Ile	Ser 5830	Gly	Pro	Asp	His	Ser 5835	Lys	Met	Ser
Pro 5840	Tyr	Ile	Ser	Thr	Glu	Thr 5845	Ile	Thr	Arg	Leu	Ser 5850	Thr	Phe	Pro
Phe 5855	Val	Thr	Gly	Ser	Thr	Glu 5860	Met	Ala	Ile	Thr	Asn 5865	Gln	Thr	Gly
Pro 5870	Ile	Gly	Thr	Ile	Ser	Gln 5875	Ala	Thr	Leu	Thr	Leu 5880	Asp	Thr	Ser
Ser 5885	Thr	Ala	Ser	Trp	Glu	Gly 5890	Thr	His	Ser	Pro	Val 5895	Thr	Gln	Arg
Phe 5900	Pro	His	Ser	Glu	Glu	Thr 5905	Thr	Thr	Met	Ser	Arg 5910	Ser	Thr	Lys
Gly 5915	Val	Ser	Trp	Gln	Ser	Pro 5920	Pro	Ser	Val	Glu	Glu 5925	Thr	Ser	Ser
Pro 5930	Ser	Ser	Pro	Val	Pro	Leu 5935	Pro	Ala	Ile	Thr	Ser 5940	His	Ser	Ser
Leu 5945	Tyr	Ser	Ala	Val	Ser	Gly 5950	Ser	Ser	Pro	Thr	Ser 5955	Ala	Leu	Pro
Val 5960	Thr	Ser	Leu	Leu	Thr	Ser 5965	Gly	Arg	Arg	Lys	Thr 5970	Ile	Asp	Met
Leu 5975	Asp	Thr	His	Ser	Glu	Leu 5980	Val	Thr	Ser	Ser	Leu 5985	Pro	Ser	Ala
Ser 5990	Ser	Phe	Ser	Gly	Glu	Ile 5995	Leu	Thr	Ser	Glu	Ala 6000	Ser	Thr	Asn
Thr 6005	Glu	Thr	Ile	His	Phe	Ser 6010	Glu	Asn	Thr	Ala	Glu 6015	Thr	Asn	Met
Gly 6020	Thr	Thr	Asn	Ser	Met	His 6025	Lys	Leu	His	Ser	Ser 6030	Val	Ser	Ile

463

His 6035	Ser	Gln	Pro	Ser	Gly	His 6040	Thr	Pro	Pro	Lys	Val 6045	Thr	Gly	Ser
Met 6050	Met	Glu	Asp	Ala	Ile	Val 6055	Ser	Thr	Ser	Thr	Pro 6060	Gly	Ser	Pro
Glu 6065	Thr	Lys	Asn	Val	Asp	Arg 6070	Asp	Ser	Thr	Ser	Pro 6075	Leu	Thr	Pro
Glu 6080	Leu	Lys	Glu	Asp	Ser	Thr 6085	Ala	Leu	Val	Met	Asn 6090	Ser	Thr	Thr
Glu 6095	Ser	Asn	Thr	Val	Phe	Ser 6100	Ser	Val	Ser	Leu	Asp 6105	Ala	Ala	Thr
Glu 6110	Val	Ser	Arg	Ala	Glu	Val 6115	Thr	Tyr	Tyr	Asp	Pro 6120	Thr	Phe	Met
Pro 6125	Ala	Ser	Ala	Gln	Ser	Thr 6130	Lys	Ser	Pro	Asp	Ile 6135	Ser	Pro	Glu
Ala 6140	Ser	Ser	Ser	His	Ser	Asn 6145	Ser	Pro	Pro	Leu	Thr 6150	Ile	Ser	Thr
His 6155	Lys	Thr	Ile	Ala	Thr	Gln 6160	Thr	Gly	Pro	Ser	Gly 6165	Val	Thr	Ser
Leu 6170	Gly	Gln	Leu	Thr	Leu	Asp 6175	Thr	Ser	Thr	Ile	Ala 6180	Thr	Ser	Ala
Gly 6185	Thr	Pro	Ser	Ala	Arg	Thr 6190	Gln	Asp	Phe	Val	Asp 6195	Ser	Glu	Thr
Thr 6200	Ser	Val	Met	Asn	Asn	Asp 6205	Leu	Asn	Asp	Val	Leu 6210	Lys	Thr	Ser
Pro 6215	Phe	Ser	Ala	Glu	Glu	Ala 6220	Asn	Ser	Leu	Ser	Ser 6225	Gln	Ala	Pro

464

Leu Leu Val Thr Thr Ser Pro Ser Pro Val Thr Ser Thr Leu Gln
 6230 6235 6240

Glu His Ser Thr Ser Ser Leu Val Ser Val Thr Ser Val Pro Thr
 6245 6250 6255

Pro Thr Leu Ala Lys Ile Thr Asp Met Asp Thr Asn Leu Glu Pro
 6260 6265 6270

Val Thr Arg Ser Pro Gln Asn Leu Arg Asn Thr Leu Ala Thr Ser
 6275 6280 6285

Glu Ala Thr Thr Asp Thr His Thr Met His Pro Ser Ile Asn Thr
 6290 6295 6300

Ala Met Ala Asn Val Gly Thr Thr Ser Ser Pro Asn Glu Phe Tyr
 6305 6310 6315

Phe Thr Val Ser Pro Asp Ser Asp Pro Tyr Lys Ala Thr Ser Ala
 6320 6325 6330

Val Val Ile Thr Ser Thr Ser Gly Asp Ser Ile Val Ser Thr Ser
 6335 6340 6345

Met Pro Arg Ser Ser Ala Met Lys Lys Ile Glu Ser Glu Thr Thr
 6350 6355 6360

Phe Ser Leu Ile Phe Arg Leu Arg Glu Thr Ser Thr Ser Gln Lys
 6365 6370 6375

Ile Gly Ser Ser Ser Asp Thr Ser Thr Val Phe Asp Lys Ala Phe
 6380 6385 6390

Thr Ala Ala Thr Thr Glu Val Ser Arg Thr Glu Leu Thr Ser Ser
 6395 6400 6405

Ser Arg Thr Ser Ile Gln Gly Thr Glu Lys Pro Thr Met Ser Pro
 6410 6415 6420

Asp Thr Ser Thr Arg Ser Val Thr Met Leu Ser Thr Phe Ala Gly
 6425 6430 6435

Leu	Thr	Lys	Ser	Glu	Glu	Arg	Thr	Ile	Ala	Thr	Gln	Thr	Gly	Pro
6440						6445							6450	
His	Arg	Ala	Thr	Ser	Gln	Gly	Thr	Leu	Thr	Trp	Asp	Thr	Ser	Ile
6455						6460					6465			
Thr	Thr	Ser	Gln	Ala	Gly	Thr	His	Ser	Ala	Met	Thr	His	Gly	Phe
6470						6475					6480			
Ser	Gln	Leu	Asp	Leu	Ser	Thr	Leu	Thr	Ser	Arg	Val	Pro	Glu	Tyr
6485						6490					6495			
Ile	Ser	Gly	Thr	Ser	Pro	Pro	Ser	Val	Glu	Lys	Thr	Ser	Ser	Ser
6500						6505					6510			
Ser	Ser	Leu	Leu	Ser	Leu	Pro	Ala	Ile	Thr	Ser	Pro	Ser	Pro	Val
6515						6520					6525			
Pro	Thr	Thr	Leu	Pro	Glu	Ser	Arg	Pro	Ser	Ser	Pro	Val	His	Leu
6530						6535					6540			
Thr	Ser	Leu	Pro	Thr	Ser	Gly	Leu	Val	Lys	Thr	Thr	Asp	Met	Leu
6545						6550					6555			
Ala	Ser	Val	Ala	Ser	Leu	Pro	Pro	Asn	Leu	Gly	Ser	Thr	Ser	His
6560						6565					6570			
Lys	Ile	Pro	Thr	Thr	Ser	Glu	Asp	Ile	Lys	Asp	Thr	Glu	Lys	Met
6575						6580					6585			
Tyr	Pro	Ser	Thr	Asn	Ile	Ala	Val	Thr	Asn	Val	Gly	Thr	Thr	Thr
6590						6595					6600			
Ser	Glu	Lys	Glu	Ser	Tyr	Ser	Ser	Val	Pro	Ala	Tyr	Ser	Glu	Pro
6605						6610					6615			
Pro	Lys	Val	Thr	Ser	Pro	Met	Val	Thr	Ser	Phe	Asn	Ile	Arg	Asp
6620						6625					6630			

466

Thr Ile	Val Ser	Thr Ser	Met	Pro Gly	Ser Ser	Glu	Ile Thr	Arg
6635			6640			6645		
Ile Glu	Met Glu	Ser Thr	Phe	Ser Val	Ala His	Gly	Leu Lys	Gly
6650			6655			6660		
Thr Ser	Thr Ser	Gln Asp	Pro	Ile Val	Ser Thr	Glu	Lys Ser	Ala
6665			6670			6675		
Val Leu	His Lys	Leu Thr	Thr	Gly Ala	Thr Glu	Thr	Ser Arg	Thr
6680			6685			6690		
Glu Val	Ala Ser	Ser Arg	Arg	Thr Ser	Ile Pro	Gly	Pro Asp	His
6695			6700			6705		
Ser Thr	Glu Ser	Pro Asp	Ile	Ser Thr	Glu Val	Ile	Pro Ser	Leu
6710			6715			6720		
Pro Ile	Ser Leu	Gly Ile	Thr	Glu Ser	Ser Asn	Met	Thr Ile	Ile
6725			6730			6735		
Thr Arg	Thr Gly	Pro Pro	Leu	Gly Ser	Thr Ser	Gln	Gly Thr	Phe
6740			6745			6750		
Thr Leu	Asp Thr	Pro Thr	Thr	Ser Ser	Arg Ala	Gly	Thr His	Ser
6755			6760			6765		
Met Ala	Thr Gln	Glu Phe	Pro	His Ser	Glu Met	Thr	Thr Val	Met
6770			6775			6780		
Asn Lys	Asp Pro	Glu Ile	Leu	Ser Trp	Thr Ile	Pro	Pro Ser	Ile
6785			6790			6795		
Glu Lys	Thr Ser	Phe Ser	Ser	Ser Leu	Met Pro	Ser	Pro Ala	Met
6800			6805			6810		
Thr Ser	Pro Pro	Val Ser	Ser	Thr Leu	Pro Lys	Thr	Ile His	Thr
6815			6820			6825		
Thr Pro	Ser Pro	Met Thr	Ser	Leu Leu	Thr Pro	Ser	Leu Val	Met
6830			6835			6840		

467

Thr	Thr	Asp	Thr	Leu	Gly	Thr	Ser	Pro	Glu	Pro	Thr	Thr	Ser	Ser
6845						6850					6855			
Pro	Pro	Asn	Leu	Ser	Ser	Thr	Ser	His	Glu	Ile	Leu	Thr	Thr	Asp
6860						6865					6870			
Glu	Asp	Thr	Thr	Ala	Ile	Glu	Ala	Met	His	Pro	Ser	Thr	Ser	Thr
6875						6880					6885			
Ala	Ala	Thr	Asn	Val	Glu	Thr	Thr	Ser	Ser	Gly	His	Gly	Ser	Gln
6890						6895					6900			
Ser	Ser	Val	Leu	Ala	Asp	Ser	Glu	Lys	Thr	Lys	Ala	Thr	Ala	Pro
6905						6910					6915			
Met	Asp	Thr	Thr	Ser	Thr	Met	Gly	His	Thr	Thr	Val	Ser	Thr	Ser
6920						6925					6930			
Met	Ser	Val	Ser	Ser	Glu	Thr	Thr	Lys	Ile	Lys	Arg	Glu	Ser	Thr
6935						6940					6945			
Tyr	Ser	Leu	Thr	Pro	Gly	Leu	Arg	Glu	Thr	Ser	Ile	Ser	Gln	Asn
6950						6955					6960			
Ala	Ser	Phe	Ser	Thr	Asp	Thr	Ser	Ile	Val	Leu	Ser	Glu	Val	Pro
6965						6970					6975			
Thr	Gly	Thr	Thr	Ala	Glu	Val	Ser	Arg	Thr	Glu	Val	Thr	Ser	Ser
6980						6985					6990			
Gly	Arg	Thr	Ser	Ile	Pro	Gly	Pro	Ser	Gln	Ser	Thr	Val	Leu	Pro
6995						7000					7005			
Glu	Ile	Ser	Thr	Arg	Thr	Met	Thr	Arg	Leu	Phe	Ala	Ser	Pro	Thr
7010						7015					7020			
Met	Thr	Glu	Ser	Ala	Glu	Met	Thr	Ile	Pro	Thr	Gln	Thr	Gly	Pro
7025						7030					7035			

468

Ser Gly Ser Thr Ser Gln Asp Thr Leu Thr Leu Asp Thr Ser Thr
 7040 7045 7050

Thr Lys Ser Gln Ala Lys Thr His Ser Thr Leu Thr Gln Arg Phe
 7055 7060 7065

Pro His Ser Glu Met Thr Thr Leu Met Ser Arg Gly Pro Gly Asp
 7070 7075 7080

Met Ser Trp Gln Ser Ser Pro Ser Leu Glu Asn Pro Ser Ser Leu
 7085 7090 7095

Pro Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Pro Pro Ile
 7100 7105 7110

Ser Ser Thr Leu Pro Val Thr Ile Ser Ser Ser Pro Leu Pro Val
 7115 7120 7125

Thr Ser Leu Leu Thr Ser Ser Pro Val Thr Thr Thr Asp Met Leu
 7130 7135 7140

His Thr Ser Pro Glu Leu Val Thr Ser Ser Pro Pro Lys Leu Ser
 7145 7150 7155

His Thr Ser Asp Glu Arg Leu Thr Thr Gly Lys Asp Thr Thr Asn
 7160 7165 7170

Thr Glu Ala Val His Pro Ser Thr Asn Thr Ala Ala Ser Asn Val
 7175 7180 7185

Glu Ile Pro Ser Ser Gly His Glu Ser Pro Ser Ser Ala Leu Ala
 7190 7195 7200

Asp Ser Glu Thr Ser Lys Ala Thr Ser Pro Met Phe Ile Thr Ser
 7205 7210 7215

Thr Gln Glu Asp Thr Thr Val Ala Ile Ser Thr Pro His Phe Leu
 7220 7225 7230

Glu Thr Ser Arg Ile Gln Lys Glu Ser Ile Ser Ser Leu Ser Pro
 7235 7240 7245

469

Lys	Leu	Arg	Glu	Thr	Gly	Ser	Ser	Val	Glu	Thr	Ser	Ser	Ala	Ile
7250						7255					7260			
Glu	Thr	Ser	Ala	Val	Leu	Ser	Glu	Val	Ser	Val	Gly	Ala	Thr	Thr
7265						7270					7275			
Glu	Ile	Ser	Arg	Thr	Glu	Val	Thr	Ser	Ser	Ser	Arg	Thr	Ser	Ile
7280						7285					7290			
Ser	Gly	Ser	Ala	Glu	Ser	Thr	Met	Leu	Pro	Glu	Ile	Ser	Thr	Thr
7295						7300					7305			
Arg	Lys	Ile	Ile	Lys	Phe	Pro	Thr	Ser	Pro	Ile	Leu	Ala	Glu	Ser
7310						7315					7320			
Ser	Glu	Met	Thr	Ile	Lys	Thr	Gln	Thr	Ser	Pro	Pro	Gly	Ser	Thr
7325						7330					7335			
Ser	Glu	Ser	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Thr	Pro	Ser	Leu
7340						7345					7350			
Val	Ile	Thr	His	Ser	Thr	Met	Thr	Gln	Arg	Leu	Pro	His	Ser	Glu
7355						7360					7365			
Ile	Thr	Thr	Leu	Val	Ser	Arg	Gly	Ala	Gly	Asp	Val	Pro	Arg	Pro
7370						7375					7380			
Ser	Ser	Leu	Pro	Val	Glu	Glu	Thr	Ser	Pro	Pro	Ser	Ser	Gln	Leu
7385						7390					7395			
Ser	Leu	Ser	Ala	Met	Ile	Ser	Pro	Ser	Pro	Val	Ser	Ser	Thr	Leu
7400						7405					7410			
Pro	Ala	Ser	Ser	His	Ser	Ser	Ser	Ala	Ser	Val	Thr	Ser	Leu	Leu
7415						7420					7425			
Thr	Pro	Gly	Gln	Val	Lys	Thr	Thr	Glu	Val	Leu	Asp	Ala	Ser	Ala
7430						7435					7440			

470

Glu Pro	Glu Thr	Ser Ser	Pro	Pro Ser	Leu Ser	Ser	Thr Ser	Val	7445	7450	7455
Glu Ile	Leu Ala	Thr Ser	Glu	Val Thr	Thr Asp	Thr	Glu Lys	Ile	7460	7465	7470
His Pro	Phe Ser	Asn Thr	Ala	Val Thr	Lys Val	Gly	Thr Ser	Ser	7475	7480	7485
Ser Gly	His Glu	Ser Pro	Ser	Ser Val	Leu Pro	Asp	Ser Glu	Thr	7490	7495	7500
Thr Lys	Ala Thr	Ser Ala	Met	Gly Thr	Ile Ser	Ile	Met Gly	Asp	7505	7510	7515
Thr Ser	Val Ser	Thr Leu	Thr	Pro Ala	Leu Ser	Asn	Thr Arg	Lys	7520	7525	7530
Ile Gln	Ser Glu	Pro Ala	Ser	Ser Leu	Thr Thr	Arg	Leu Arg	Glu	7535	7540	7545
Thr Ser	Thr Ser	Glu Glu	Thr	Ser Leu	Ala Thr	Glu	Ala Asn	Thr	7550	7555	7560
Val Leu	Ser Lys	Val Ser	Thr	Gly Ala	Thr Thr	Glu	Val Ser	Arg	7565	7570	7575
Thr Glu	Ala Ile	Ser Phe	Ser	Arg Thr	Ser Met	Ser	Gly Pro	Glu	7580	7585	7590
Gln Ser	Thr Met	Ser Gln	Asp	Ile Ser	Ile Gly	Thr	Ile Pro	Arg	7595	7600	7605
Ile Ser	Ala Ser	Ser Val	Leu	Thr Glu	Ser Ala	Lys	Met Thr	Ile	7610	7615	7620
Thr Thr	Gln Thr	Gly Pro	Ser	Glu Ser	Thr Leu	Glu	Ser Thr	Leu	7625	7630	7635
Asn Leu	Asn Thr	Ala Thr	Thr	Pro Ser	Trp Val	Glu	Thr His	Ser	7640	7645	7650

471

Ile Val Ile Gln Gly Phe Pro His Pro Glu Met Thr Thr Ser Met
 7655 7660 7665

Gly Arg Gly Pro Gly Gly Val Ser Trp Pro Ser Pro Pro Phe Val
 7670 7675 7680

Lys Glu Thr Ser Pro Pro Ser Ser Pro Leu Ser Leu Pro Ala Val
 7685 7690 7695

Thr Ser Pro His Pro Val Ser Thr Thr Phe Leu Ala His Ile Pro
 7700 7705 7710

Pro Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Pro Ala
 7715 7720 7725

Thr Thr Thr Asp Ile Leu Gly Thr Ser Thr Glu Pro Gly Thr Ser
 7730 7735 7740

Ser Ser Ser Ser Leu Ser Thr Thr Ser His Glu Arg Leu Thr Thr
 7745 7750 7755

Tyr Lys Asp Thr Ala His Thr Glu Ala Val His Pro Ser Thr Asn
 7760 7765 7770

Thr Gly Gly Thr Asn Val Ala Thr Thr Ser Ser Gly Tyr Lys Ser
 7775 7780 7785

Gln Ser Ser Val Leu Ala Asp Ser Ser Pro Met Cys Thr Thr Ser
 7790 7795 7800

Thr Met Gly Asp Thr Ser Val Leu Thr Ser Thr Pro Ala Phe Leu
 7805 7810 7815

Glu Thr Arg Arg Ile Gln Thr Glu Leu Ala Ser Ser Leu Thr Pro
 7820 7825 7830

Gly Leu Arg Glu Ser Ser Gly Ser Glu Gly Thr Ser Ser Gly Thr
 7835 7840 7845

472

Lys Met 7850	Ser Thr Val Leu Ser 7855	Lys Val Pro Thr Gly 7860	Ala Thr Thr
Glu Ile 7865	Ser Lys Glu Asp Val 7870	Thr Ser Ile Pro Gly 7875	Pro Ala Gln
Ser Thr 7880	Ile Ser Pro Asp Ile 7885	Ser Thr Arg Thr Val 7890	Ser Trp Phe
Ser Thr 7895	Ser Pro Val Met Thr 7900	Glu Ser Ala Glu Ile 7905	Thr Met Asn
Thr His 7910	Thr Ser Pro Leu Gly 7915	Ala Thr Thr Gln Gly 7920	Thr Ser Thr
Leu Ala 7925	Thr Ser Ser Thr Thr 7930	Ser Leu Thr Met Thr 7935	His Ser Thr
Ile Ser 7940	Gln Gly Phe Ser His 7945	Ser Gln Met Ser Thr 7950	Leu Met Arg
Arg Gly 7955	Pro Glu Asp Val Ser 7960	Trp Met Ser Pro Pro 7965	Leu Leu Glu
Lys Thr 7970	Arg Pro Ser Phe Ser 7975	Leu Met Ser Ser Pro 7980	Ala Thr Thr
Ser Pro 7985	Ser Pro Val Ser Ser 7990	Thr Leu Pro Glu Ser 7995	Ile Ser Ser
Ser Pro 8000	Leu Pro Val Thr Ser 8005	Leu Leu Thr Ser Gly 8010	Leu Ala Lys
Thr Thr 8015	Asp Met Leu His Lys 8020	Ser Ser Glu Pro Val 8025	Thr Asn Ser
Pro Ala 8030	Asn Leu Ser Ser Thr 8035	Ser Val Glu Ile Leu 8040	Ala Thr Ser
Glu Val 8045	Thr Thr Asp Thr Glu 8050	Lys Thr His Pro Ser 8055	Ser Asn Arg

473

Thr Val 8060	Thr Asp Val Gly Thr 8065	Ser Ser Ser Gly His 8070	Glu Ser Thr
Ser Phe 8075	Val Leu Ala Asp Ser 8080	Gln Thr Ser Lys Val 8085	Thr Ser Pro
Met Val 8090	Ile Thr Ser Thr Met 8095	Glu Asp Thr Ser Val 8100	Ser Thr Ser
Thr Pro 8105	Gly Phe Phe Glu Thr 8110	Ser Arg Ile Gln Thr 8115	Glu Pro Thr
Ser Ser 8120	Leu Thr Leu Gly Leu 8125	Arg Lys Thr Ser Ser 8130	Ser Glu Gly
Thr Ser 8135	Leu Ala Thr Glu Met 8140	Ser Thr Val Leu Ser 8145	Gly Val Pro
Thr Gly 8150	Ala Thr Ala Glu Val 8155	Ser Arg Thr Glu Val 8160	Thr Ser Ser
Ser Arg 8165	Thr Ser Ile Ser Gly 8170	Phe Ala Gln Leu Thr 8175	Val Ser Pro
Glu Thr 8180	Ser Thr Glu Thr Ile 8185	Thr Arg Leu Pro Thr 8190	Ser Ser Ile
Met Thr 8195	Glu Ser Ala Glu Met 8200	Met Ile Lys Thr Gln 8205	Thr Asp Pro
Pro Gly 8210	Ser Thr Pro Glu Ser 8215	Thr His Thr Val Asp 8220	Ile Ser Thr
Thr Pro 8225	Asn Trp Val Glu Thr 8230	His Ser Thr Val Thr 8235	Gln Arg Phe
Ser His 8240	Ser Glu Met Thr Thr 8245	Leu Val Ser Arg Ser 8250	Pro Gly Asp

474

Met Leu Trp Pro Ser Gln Ser Ser Val Glu Glu Thr Ser Ser Ala
8255 8260 8265

Ser Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Ser Pro Val
8270 8275 8280

Ser Ser Thr Leu Val Glu Asp Phe Pro Ser Ala Ser Leu Pro Val
8285 8290 8295

Thr Ser Leu Leu Thr Pro Gly Leu Val Ile Thr Thr Asp Arg Met
8300 8305 8310

Gly Ile Ser Arg Glu Pro Gly Thr Ser Ser Thr Ser Asn Leu Ser
8315 8320 8325

Ser Thr Ser His Glu Arg Leu Thr Thr Leu Glu Asp Thr Val Asp
8330 8335 8340

Thr Glu Asp Met Gln Pro Ser Thr His Thr Ala Val Thr Asn Val
8345 8350 8355

Arg Thr Ser Ile Ser Gly His Glu Ser Gln Ser Ser Val Leu Ser
8360 8365 8370

Asp Ser Glu Thr Pro Lys Ala Thr Ser Pro Met Gly Thr Thr Tyr
8375 8380 8385

Thr Met Gly Glu Thr Ser Val Ser Ile Ser Thr Ser Asp Phe Phe
8390 8395 8400

Glu Thr Ser Arg Ile Gln Ile Glu Pro Thr Ser Ser Leu Thr Ser
8405 8410 8415

Gly Leu Arg Glu Thr Ser Ser Ser Glu Arg Ile Ser Ser Ala Thr
8420 8425 8430

Glu Gly Ser Thr Val Leu Ser Glu Val Pro Ser Gly Ala Thr Thr
8435 8440 8445

Glu Val Ser Arg Thr Glu Val Ile Ser Ser Arg Gly Thr Ser Met
8450 8455 8460

475

Ser Gly 8465	Pro Asp Gln Phe Thr 8470	Ile Ser Pro Asp Ile 8475	Ser Thr Glu
Ala Ile 8480	Thr Arg Leu Ser Thr 8485	Ser Pro Ile Met Thr 8490	Glu Ser Ala
Glu Ser 8495	Ala Ile Thr Ile Glu 8500	Thr Gly Ser Pro Gly 8505	Ala Thr Ser
Glu Gly 8510	Thr Leu Thr Leu Asp 8515	Thr Ser Thr Thr Thr 8520	Phe Trp Ser
Gly Thr 8525	His Ser Thr Ala Ser 8530	Pro Gly Phe Ser His 8535	Ser Glu Met
Thr Thr 8540	Leu Met Ser Arg Thr 8545	Pro Gly Asp Val Pro 8550	Trp Pro Ser
Leu Pro 8555	Ser Val Glu Glu Ala 8560	Ser Ser Val Ser Ser 8565	Ser Leu Ser
Ser Pro 8570	Ala Met Thr Ser Thr 8575	Ser Phe Phe Ser Thr 8580	Leu Pro Glu
Ser Ile 8585	Ser Ser Ser Pro His 8590	Pro Val Thr Ala Leu 8595	Leu Thr Leu
Gly Pro 8600	Val Lys Thr Thr Asp 8605	Met Leu Arg Thr Ser 8610	Ser Glu Pro
Glu Thr 8615	Ser Ser Pro Pro Asn 8620	Leu Ser Ser Thr Ser 8625	Ala Glu Ile
Leu Ala 8630	Thr Ser Glu Val Thr 8635	Lys Asp Arg Glu Lys 8640	Ile His Pro
Ser Ser 8645	Asn Thr Pro Val Val 8650	Asn Val Gly Thr Val 8655	Ile Tyr Lys

476

His Leu Ser Pro Ser Ser Val Leu Ala Asp Leu Val Thr Thr Lys
 8660 8665 8670

Pro Thr Ser Pro Met Ala Thr Thr Ser Thr Leu Gly Asn Thr Ser
 8675 8680 8685

Val Ser Thr Ser Thr Pro Ala Phe Pro Glu Thr Met Met Thr Gln
 8690 8695 8700

Pro Thr Ser Ser Leu Thr Ser Gly Leu Arg Glu Ile Ser Thr Ser
 8705 8710 8715

Gln Glu Thr Ser Ser Ala Thr Glu Arg Ser Ala Ser Leu Ser Gly
 8720 8725 8730

Met Pro Thr Gly Ala Thr Thr Lys Val Ser Arg Thr Glu Ala Leu
 8735 8740 8745

Ser Leu Gly Arg Thr Ser Thr Pro Gly Pro Ala Gln Ser Thr Ile
 8750 8755 8760

Ser Pro Glu Ile Ser Thr Glu Thr Ile Thr Arg Ile Ser Thr Pro
 8765 8770 8775

Leu Thr Thr Thr Gly Ser Ala Glu Met Thr Ile Thr Pro Lys Thr
 8780 8785 8790

Gly His Ser Gly Ala Ser Ser Gln Gly Thr Phe Thr Leu Asp Thr
 8795 8800 8805

Ser Ser Arg Ala Ser Trp Pro Gly Thr His Ser Ala Ala Thr His
 8810 8815 8820

Arg Ser Pro His Ser Gly Met Thr Thr Pro Met Ser Arg Gly Pro
 8825 8830 8835

Glu Asp Val Ser Trp Pro Ser Arg Pro Ser Val Glu Lys Thr Ser
 8840 8845 8850

Pro Pro Ser Ser Leu Val Ser Leu Ser Ala Val Thr Ser Pro Ser
 8855 8860 8865

477

Pro	Leu	Tyr	Ser	Thr	Pro	Ser	Glu	Ser	Ser	His	Ser	Ser	Pro	Leu
8870						8875					8880			
Arg	Val	Thr	Ser	Leu	Phe	Thr	Pro	Val	Met	Met	Lys	Thr	Thr	Asp
8885						8890					8895			
Met	Leu	Asp	Thr	Ser	Leu	Glu	Pro	Val	Thr	Thr	Ser	Pro	Pro	Ser
8900						8905					8910			
Met	Asn	Ile	Thr	Ser	Asp	Glu	Ser	Leu	Ala	Thr	Ser	Lys	Ala	Thr
8915						8920					8925			
Met	Glu	Thr	Glu	Ala	Ile	Gln	Leu	Ser	Glu	Asn	Thr	Ala	Val	Thr
8930						8935					8940			
Gln	Met	Gly	Thr	Ile	Ser	Ala	Arg	Gln	Glu	Phe	Tyr	Ser	Ser	Tyr
8945						8950					8955			
Pro	Gly	Leu	Pro	Glu	Pro	Ser	Lys	Val	Thr	Ser	Pro	Val	Val	Thr
8960						8965					8970			
Ser	Ser	Thr	Ile	Lys	Asp	Ile	Val	Ser	Thr	Thr	Ile	Pro	Ala	Ser
8975						8980					8985			
Ser	Glu	Ile	Thr	Arg	Ile	Glu	Met	Glu	Ser	Thr	Ser	Thr	Leu	Thr
8990						8995					9000			
Pro	Thr	Pro	Arg	Glu	Thr	Ser	Thr	Ser	Gln	Glu	Ile	His	Ser	Ala
9005						9010					9015			
Thr	Lys	Pro	Ser	Thr	Val	Pro	Tyr	Lys	Ala	Leu	Thr	Ser	Ala	Thr
9020						9025					9030			
Ile	Glu	Asp	Ser	Met	Thr	Gln	Val	Met	Ser	Ser	Ser	Arg	Gly	Pro
9035						9040					9045			
Ser	Pro	Asp	Gln	Ser	Thr	Met	Ser	Gln	Asp	Ile	Ser	Ser	Glu	Val
9050						9055					9060			

478

Ile Thr	Arg Leu Ser Thr Ser	Pro Ile Lys Ala Glu	Ser Thr Glu
9065	9070	9075	
Met Thr	Ile Thr Thr Gln Thr Gly Ser Pro Gly	Ala Thr Ser Arg	
9080	9085	9090	
Gly Thr	Leu Thr Leu Asp Thr Ser Thr Thr Phe Met	Ser Gly Thr	
9095	9100	9105	
His Ser	Thr Ala Ser Gln Gly Phe Ser His Ser	Gln Met Thr Ala	
9110	9115	9120	
Leu Met	Ser Arg Thr Pro Gly Asp Val Pro Trp Leu	Ser His Pro	
9125	9130	9135	
Ser Val	Glu Glu Ala Ser Ser Ala Ser Phe Ser	Leu Ser Ser Pro	
9140	9145	9150	
Val Met	Thr Ser Ser Ser Pro Val Ser Ser Thr	Leu Pro Asp Ser	
9155	9160	9165	
Ile His	Ser Ser Ser Leu Pro Val Thr Ser Leu	Leu Thr Ser Gly	
9170	9175	9180	
Leu Val	Lys Thr Thr Glu Leu Leu Gly Thr Ser	Ser Glu Pro Glu	
9185	9190	9195	
Thr Ser	Ser Pro Pro Asn Leu Ser Ser Thr Ser	Ala Glu Ile Leu	
9200	9205	9210	
Ala Thr	Thr Glu Val Thr Thr Asp Thr Glu Lys	Leu Glu Met Thr	
9215	9220	9225	
Asn Val	Val Thr Ser Gly Tyr Thr His Glu Ser	Pro Ser Ser Val	
9230	9235	9240	
Leu Ala	Asp Ser Val Thr Thr Lys Ala Thr Ser	Ser Met Gly Ile	
9245	9250	9255	
Thr Tyr	Pro Thr Gly Asp Thr Asn Val Leu Thr	Ser Thr Pro Ala	
9260	9265	9270	

479

Phe	Ser	Asp	Thr	Ser	Arg	Ile	Gln	Thr	Lys	Ser	Lys	Leu	Ser	Leu
9275						9280					9285			
Thr	Pro	Gly	Leu	Met	Glu	Thr	Ser	Ile	Ser	Glu	Glu	Thr	Ser	Ser
9290						9295					9300			
Ala	Thr	Glu	Lys	Ser	Thr	Val	Leu	Ser	Ser	Val	Pro	Thr	Gly	Ala
9305						9310					9315			
Thr	Thr	Glu	Val	Ser	Arg	Thr	Glu	Ala	Ile	Ser	Ser	Ser	Arg	Thr
9320						9325					9330			
Ser	Ile	Pro	Gly	Pro	Ala	Gln	Ser	Thr	Met	Ser	Ser	Asp	Thr	Ser
9335						9340					9345			
Met	Glu	Thr	Ile	Thr	Arg	Ile	Ser	Thr	Pro	Leu	Thr	Arg	Lys	Glu
9350						9355					9360			
Ser	Thr	Asp	Met	Ala	Ile	Thr	Pro	Lys	Thr	Gly	Pro	Ser	Gly	Ala
9365						9370					9375			
Thr	Ser	Gln	Gly	Thr	Phe	Thr	Leu	Asp	Ser	Ser	Ser	Thr	Ala	Ser
9380						9385					9390			
Trp	Pro	Gly	Thr	His	Ser	Ala	Thr	Thr	Gln	Arg	Phe	Pro	Gln	Ser
9395						9400					9405			
Val	Val	Thr	Thr	Pro	Met	Ser	Arg	Gly	Pro	Glu	Asp	Val	Ser	Trp
9410						9415					9420			
Pro	Ser	Pro	Leu	Ser	Val	Glu	Lys	Asn	Ser	Pro	Pro	Ser	Ser	Leu
9425						9430					9435			
Val	Ser	Ser	Ser	Ser	Val	Thr	Ser	Pro	Ser	Pro	Leu	Tyr	Ser	Thr
9440						9445					9450			
Pro	Ser	Gly	Ser	Ser	His	Ser	Ser	Pro	Val	Pro	Val	Thr	Ser	Leu
9455						9460					9465			

480

Phe Thr Ser Ile Met Met Lys Ala Thr Asp Met Leu Asp Ala Ser
 9470 9475 9480

Leu Glu Pro Glu Thr Thr Ser Ala Pro Asn Met Asn Ile Thr Ser
 9485 9490 9495

Asp Glu Ser Leu Ala Ala Ser Lys Ala Thr Thr Glu Thr Glu Ala
 9500 9505 9510

Ile His Val Phe Glu Asn Thr Ala Ala Ser His Val Glu Thr Thr
 9515 9520 9525

Ser Ala Thr Glu Glu Leu Tyr Ser Ser Ser Pro Gly Phe Ser Glu
 9530 9535 9540

Pro Thr Lys Val Ile Ser Pro Val Val Thr Ser Ser Ser Ile Arg
 9545 9550 9555

Asp Asn Met Val Ser Thr Thr Met Pro Gly Ser Ser Gly Ile Thr
 9560 9565 9570

Arg Ile Glu Ile Glu Ser Met Ser Ser Leu Thr Pro Gly Leu Arg
 9575 9580 9585

Glu Thr Arg Thr Ser Gln Asp Ile Thr Ser Ser Thr Glu Thr Ser
 9590 9595 9600

Thr Val Leu Tyr Lys Met Pro Ser Gly Ala Thr Pro Glu Val Ser
 9605 9610 9615

Arg Thr Glu Val Met Pro Ser Ser Arg Thr Ser Ile Pro Gly Pro
 9620 9625 9630

Ala Gln Ser Thr Met Ser Leu Asp Ile Ser Asp Glu Val Val Thr
 9635 9640 9645

Arg Leu Ser Thr Ser Pro Ile Met Thr Glu Ser Ala Glu Ile Thr
 9650 9655 9660

Ile Thr Thr Gln Thr Gly Tyr Ser Leu Ala Thr Ser Gln Val Thr
 9665 9670 9675

481

Leu Pro 9680	Leu Gly Thr Ser Met 9685	Thr Phe Leu Ser Gly 9690	Thr His Ser
Thr Met 9695	Ser Gln Gly Leu Ser 9700	His Ser Glu Met Thr 9705	Asn Leu Met
Ser Arg 9710	Gly Pro Glu Ser Leu 9715	Ser Trp Thr Ser Pro 9720	Arg Phe Val
Glu Thr 9725	Thr Arg Ser Ser Ser 9730	Ser Leu Thr Ser Leu 9735	Pro Leu Thr
Thr Ser 9740	Leu Ser Pro Val Ser 9745	Ser Thr Leu Leu Asp 9750	Ser Ser Pro
Ser Ser 9755	Pro Leu Pro Val Thr 9760	Ser Leu Ile Leu Pro 9765	Gly Leu Val
Lys Thr 9770	Thr Glu Val Leu Asp 9775	Thr Ser Ser Glu Pro 9780	Lys Thr Ser
Ser Ser 9785	Pro Asn Leu Ser Ser 9790	Thr Ser Val Glu Ile 9795	Pro Ala Thr
Ser Glu 9800	Ile Met Thr Asp Thr 9805	Glu Lys Ile His Pro 9810	Ser Ser Asn
Thr Ala 9815	Val Ala Lys Val Arg 9820	Thr Ser Ser Ser Val 9825	His Glu Ser
His Ser 9830	Ser Val Leu Ala Asp 9835	Ser Glu Thr Thr Ile 9840	Thr Ile Pro
Ser Met 9845	Gly Ile Thr Ser Ala 9850	Val Asp Asp Thr Thr 9855	Val Phe Thr
Ser Asn 9860	Pro Ala Phe Ser Glu 9865	Thr Arg Arg Ile Pro 9870	Thr Glu Pro

482

Thr Phe Ser Leu Thr Pro Gly Phe Arg Glu Thr Ser Thr Ser Glu
 9875 9880 9885

Glu Thr Thr Ser Ile Thr Glu Thr Ser Ala Val Leu Tyr Gly Val
 9890 9895 9900

Pro Thr Ser Ala Thr Thr Glu Val Ser Met Thr Glu Ile Met Ser
 9905 9910 9915

Ser Asn Arg Thr His Ile Pro Asp Ser Asp Gln Ser Thr Met Ser
 9920 9925 9930

Pro Asp Ile Ile Thr Glu Val Ile Thr Arg Leu Ser Ser Ser Ser
 9935 9940 9945

Met Met Ser Glu Ser Thr Gln Met Thr Ile Thr Thr Gln Lys Ser
 9950 9955 9960

Ser Pro Gly Ala Thr Ala Gln Ser Thr Leu Thr Leu Ala Thr Thr
 9965 9970 9975

Thr Ala Pro Leu Ala Arg Thr His Ser Thr Val Pro Pro Arg Phe
 9980 9985 9990

Leu His Ser Glu Met Thr Thr Leu Met Ser Arg Ser Pro Glu Asn
 9995 10000 10005

Pro Ser Trp Lys Ser Ser Pro Phe Val Glu Lys Thr Ser Ser Ser
 10010 10015 10020

Ser Ser Leu Leu Ser Leu Pro Val Thr Thr Ser Pro Ser Val Ser
 10025 10030 10035

Ser Thr Leu Pro Gln Ser Ile Pro Ser Ser Ser Phe Ser Val Thr
 10040 10045 10050

Ser Leu Leu Thr Pro Gly Met Val Lys Thr Thr Asp Thr Ser Thr
 10055 10060 10065

Glu Pro Gly Thr Ser Leu Ser Pro Asn Leu Ser Gly Thr Ser Val
 10070 10075 10080

483

Glu Ile 10085	Leu Ala Ala Ser 10090	Glu Val Thr Thr Asp Thr 10095	Glu Lys Ile
His Pro 10100	Ser Ser Ser Met Ala 10105	Val Thr Asn Val Gly 10110	Thr Thr Ser
Ser Gly 10115	His Glu Leu Tyr Ser 10120	Ser Val Ser Ile His 10125	Ser Glu Pro
Ser Lys 10130	Ala Thr Tyr Pro Val 10135	Gly Thr Pro Ser Ser 10140	Met Ala Glu
Thr Ser 10145	Ile Ser Thr Ser Met 10150	Pro Ala Asn Phe Glu 10155	Thr Thr Gly
Phe Glu 10160	Ala Glu Pro Phe Ser 10165	His Leu Thr Ser Gly 10170	Phe Arg Lys
Thr Asn 10175	Met Ser Leu Asp Thr 10180	Ser Ser Val Thr Pro 10185	Thr Asn Thr
Pro Ser 10190	Ser Pro Gly Ser Thr 10195	His Leu Leu Gln Ser 10200	Ser Lys Thr
Asp Phe 10205	Thr Ser Ser Ala Lys 10210	Thr Ser Ser Pro Asp 10215	Trp Pro Pro
Ala Ser 10220	Gln Tyr Thr Glu Ile 10225	Pro Val Asp Ile Ile 10230	Thr Pro Phe
Asn Ala 10235	Ser Pro Ser Ile Thr 10240	Glu Ser Thr Gly Ile 10245	Thr Ser Phe
Pro Glu 10250	Ser Arg Phe Thr Met 10255	Ser Val Thr Glu Ser 10260	Thr His His
Leu Ser 10265	Thr Asp Leu Leu Pro 10270	Ser Ala Glu Thr Ile 10275	Ser Thr Gly

484

Thr Val 10280	Met Pro Ser Leu Ser 10285	Glu Ala Met Thr Ser 10290	Phe Ala Thr
Thr Gly 10295	Val Pro Arg Ala Ile 10300	Ser Gly Ser Gly Ser 10305	Pro Phe Ser
Arg Thr 10310	Glu Ser Gly Pro Gly 10315	Asp Ala Thr Leu Ser 10320	Thr Ile Ala
Glu Ser 10325	Leu Pro Ser Ser Thr 10330	Pro Val Pro Phe Ser 10335	Ser Ser Thr
Phe Thr 10340	Thr Thr Asp Ser Ser 10345	Thr Ile Pro Ala Leu 10350	His Glu Ile
Thr Ser 10355	Ser Ser Ala Thr Pro 10360	Tyr Arg Val Asp Thr 10365	Ser Leu Gly
Thr Glu 10370	Ser Ser Thr Thr Glu 10375	Gly Arg Leu Val Met 10380	Val Ser Thr
Leu Asp 10385	Thr Ser Ser Gln Pro 10390	Gly Arg Thr Ser Ser 10395	Thr Pro Ile
Leu Asp 10400	Thr Arg Met Thr Glu 10405	Ser Val Glu Leu Gly 10410	Thr Val Thr
Ser Ala 10415	Tyr Gln Val Pro Ser 10420	Leu Ser Thr Arg Leu 10425	Thr Arg Thr
Asp Gly 10430	Ile		

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)